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(54) Title: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING THESE PROTEINS

(57) Abstract: The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs, transformed eukaryotic cells expressing these DNAs and antibodies directed to these proteins.



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## DESCRIPTION

Human Proteins Having Hydrophobic  
Domains and DNAs Encoding These Proteins

5

## TECHNICAL FIELD

The present invention relates to human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs, eukaryotic cells  
10 expressing these DNAs and antibodies directed to these proteins. The proteins of the present invention can be employed as pharmaceuticals or as antigens for preparing antibodies directed to these proteins. The human cDNAs of the present invention can be utilized as probes for genetic  
15 diagnosis and gene sources for gene therapy. Furthermore, the cDNAs can be utilized as gene sources for producing the proteins encoded by these cDNAs in large quantities. Cells into which these genes are introduced to express secretory proteins or membrane proteins in large quantities can be  
20 utilized for detection of the corresponding receptors or ligands, screening of novel small molecule pharmaceuticals and the like. The antibodies of the present invention can be utilized for the detection, quantification, purification and the like of the proteins of the present invention.

25



## BACKGROUND ART

Cells secrete many proteins extracellularly. These secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport, the biophylaxis, and the like of the cells. Unlike intracellular proteins, the secretory proteins exert their actions outside the cells. Therefore, they can be administered in the intracorporeal manner such as the injection or the drip, so that they possess hidden potentialities as pharmaceuticals. In fact, a number of human secretory proteins such as interferons, interleukins, erythropoietin, thrombolytic agents and the like are currently employed as pharmaceuticals. In addition, secretory proteins other than those described above are undergoing clinical trials for developing their use as pharmaceuticals. It is believed that the human cells produce many unknown secretory proteins. Availability of these secretory proteins as well as genes encoding them is expected to lead to development of novel pharmaceuticals utilizing them.

On the other hand, membrane proteins play important roles, as signal receptors, ion channels, transporters and the like in the material transport and the signal transduction through the cell membrane. Examples thereof include receptors for various cytokines, ion

channels for the sodium ion, the potassium ion, the chloride ion and the like, transporters for saccharides and amino acids and the like. The genes for many of them have already been cloned. It has been clarified that abnormalities in these membrane proteins are involved in a number of previously cryptogenic diseases. Therefore, discovery of a new membrane protein is expected to lead to elucidation of the causes of many diseases, so that isolation of new genes encoding the membrane proteins has been desired.

Heretofore, due to difficulty in the purification from human cells, many of these secretory proteins and membrane proteins have been isolated by genetic approaches. A general method is the so-called expression cloning method, in which a cDNA library is introduced into eukaryotic cells to express cDNAs, and the cells secreting, or expressing on the surface of membrane, the protein having the activity of interest are then screened. However, only genes for proteins with known functions can be cloned by using this method.

In general, a secretory protein or a membrane protein possesses at least one hydrophobic domain within the protein. After synthesis on ribosomes, such domain works as a secretory signal or remains in the phospholipid membrane to be entrapped in the membrane. Accordingly, if the existence of a highly hydrophobic domain is observed in the amino acid sequence of a protein encoded by a cDNA when the

whole base sequence of the full-length cDNA is determined, it is considered that the cDNA encodes a secretory protein or a membrane protein.

5 OBJECTS OF INVENTION

The main object of the present invention is to provide novel human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs, transformed eukaryotic cells that are capable of  
10 expressing these DNAs and antibodies directed to these proteins. This object as well as other objects and advantages of the present invention will become apparent to those skilled in the art from the following description with reference to the accompanying drawings.

15

SUMMARY OF INVENTION

As the result of intensive studies, the present inventors have successfully cloned cDNAs encoding proteins having hydrophobic domains from the human full-length cDNA  
20 bank, thereby completing the present invention. Thus, the present invention provides a human protein having hydrophobic domain(s), namely a protein comprising any one of an amino acid sequence selected from the group consisting of SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and  
25 121 to 130. Moreover, the present invention provides a DNA

encoding said protein, exemplified by a cDNA comprising any one of a base sequence selected from the group consisting of SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131 to 150, an expression vector that is capable of expressing  
5 said DNA by in vitro translation or in eukaryotic cells, a transformed eukaryotic cell that is capable of expressing said DNA and of producing said protein and an antibody directed to said protein.

10 BRIEF DESCRIPTION OF DRAWINGS

Fig. 1 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03171.

Fig. 2 illustrates the  
15 hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03424.

Fig. 3 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03444.

20 Fig. 4 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03478.

Fig. 5 illustrates the  
25 hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03499.

Fig. 6 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03500.

Fig. 7 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10691.

Fig. 8 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10703.

Fig. 9 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10711.

Fig. 10 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10712.

Fig. 11 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03010.

Fig. 12 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03576.

Fig. 13 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03611.

Fig. 14 illustrates the

hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP03612.

Fig. 15 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
5 by clone HP10407.

Fig. 16 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP10713.

Fig. 17 illustrates the  
10 hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP10714.

Fig. 18 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP10716.

15 Fig. 19 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP10717.

Fig. 20 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
20 by clone HP10718.

Fig. 21 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP03745.

Fig. 22 illustrates the  
25 hydrophobicity/hydrophilicity profile of the protein encoded

by clone HP03747.

Fig. 23 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10719.

5 Fig. 24 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10720.

Fig. 25 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded  
10 by clone HP10721.

Fig. 26 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10725.

Fig. 27 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded  
15 by clone HP10727.

Fig. 28 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10728.

20 Fig. 29 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10730.

Fig. 30 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded  
25 by clone HP10742.

Fig. 31 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03800.

Fig. 32 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03831.

Fig. 33 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03879.

Fig. 34 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03880.

Fig. 35 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10704.

Fig. 36 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10715.

Fig. 37 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10724.

Fig. 38 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10733.

Fig. 39 illustrates the



hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP10734.

Fig. 40 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
5 by clone HP10756.

Fig. 41 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP03670.

Fig. 42 illustrates the  
10 hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP03688.

Fig. 43 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP03825

15 Fig. 44 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP03877.

Fig. 45 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
20 by clone HP10765.

Fig. 46 illustrates the  
hydrophobicity/hydrophilicity profile of the protein encoded  
by clone HP10766.

Fig. 47 illustrates the  
25 hydrophobicity/hydrophilicity profile of the protein encoded

by clone HP10770.

Fig. 48 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10772.

5 Fig. 49 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10773.

Fig. 50 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded  
10 by clone HP10776.

#### DETAILED DESCRIPTION OF THE INVENTION

The proteins of the present invention can be obtained, for example, by a method for isolating proteins  
15 from human organs, cell lines or the like, a method for preparing peptides by the chemical synthesis based on the amino acid sequences of the present invention, or a method for producing proteins by the recombinant DNA technology using the DNAs encoding the hydrophobic domains of the  
20 present invention. Among these, the method for producing proteins by the recombinant DNA technology is preferably employed. For example, the proteins can be expressed in vitro by preparing an RNA by in vitro transcription from a vector having the cDNA of the present invention, and then  
25 carrying out in vitro translation using this RNA as a

template. Alternatively, incorporation of the translated region into a suitable expression vector by the method known in the art may lead to expression of a large amount of the encoded protein in prokaryotic cells such as *Escherichia coli*, *Bacillus subtilis*, etc., and eukaryotic cells such as yeasts, insect cells, mammalian cells, etc.

In the case where the protein of the present invention is produced by expressing the DNA by in vitro translation, the protein of the present invention can be produced in vitro by incorporating the translated region of this cDNA into a vector having an RNA polymerase promoter, and then adding the vector to an in vitro translation system such as a rabbit reticulocyte lysate or a wheat germ extract, which contains an RNA polymerase corresponding to the promoter. The RNA polymerase promoters are exemplified by T7, T3, SP6 and the like. The vectors containing promoters for these RNA polymerases are exemplified by pKA1, pCDM8, pT3/T7 18, pT7/3 19, pBluescript II and the like. Furthermore, the protein of the present invention can be expressed in the secreted form or the form incorporated in the microsome membrane when a canine pancreas microsome or the like is added to the reaction system.

In the case where the protein of the present invention is produced by expressing the DNA in a microorganism such as *Escherichia coli* etc., a recombinant

expression vector in which the translated region of the cDNA of the present invention is incorporated into an expression vector having an origin which is capable of replicating in the microorganism, a promoter, a ribosome-binding site, a cDNA-cloning site, a terminator and the like is constructed. After transformation of the host cells with this expression vector, the resulting transformant is cultivated, whereby the protein encoded by the cDNA can be produced in large quantities in the microorganism. In this case, a protein fragment containing any translated region can be obtained by adding an initiation codon and a termination codon in front of and behind the selected translated region to express the protein. Alternatively, the protein can be expressed as a fusion protein with another protein. Only the portion of the protein encoded by the cDNA can be obtained by cleaving this fusion protein with a suitable protease. The expression vectors for *Escherichia coli* are exemplified by the pUC series, pBluescript II, the pET expression system, the pGEX expression system and the like.

In the case where the protein of the present invention is produced by expressing the DNA in eukaryotic cells, the protein of the present invention can be produced as a secretory protein, or as a membrane protein on the surface of cell membrane, by incorporating the translated region of the cDNA into an expression vector for eukaryotic

cells that has a promoter, a splicing region, a poly(A) addition site and the like, and then introducing the vector into the eukaryotic cells. The expression vectors are exemplified by pKA1, pED6dpc2, pCDM8, pSVK3, pMSG, pSVL, 5 pBK-CMV, pBK-RSV, EBV vectors, pRS, pYES2 and the like. Examples of eukaryotic cells to be used in general include mammalian cultured cells such as monkey kidney COS7 cells, Chinese hamster ovary CHO cells and the like, budding yeasts, fission yeasts, silkworm cells, *Xenopus* oocytes and the like. 10 Any eukaryotic cells may be used as long as they are capable of expressing the proteins of the present invention. The expression vector can be introduced into the eukaryotic cells by using a method known in the art such as the electroporation method, the calcium phosphate method, the 15 liposome method, the DEAE-dextran method and the like.

After the protein of the present invention is expressed in prokaryotic cells or eukaryotic cells, the protein of interest can be isolated and purified from the culture by a combination of separation procedures known in 20 the art. Examples of the separation procedures include treatment with a denaturing agent such as urea or a detergent, sonication, enzymatic digestion, salting-out or solvent precipitation, dialysis, centrifugation, ultrafiltration, gel filtration, SDS-PAGE, isoelectric 25 focusing, ion-exchange chromatography, hydrophobic

chromatography, affinity chromatography, reverse phase chromatography and the like.

The proteins of the present invention also include peptide fragments (of 5 amino acid residues or more) containing any partial amino acid sequences in the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130. These peptide fragments can be utilized as antigens for preparation of antibodies. Among the proteins of the present invention, those having the signal sequences are secreted in the form of mature proteins after the signal sequences are removed. Therefore, these mature proteins shall come within the scope of the protein of the present invention. The N-terminal amino acid sequences of the mature proteins can be easily determined by using the method for the determination of cleavage site of a signal sequence [JP-A 8-187100]. Furthermore, some membrane proteins undergo the processing on the cell surface to be converted to the secreted forms. Such proteins or peptides in the secreted forms shall also come within the scope of the protein of the present invention. In the case where sugar chain-binding sites are present in the amino acid sequences of the proteins, expression of the proteins in appropriate eukaryotic cells affords the proteins to which sugar chains are added. Accordingly, such proteins or peptides to which sugar chains are added shall also come

within the scope of the protein of the present invention.

The DNAs of the present invention include all the DNAs encoding the above-mentioned proteins. These DNAs can be obtained by using a method for chemical synthesis, a  
5 method for cDNA cloning and the like.

The cDNAs of the present invention can be cloned, for example, from cDNA libraries derived from the human cells. The cDNAs are synthesized by using poly(A)<sup>+</sup> RNAs extracted from human cells as templates. The human cells may  
10 be cells delivered from the human body, for example, by the operation or may be the cultured cells. The cDNAs can be synthesized by using any method such as the Okayama-Berg method [Okayama, H. and Berg, P., Mol. Cell. Biol. 2: 161-170 (1982)], the Gubler-Hoffman method [Gubler, U. and  
15 Hoffman, J., Gene 25: 263-269 (1983)] and the like. However, it is desirable to use the capping method [Kato, S. et al., Gene 150: 243-250 (1994)], as exemplified in Examples, in order to obtain a full-length clone in an effective manner. In addition, commercially available human cDNA libraries can  
20 be utilized. The cDNAs of the present invention can be cloned from the cDNA libraries by synthesizing an oligonucleotide on the basis of base sequences of any portion in the cDNA of the present invention and screening the cDNA libraries using this oligonucleotide as a probe for  
25 colony or plaque hybridization according to a method known

in the art. In addition, the cDNA fragments of the present invention can be prepared from an mRNA isolated from human cells by the RT-PCR method in which oligonucleotides which hybridize with both termini of the cDNA fragment of interest  
5 are synthesized, which oligonucleotides are then used as the primers.

The cDNAs of the present invention are characterized in that they comprise any one of the base sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71  
10 to 80, 101 to 110 and 131 to 140 or the base sequences represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141 to 150. Tables 1 and 2 summarizes the clone number (HP number), the cell from which the cDNA clone was obtained, the total number of bases of the cDNA, and the  
15 number of the amino acid residues of the encoded protein, for each of the cDNAs.



Table 1

| SEQ ID NO. |     |    | HP<br>number | Cell                 | Number<br>of<br>bases | Number<br>of amino<br>acid<br>residues |
|------------|-----|----|--------------|----------------------|-----------------------|--|
| 1,         | 11, | 21 | HP03171      | Thymus               | 2042                  | 267                                    |
| 2,         | 12, | 22 | HP03424      | Liver                | 1433                  | 419                                    |
| 3,         | 13, | 23 | HP03444      | Kidney               | 1917                  | 415                                    |
| 4,         | 14, | 24 | HP03478      | Umbilical cord blood | 2258                  | 380                                    |
| 5,         | 15, | 25 | HP03499      | Kidney               | 1973                  | 585                                    |
| 6,         | 16, | 26 | HP03500      | kidney               | 1606                  | 331                                    |
| 7,         | 17, | 27 | HP10691      | Umbilical cord blood | 2380                  | 345                                    |
| 8,         | 18, | 28 | HP10703      | Kidney               | 2017                  | 89                                     |
| 9,         | 19, | 29 | HP10711      | Kidney               | 1606                  | 406                                    |
| 10,        | 20, | 30 | HP10712      | Kidney               | 1695                  | 192                                    |
| 31,        | 41, | 51 | HP03010      | Kidney               | 1551                  | 377                                    |
| 32,        | 42, | 52 | HP03576      | Kidney               | 1713                  | 81                                     |
| 33,        | 43, | 53 | HP03611      | Kidney               | 1758                  | 487                                    |
| 34,        | 44, | 54 | HP03612      | Kidney               | 1550                  | 375                                    |
| 35,        | 45, | 55 | HP10407      | Stomach cancer       | 1485                  | 350                                    |
| 36,        | 46, | 56 | HP10713      | Kidney               | 2694                  | 667                                    |
| 37,        | 47, | 57 | HP10714      | Umbilical cord blood | 3297                  | 464                                    |
| 38,        | 48, | 58 | HP10716      | Umbilical cord blood | 2126                  | 470                                    |
| 39,        | 49, | 59 | HP10717      | Kidney               | 1781                  | 243                                    |
| 40,        | 50, | 60 | HP10718      | Umbilical cord blood | 1788                  | 270                                    |
| 61,        | 71, | 81 | HP03745      | Kidney               | 1376                  | 389                                    |
| 62,        | 72, | 82 | HP03747      | Umbilical cord blood | 2392                  | 348                                    |
| 63,        | 73, | 83 | HP10719      | Kidney               | 1416                  | 261                                    |
| 64,        | 74, | 84 | HP10720      | Kidney               | 1347                  | 222                                    |
| 65,        | 75, | 85 | HP10721      | Kidney               | 2284                  | 183                                    |

Table 2

| SEQ ID NO     | HP<br>number | Cell                 | Number<br>of<br>bases | Number<br>of amino<br>acid<br>residues |
|---------------|--------------|----------------------|-----------------------|--|
| 66, 76, 86    | HP10725      | Kidney               | 1737                  | 262                                    |
| 67, 77, 87    | HP10727      | Umbilical cord blood | 1556                  | 168                                    |
| 68, 78, 88    | HP10728      | Umbilical cord blood | 1855                  | 243                                    |
| 69, 79, 89    | HP10730      | Umbilical cord blood | 2530                  | 428                                    |
| 70, 80, 90    | HP10742      | Umbilical cord blood | 1911                  | 283                                    |
| 91, 101, 111  | HP03800      | Umbilical cord blood | 1633                  | 476                                    |
| 92, 102, 112  | HP03831      | Kidney               | 1095                  | 226                                    |
| 93, 103, 113  | HP03879      | Kidney               | 1602                  | 305                                    |
| 94, 104, 114  | HP03880      | Kidney               | 897                   | 227                                    |
| 95, 105, 115  | HP10704      | Kidney               | 1866                  | 441                                    |
| 96, 106, 116  | HP10715      | Umbilical cord blood | 2198                  | 265                                    |
| 97, 107, 117  | HP10724      | Umbilical cord blood | 2180                  | 208                                    |
| 98, 108, 118  | HP10733      | Umbilical cord blood | 1527                  | 400                                    |
| 99, 109, 119  | HP10734      | Umbilical cord blood | 1905                  | 192                                    |
| 100, 110, 120 | HP10756      | Kidney               | 998                   | 260                                    |
| 121, 131, 141 | HP03670      | Umbilical cord blood | 1622                  | 337                                    |
| 122, 132, 142 | HP03688      | Umbilical cord blood | 2475                  | 236                                    |
| 123, 133, 143 | HP03825      | Kidney               | 1739                  | 560                                    |
| 124, 134, 144 | HP03877      | Kidney               | 2005                  | 406                                    |
| 125, 135, 145 | HP10765      | Umbilical cord blood | 1558                  | 453                                    |
| 126, 136, 146 | HP10766      | Kidney               | 1005                  | 59                                     |
| 127, 137, 147 | HP10770      | Kidney               | 969                   | 210                                    |
| 128, 138, 148 | HP10772      | Kidney               | 1241                  | 165                                    |
| 129, 139, 149 | HP10773      | Kidney               | 1174                  | 162                                    |
| 130, 140, 150 | HP10776      | Kidney               | 1012                  | 221                                    |

The same clones as the cDNAs of the present invention can be easily obtained by screening the cDNA libraries constructed from the human cell lines or human

tissues utilized in the present invention using an oligonucleotide probe synthesized on the basis of the base sequence of the cDNA provided in any one of SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131 to 150.

5           In general, the polymorphism due to the individual differences is frequently observed in human genes. Accordingly, any cDNA in which one or plural nucleotides are added, deleted and/or substituted with other nucleotides in SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131  
10 to 150 shall come within the scope of the present invention.

          Similarly, any protein in which one or plural amino acids are added, deleted and/or substituted with other amino acids resulting from the above-mentioned changes shall come within the scope of the present invention, as long as  
15 the protein possesses the activity of the protein having any one of the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130.

          The cDNAs of the present invention also include cDNA fragments (of 10 bp or more) containing any partial  
20 base sequence in the base sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71 to 80, 101 to 110 and 131 to 140 or in the base sequences represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141 to 150. Also, DNA fragments consisting of a sense strand and an anti-sense  
25 strand shall come within this scope. These DNA fragments can

be utilized as the probes for the genetic diagnosis.

The antibody of the present invention can be obtained from a serum after immunizing an animal using the protein of the present invention as an antigen. A peptide  
5 that is chemically synthesized based on the amino acid sequence of the present invention and a protein expressed in eukaryotic or prokaryotic cells can be used as an antigen. Alternatively, an antibody can be prepared by introducing the above-mentioned expression vector for eukaryotic cells  
10 into the muscle or the skin of an animal by injection or by using a gene gun and then collecting a serum therefrom (JP-A 7-313187). Animals that can be used include a mouse, a rat, a rabbit, a goat, a chicken and the like. A monoclonal antibody directed to the protein of the present invention  
15 can be produced by fusing B cells collected from the spleen of the immunized animal with myelomas to generate hybridomas.

In addition to the activities and uses described above, the polynucleotides and proteins of the present invention may exhibit one or more of the uses or biological  
20 activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as,  
25 for example, in gene therapies or vectors suitable for

introduction of DNA).

#### Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein

(such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell '75:791-803 (1993)) to identify polynucleotides  
5 encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-  
10 throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding  
15 protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for  
20 example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or  
25 agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

#### Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation

Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol.



145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

5                    Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In Current Protocols in Immunology. J.E.e.a. Coligan  
10 eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon  $\gamma$ , Schreiber, R.D. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

15                    Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In Current Protocols in Immunology.  
20 J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6-  
25 Nordan, R. In Current Protocols in Immunology. J.E.e.a.

Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In  
5 Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John  
10 Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include,  
15 without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines  
20 and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune

pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by

the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant.

Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate

activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy.

Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function  
5 may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be  
10 enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing  
15 the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a  
20 portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

In another application, up regulation or  
25 enhancement of antigen function (preferably B lymphocyte



antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a

cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$  microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19;

Chapter 7, Immunologic studies in Humans); Herrmann et al.,  
Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et  
al., J. Immunol. 128:1968-1974, 1982; Handa et al., J.  
Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol.  
5 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512,  
1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-  
2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974,  
1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai  
et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J.  
10 Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512,  
1988; Bertagnolli et al., Cellular Immunology 133:327-341,  
1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin  
responses and isotype switching (which will identify, among  
15 others, proteins that modulate T-cell dependent antibody  
responses and that affect Th1/Th2 profiles) include, without  
limitation, those described in: Maliszewski, J. Immunol.  
144:3028-3033, 1990; and Assays for B cell function: In  
vitro antibody production, Mond, J.J. and Brunswick, M. In  
20 Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1  
pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will  
identify, among others, proteins that generate predominantly  
Th1 and CTL responses) include, without limitation, those  
25 described in: Current Protocols in Immunology, Ed by J. E.

Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W  
Strober, Pub. Greene Publishing Associates and Wiley-  
Interscience (Chapter 3, In Vitro assays for Mouse  
Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies  
5 in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986;  
Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et  
al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will  
identify, among others, proteins expressed by dendritic  
10 cells that activate naive T-cells) include, without  
limitation, those described in: Guery et al., J. Immunol.  
134:536-544, 1995; Inaba et al., Journal of Experimental  
Medicine 173:549-559, 1991; Macatonia et al., Journal of  
Immunology 154:5071-5079, 1995; Porgador et al., Journal of  
15 Experimental Medicine 182:255-260, 1995; Nair et al.,  
Journal of Virology 67:4062-4069, 1993; Huang et al.,  
Science 264:961-965, 1994; Macatonia et al., Journal of  
Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al.,  
Journal of Clinical Investigation 94:797-807, 1994; and  
20 Inaba et al., Journal of Experimental Medicine 172:631-640,  
1990.

Assays for lymphocyte survival/apoptosis (which  
will identify, among others, proteins that prevent apoptosis  
after superantigen induction and proteins that regulate  
25 lymphocyte homeostasis) include, without limitation, those

described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

#### Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or

erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complementary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and

differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the

presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

#### Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth



repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful  
5 in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

10 Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue  
15 is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to  
20 tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the  
25 repair of congenital, trauma induced, or other tendon or

ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon or ligament-forming  
5 cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be  
10 useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be  
15 useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to  
20 neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's,  
25 Parkinson's disease, Huntington's disease, amyotrophic

lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and  
5 cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to  
10 promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds and the like.

It is expected that a protein of the present  
15 invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for  
20 promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

25 A protein of the present invention may also be

useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

5           A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

          The activity of a protein of the invention may, 10 among other means, be measured by the following methods:

          Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, 15 neuronal); International Patent Publication No. WO91/07491 (skin, endothelium ).

          Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year 20 Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

#### Activin/Inhibin Activity

          A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are 25 characterized by their ability to inhibit the release of

follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin  $\alpha$  family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- $\beta$  group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et

al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

#### Chemotactic/Chemokinetic Activity

A protein of the present invention may have  
5 chemotactic or chemokinetic activity (e.g., act as a  
chemokine) for mammalian cells, including, for example,  
monocytes, fibroblasts, neutrophils, T-cells, mast cells,  
eosinophils, epithelial and/or endothelial cells.  
Chemotactic and chemokinetic proteins can be used to  
10 mobilize or attract a desired cell population to a desired  
site of action. Chemotactic or chemokinetic proteins provide  
particular advantages in treatment of wounds and other  
trauma to tissues, as well as in treatment of localized  
infections. For example, attraction of lymphocytes,  
15 monocytes or neutrophils to tumors or sites of infection may  
result in improved immune responses against the tumor or  
infecting agent.

A protein or peptide has chemotactic activity for  
a particular cell population if it can stimulate, directly  
20 or indirectly, the directed orientation or movement of such  
cell population. Preferably, the protein or peptide has the  
ability to directly stimulate directed movement of cells.  
Whether a particular protein has chemotactic activity for a  
population of cells can be readily determined by employing  
25 such protein or peptide in any known assay for cell

chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will  
5 identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for  
10 movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta  
15 Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

#### 20 Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such  
25 as hemophilias) or to enhance coagulation and other

hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions  
5 resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke)).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity  
10 include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

15           Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without  
20 limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their  
25 ligands) and receptor/ligand pairs involved in antigen



presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

#### Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity

may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

#### 20                    Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly

(such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by  
5 inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

#### Other Activities

10 A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing  
15 or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape);  
20 effecting biorhythms or cardiac cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other

nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

#### Examples

The present invention is specifically illustrated in more detail by the following Examples, but Examples are not intended to restrict the present invention. The basic procedures with regard to the recombinant DNA and the enzymatic reactions were carried out according to the literature ["Molecular Cloning. A Laboratory Manual", Cold

Spring Harbor Laboratory, 1989]. Unless otherwise stated, restriction enzymes and various modifying enzymes to be used were those available from Takara Shuzo. The buffer compositions and the reaction conditions for each of the enzyme reactions were as described in the attached instructions. The cDNA synthesis was carried out according to the literature [Kato, S. et al., Gene 150: 243-250 (1994)].

(1) Selection of cDNAs Encoding Proteins Having  
Hydrophobic Domains

Human liver cDNA library (WO 98/21328) and human stomach cancer cDNA library (WO 98/21328), as well as the cDNA libraries constructed from human kidney mRNA (Clontech), human thymus mRNA (Clontech) and human umbilical cord blood mRNA were used as cDNA libraries.

Full-length cDNA clones were selected from the respective libraries and the whole base sequences thereof were determined to construct a homo-protein cDNA bank consisting of the full-length cDNA clones. The hydrophobicity/hydrophilicity profiles were determined for the proteins encoded by the full-length cDNA clones registered in the homo-protein cDNA bank by the Kyte-Doolittle method [Kyte, J. & Doolittle, R. F., J. Mol. Biol. 157: 105-132 (1982)] to examine the presence or absence of a hydrophobic domain. A clone that has a hydrophobic region

being assumed as a secretory signal or a transmembrane domain in the amino acid sequence of the encoded protein was selected as a clone candidate.

## (2) Protein Synthesis by In Vitro Translation

5           The plasmid vector bearing the cDNA of the present invention was used for in vitro transcription/translation with a T<sub>N</sub>T rabbit reticulocyte lysate kit (Promega). In this case, [<sup>35</sup>S]methionine was added to label the expression product with a radioisotope. Each of the reactions was  
10           carried out according to the protocols attached to the kit. Two micrograms of the plasmid was subjected to the reaction at 30°C for 90 minutes in the reaction solution of a total volume of 25 µl containing 12.5 µl µ of T<sub>N</sub>T rabbit reticulocyte lysate, 0.5 µl of a buffer solution (attached  
15           to the kit), 2 µl of an amino acid mixture (without methionine), 2 µl of [<sup>35</sup>S]methionine (Amersham) (0.37 MBq/µl), 0.5 µl of T7 RNA polymerase, and 20 U of RNasin. The experiment in the presence of a membrane system was carried out by adding 2.5 µl of a canine pancreas microsomal fraction  
20           (Promega) to the reaction system. To 3 µl of the reaction solution was added 2 µl of the SDS sampling buffer (125 mM Tris-hydrochloride buffer, pH 6.8, 120 mM 2-mercaptoethanol, 2% SDS solution, 0.025% bromophenol blue and 20% glycerol) and the resulting mixture was heated at 95°C for 3 minutes  
25           and then subjected to SDS-polyacrylamide gel electrophoresis.

The molecular weight of the translation product was determined by carrying out the autoradiography.

(3) Expression in COS7

*Escherichia coli* cells harboring the expression  
5 vector for the protein of the present invention were  
cultured at 37°C for 2 hours in 2 ml of the 2 x YT culture  
medium containing 100 µg/ml of ampicillin, the helper phage  
M13K07 (50 µl) was added thereto, and the cells were then  
cultured at 37°C overnight. Single-stranded phage particles  
10 were obtained by polyethylene glycol precipitation from a  
supernatant separated by centrifugation. The particles were  
suspended in 100 µl of 1 mM Tris-0.1 mM EDTA, pH 8 (TE).

The cultured cells derived from monkey kidney,  
COS7, were cultured at 37°C in the presence of 5% CO<sub>2</sub> in the  
15 Dulbecco's modified Eagle's medium (DMEM) containing 10%  
fetal calf serum. 1 x 10<sup>5</sup> COS7 cells were inoculated into a  
6-well plate (Nunc, well diameter: 3 cm) and cultured at  
37°C for 22 hours in the presence of 5% CO<sub>2</sub>. After the medium  
was removed, the cell surface was washed with a phosphate  
20 buffer solution followed by DMEM containing 50 mM Tris-  
hydrochloride (pH 7.5) (TDMEM). A suspension containing 1 µl  
of the single-stranded phage suspension, 0.6 ml of the DMEM  
medium and 3 µl of TRANSFECTAM™ (IBF) was added to the cells  
and the cells were cultured at 37°C for 3 hours in the  
25 presence of 5% CO<sub>2</sub>. After the sample solution was removed,

the cell surface was washed with TDMEM, 2 ml per well of DMEM containing 10% fetal calf serum was added, and the cells were cultured at 37°C for 2 days in the presence of 5% CO<sub>2</sub>. After the medium was exchanged for a medium containing  
5 [35S]cysteine or [35S]methionine, the cells were cultured for one hour. After the medium and the cells were separated each other by centrifugation, proteins in the medium fraction and the cell membrane fraction were subjected to SDS-PAGE.

#### (4) Preparation of Antibodies

10 A plasmid vector containing the cDNA of the present invention was dissolved in a phosphate buffer solution (PBS: 145 mM NaCl, 2.68 mM KCl, 8.09 mM Na<sub>2</sub>HPO<sub>4</sub>, 2 mM KH<sub>2</sub>PO<sub>4</sub>, pH 7.2) to a concentration of 2 µg/µl. 25 µl each (a total of 50 µl) of the thus-prepared plasmid solution in  
15 PBS was injected into the right and left musculi quadriceps femoris of three mice (ICR line) using a 26 guage needle. After similar injections were repeated for one month at intervals of one week, blood was collected. The collected blood was stored at 4°C overnight to coagulate the blood,  
20 and then centrifuged at 8,000 x g for five minutes to obtain a supernatant. NaN<sub>3</sub> was added to the supernatant to a concentration of 0.01% and the mixture was then stored at 4°C. The generation of an antibody was confirmed by immunostaining of COS7 cells into which the corresponding  
25 vector had been introduced or by Western blotting using a



cell lysate or a secreted product.

(5) Clone Examples

<HP03171> (SEQ ID NOS: 1, 11 and 21)

Determination of the whole base sequence of the  
5 cDNA insert of clone HP03171 obtained from cDNA library of  
human thymus revealed the structure consisting of a 90-bp  
5'-untranslated region, a 804-bp ORF, and a 1148-bp 3'-  
untranslated region. The ORF encodes a protein consisting of  
267 amino acid residues and there existed one putative  
10 transmembrane domain. Figure 1 depicts the  
hydrophobicity/hydrophilicity profile, obtained by the Kyte-  
Doolittle method, of the present protein. In vitro  
translation resulted in formation of a translation product  
of 34 kDa that was somewhat larger than the molecular weight  
15 of 30,234 predicted from the ORF. In this case, the  
addition of a microsome led to the formation of a product of  
38 kDa. In addition, there exists in the amino acid sequence  
of this protein one site at which N-glycosylation may occur  
(Asn-Thr-Thr at position 169).

20 The search of the protein database using the amino  
acid sequence of the present protein revealed that the  
protein was similar to chicken putative transmembrane  
protein E3-16 (Accession No. AAB70816). Table 3 shows the  
comparison between amino acid sequences of the human protein  
25 of the present invention (HP) and chicken putative

transmembrane protein E3-16 (GG). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology  
 5 of 43.0% in the entire region.

Table 3

---

10 HP MVKISFQPAVAGIKGDKADKASAPAPASATEILLTPAREEQPPQHRSKRGSSVGGVCY  
 \*\*\*.\*\*.\*.\* . \*.\*..... . \*. \*.\*.. .. \*.  
 GG MVKVSFNSALAH--KEAANKKEEENSQVL-ILPPDAKEPEDVVVPAGHKRAWCWCW---CF

HP LSMGMVVLLMGLVFASVYIYRYFFLAQLARDNFFRCGVLY-EDSL-----SSQVRTQM--  
 15 \*..\*.\*.....\*.\*.\*\*..\* .\*.\*\*.\*\*\*.\* ..\*.....  
 GG ---GLAFMLAGVILGGAYLYKYFAFQQ--GGVYF-CGIKYIEDGLSLPESGAQLKSARYH

HP ELEEDVKIYLDENYERINVPVPQFGGGDPADIIHDFQRGLTAYHDISLDKCYVIELNTTI  
 ..\*....\* .\*. \*.\*.\*\*\*\*.\*...\*\*\*\*\*.\*\*\*.\* \*\*\*\*.\*.\*\*\*\*\*.\*\*\*..  
 20 GG TIEQNIQILEEEDVEFISVPVEFADSDPADIVHDFHRRLTAYLDLSLDKCYVIPLNTSV

HP VLPPRNFWEELLMNVKRGTYLPQTYIIQEEMVTEHVSDEALGSFIYHLCNGKDTYRLRR  
 \*.\*\*.\* \*\*\*. \*.\* \*\*\*\*\*.\*.\*.\*.\*.\*..... ..\*\* \*\*\*.\*\*.\*.\*.\*.\*  
 25 GG VMPPKNFLELLINIKAGTYLPQSYLIHEQMIVTDRIENVQDLGFFIYRLCRGKETYLQR

HP RATRRRINKRGAKNCNAIRHFENTFVVETLICGVV

..... \*.\*\*.\* \*\*. \*\*\*\*\* \*.\*\*\*\*\*

GG KEAMKGIQKREAVNCRKIRHFENRFAMETLICEQ

---

5

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AL036384) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03424> (SEQ ID NOS: 2, 12 and 22)

Determination of the whole base sequence of the cDNA insert of clone HP03424 obtained from cDNA library of human liver revealed the structure consisting of a 4-bp 5'-untranslated region, a 1260-bp ORF, and a 169-bp 3'-untranslated region. The ORF encodes a protein consisting of 419 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 2 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 50 kDa that was somewhat larger than the molecular weight

of 46,375 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 54 kDa. In addition, there exist in the amino acid sequence of this protein six sites at which N-glycosylation may occur  
5 (Asn-Ala-Ser at position 29, Asn-Val-Thr at position 40, Asn-Cys-Thr at position 112, Asn-Lys-Ser at position 135, Asn-Ile-Ser at position 172 and Asn-Phe-Ser at position 189). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to  
10 expect that the mature protein starts from aspartic acid at position 28.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Drosophila melanogaster* GOLIATH  
15 protein (Accession No. Q06003). Table 4 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Drosophila melanogaster* GOLIATH protein (DM). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that  
20 of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 40.8% in the intermediate region of 218 amino acid residues.

Table 4

---

|    |    |  |
|----|----|--|
|    | HP | MSCAGRAGPARLAALALLTCSLWPARADNASQEYYTALINVTVQEPGRGAPLTFRIDRGR   |
| 5  | HP | YGLDSPKAEVRGQVLAPLPLHGVADHLGCDPQTRFFVPPNIKQWIALLRGNCTFKEKIS    |
|    | HP | RAAFHNAVAVVIYNKSKEEPVTMTHPGTGDIIVMITELRGKDILSYLEKNISVQMTIA     |
|    |    | . * ** . . . * . * . * . * . * . . *                           |
|    | DM | MQLEKMQIKGKTRNIAAVITYQNIGQDLSLTLDKGYNTISII                     |
| 10 |    |  |
|    | HP | VGTR--MPPKNFSRGSVLFVSISFIVLMISSAWLIFYFIQKIRYTNARDRNQRRLGDA     |
|    |    | * * . . . . * . * . * . * . * . * . * . * . * . * . * . *      |
|    | DM | EGRRGVRTISSLNRTSVLFVSISFIVDDIL--CWLIFYIQRFRYMQAKDQQSRNLCSVT    |
| 15 | HP | KKAISKLTTRTVKKGDKETDPDFDHCAVCIESYKQNDVVRILPCKHVFHKSCVDPWLSEH   |
|    |    | **** * . * . * * . * * . * * * . * . * . * . * . * . * . * . * |
|    | DM | KKAIMKIPTKTGKFSD-EKDLDSDCCAICIEAYKPTDTIRILPCKHEFHKNCIDPWLIEH   |
|    | HP | CTCPMCKLNILKALGIVPNLPCTDNVAFDMERLTRTQAVNRRSALGDLAGDNSLGLEPLR   |
| 20 |    | ***** . ** * * . . . . . . . . . . . . . . . . * . ** .        |
|    | DM | RTCPMCKLDVLKFYGYVVGDIYQTPS--PQHTAPIASIEEVPVIVVAVPHGPQPLQLQ     |
|    | HP | TSGISPLPDGELTPRTGEINIAVTKEWFIIASFGLLSALTLCYMIIRATASLNANEVEW    |
|    |    | . * . * . . .  |
| 25 | DM | ASNMSFAPSHYFQSSRSPSSSVQQQLAPLTYQPHPQQAASERGRRNSAPATMPHAITAS    |

HP F

DM HQVTDV

5

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA082118) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03444> (SEQ ID NOS: 3, 13 and 23)

15

Determination of the whole base sequence of the cDNA insert of clone HP03444 obtained from cDNA library of human kidney revealed the structure consisting of a 209-bp 5'-untranslated region, a 1248-bp ORF, and a 460-bp 3'-untranslated region. The ORF encodes a protein consisting of 415 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 3 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 43 kDa that was somewhat smaller than the molecular

25

weight of 45,691 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 42 kDa. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamine at position 24.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human type I procollagen C-proteinase enhancer protein (Accession No. BAA23281). Table 5 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human type I procollagen C-proteinase enhancer protein (CP). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 43.6% in the entire region.

Table 5

---

HP           MRGANAWAPLCLLLAAATQLSRQQSPERPVFCTCGGILTGESGFIGSEGFPGVYP

          \* \*\*. \* \* .. .. .\*\*\*\*\* \*\*\* ..\*\*\*\*\*...\*\*\*\*\*..\*\*

CP MLPAATASLLGPLLTACALLPFA-Q-GQTPNYTRPVFLCGGDVKGESGYVASEGFPNLYP





... ..\*..\*....\*

CP VVLRPNQDQILTNLSKRKCPSQPVRAAASQD

---

5           The search of the GenBank using the base sequences  
of the present cDNA has revealed the registration of  
sequences that shared a homology of 90% or more (for example,  
Accession No. D78874) among ESTs. However, since they are  
partial sequences, it can not be judged whether or not they  
10       encode the same protein as the protein of the present  
invention.

<HP03478> (SEQ ID NOS: 4, 14 and 24)

Determination of the whole base sequence of the  
cDNA insert of clone HP03478 obtained from cDNA library of  
15       human umbilical cord blood revealed the structure consisting  
of a 224-bp 5'-untranslated region, a 1143-bp ORF, and a  
891-bp 3'-untranslated region. The ORF encodes a protein  
consisting of 380 amino acid residues and there existed five  
putative transmembrane domains. Figure 4 depicts the  
20       hydrophobicity/hydrophilicity profile, obtained by the Kyte-  
Doolittle method, of the present protein. In vitro  
translation resulted in formation of a translation product  
of high molecular weight.

25       The search of the protein database using the amino  
acid sequence of the present protein revealed that the

protein was similar to Halocynthia roretzi HrPET-1 protein (Accession No. BAA81907). Table 6 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and Halocynthia roretzi HrPET-1 protein (HR). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 36.8% in the entire region.

Table 6

---

|    |  |
|----|--|
| HP | MLQTLYDYFWWERLWLPVNLTWADLEDRDGRVYAKASDLYITLPLALLFLIVRYFFEL                 |
| 15 | . * . ** . ** * . . *** ****. **. ... .. ** . * . ** . * . * . *           |
| HR | MDLLMDLYHWFWNEKFWLPQNLTWEDLKRTEEKQFGETRDLWTFPLCITVLCIRFSVEK                |
| HP | YVATPLAALLNIKEKTRLRAPPNATLEHFYLTSGKQPKQVEVELLSRQSGLSGRQVERWF               |
| 20 | . * **. ** . * . . . . * . **. * * ... * . ** * . * . * . . . . **         |
| HR | GIARPLGKWLNLSERLHTPPRENIVLEKVYKTITRKNYSQVEDLCKQTGWRKHEINVWF                |
| HP | RRRRNQDRPSLLKKFREASWRFTFYLIAFIAGMAVIVDKPWFYDMKKVWEGYPIQSTIPS               |
| 25 | * . . . . ** . * . ** . * . ***. ***. . * . * . * . . . * . . . ** . . . . |
| HR | RKKNLVGRPTTLTKFQETFWRFAYLTSFFYGLYVMYDQECVWQTEKCFSNYPEDHVLVSQ               |

HP Q-YWYYMIELSFYWSLLFSIASDVKRKDFKEQIIHHVATIILISFSWFANYIRAGTLIMA

. \*.\*\*.\*\*\*.\*\*\* . . . . .\*\*\*\*\* \* .\*\*\*.\*\*\*. . \* .\*\*..\*..\*..

HR KIIYYYLIELAFYSATTLTQFFDVKRKDFWEMFIHHIVTIILLCGSYTLNYTKMGAFILV

5 HP LHDSSDYLLS AKMFNYAGWKNTCNNIFIVFAIVFIITRLVILPFWILHCTLVYPLELYP

.\*\*\*.\*. .\* \*\*\* .\*\* . . \* \*\* \*.\* \*...\*\*\*\*\*.\*\*.... \* . \*

HR VHDSADFYIEFAKMGKYANNSLVTVGFISFTISFFLSRLVILPLWIVPSIWFGIYTYN

HP AFFGYFFNSMMGVLQLLHIFWAYLILRMAHKFITGKLVEDERSDREETESSEGEAAAAG

10 .. ..\* ... .\*\*\*\*\*.\* \*..\* . \* ..\* . . .\*.\*.\*.\*. \* .

HR CAMA-WLFCALL-ILQLLHFYWF SHIVKAAYASILVGVIERDTRSESEDSSAEDETAKYS

HP GGAKSRLANGHPILNNNHRKND

\*,

15 HR VGSGDYTESNGIHKRVVTAR

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T27334) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

25 <HP03499> (SEQ ID NOS: 5, 15 and 25)

Determination of the whole base sequence of the cDNA insert of clone HP03499 obtained from cDNA library of human kidney revealed the structure consisting of a 129-bp 5'-untranslated region, a 1758-bp ORF, and a 86-bp 3'-untranslated region. The ORF encodes a protein consisting of 585 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 5 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 63 kDa that was almost identical with the molecular weight of 63,987 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 82 kDa. In addition, there exist in the amino acid sequence of this protein five sites at which N-glycosylation may occur (Asn-Ile-Thr at position 89, Asn-Glu-Thr at position 106, Asn-Ala-Thr at position 189, Asn-Arg-Thr at position 220 and Asn-Ala-Thr at position 315).

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to Chinese hamster hypothetical protein 2BE2121 (Accession No. A30227). Table 7 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and Chinese hamster hypothetical protein 2BE2121 (CH). Therein, the marks of -,

\*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a  
 5 homology of 44.8% in the entire region.

Table 7

---

|    |   |                                      |
|----|---|--------------------------------------|
|    | HP MVCREQLSKNQVKWVFAGITCVSVVVIAAIVLAITLRRPGCELEACSPDADMLDYLLSLG   |                                      |
| 10 |   | ..***.*.                             |
|    | CH  | SWSENILDYFLRNS                       |
|    | HP QISRRDALEVTWYHAANSKKAMTAALNSNITVLEADVNV EGLGTANETGVPIMAHPTIY   |                                      |
|    | **.   | *. *.***** *.* .**.*. ....* * *****. |
| 15 | CH QITTEDGAEEIWIYHAANHKSQMQEALRSAAHMIEADVLLPS--DGSEHGQPIMAHPPEMN  |                                      |
|    | HP SDNTLEQWLDAVLGSSQKGIKLD FKNIAVGPSLDLLRQLTEEGKVRRIWINADILKGP    |                                      |
|    | *****.***.*. *.*****. *. *. *. .... ..*.*.***.* **                |                                      |
|    | CH SDNTLQEWLAEVM-KSNKGIKLD FKS LAAARASMLFLDNVKQH--LQCPVWMNADVLPGP |                                      |
| 20 |   |                                      |
|    | HP NMLISTEVNATQFLALVQEKYPKATLSPGWTTFY MSTSPNRTYTQAMVEKMHEL VGGVPQ |                                      |
|    | * *.***.***. *. *.***.*** ***** . ...*.*.***.*. ....*             |                                      |
|    | CH NG-SSKVVD AKAFLDTVTSFFPDVTFSLGWTTGWHPEKVN EGYSWTMVKEMDYICSLTQ  |                                      |
| 25 | HP RVTFPVRSSMVRAAWPHFSWLLSQSERYS LTLWQAASDPMSVEDLLYVRDNTAVHQVYYD  |                                      |

.\*\*\*\*\*...\*\*.. . . . \*\*\*..\*.\*\*\*\*\*.\* . .\*. ..\*\*\*\*\*.\*\* . \*\*.\*\*

CH PVTFPVRAALVRQSCSQLLWLLKKSNNRYSLTVWTGKDDSYPTEDLLYIRDYFNKTQVFYD

HP IFEPLLSQFKQLALNATRKPYYTGGSLIPLLQLPGDDGLNVEWLVPDVQSGSKTATMTL

5       \*.\*\*   .\*\*\*

CH ILEPQSHEFKQAIGI

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Furthermore, the search of the GenBank using the  
 10 base sequences of the present cDNA has revealed the  
 registration of sequences that shared a homology of 90% or  
 more (for example, Accession No. R92398) among ESTs. However,  
 since they are partial sequences, it can not be judged  
 whether or not they encode the same protein as the protein  
 15 of the present invention.

<HP03500> (SEQ ID NOS: 6, 16 and 26)

Determination of the whole base sequence of the  
 cDNA insert of clone HP03500 obtained from cDNA library of  
 human kidney revealed the structure consisting of a 134-bp  
 20 5'-untranslated region, a 996-bp ORF, and a 476-bp 3'-  
 untranslated region. The ORF encodes a protein consisting of  
 331 amino acid residues and there existed one putative  
 transmembrane domain at the N-terminus. Figure 6 depicts the  
 hydrophobicity/hydrophilicity profile, obtained by the Kyte-  
 25 Doolittle method, of the present protein. In vitro

translation resulted in formation of a translation product of 38 kDa that was almost identical with the molecular weight of 37,694 predicted from the ORF.

5 The search of the protein database using the amino acid sequence of the present protein revealed that the amino acid sequence of the protein matched with that of human hypothetical protein (Accession No. AAC05803) in which a region of 62 amino acid residues from glycine at position 88 to lysine at position 149 was deleted.

10 The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA340631) among ESTs. However, since they are partial sequences, it can not be judged whether or not they  
15 encode the same protein as the protein of the present invention.

<HP10691> (SEQ ID NOS: 7, 17 and 27)

Determination of the whole base sequence of the cDNA insert of clone HP10691 obtained from cDNA library of  
20 human umbilical cord blood revealed the structure consisting of a 246-bp 5'-untranslated region, a 1038-bp ORF, and a 1096-bp 3'-untranslated region. The ORF encodes a protein consisting of 345 amino acid residues and there existed at least two putative transmembrane domains. Figure 7 depicts  
25 the hydrophobicity/hydrophilicity profile, obtained by the

Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human BB1 protein (Accession No. AAB37433). Table 8 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human BB1 protein (BB). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The C-terminal region of 215 amino acid residues of the present protein shared a homology of 81.9% with the N-terminal region of human BB1 protein.

Table 8

---

|    |   |
|----|---|
|    | HP MSPEEWTYLVLLISIPIGFLFKKAGPGLKRWGAAVGLGLTLFTCGPHTLHSLVTILGT   |
| 20 | HP WALIQAQPCSCHALALAWTFSYLLFFRALSLLGLPTPTPFTNAVQLLLTLKLVSLASEVQ |
|    | HP DLHLAQRKEMASGFSKGPTLGLLPDVPSLMETLSYSYCYVGIMTGPFPRYRTYLDWLEQP |
|    | *****. . . .*   |
| 25 | BB MASGFSKGPTLGLLRRALPDGDT-QLQLLLRGNHDPVLPLPHLPGLAGAA           |



HP FPGAVPSLRPLLRRWPAPLFGLLFLLSSHLPLEAVREDAFYARPLPARLFYMIPVFFA

. \* . \*\*\*\*\*

BB LPRGSASLRPLLRRWPAPLFGLLFLLSSHLPLEAVREDAFYARPLPARLFYMIPVFFA

5

HP FRMRFYVAWIAAECGCIAAGFGAYPVA AKARAGGGPTLQCPPSSPEKAASLEYDYETIR

\*\*\*\*\*

BB FRMRFYVAWIAAECGCIAAGFGAYPVA AKARAGGGPTLQCPPSSPEKAASLEYDYETIR

10

HP NIDCYSTDFCVRVRDGMRYWNMTVQWWLAQYIYKSAPARSYVLRL

\*\*\*\*\*

BB NIDCYSTDFCVRVRDGMRYWNMTVQWWLAQYIYKSAPARSYVLRTAWTMLLSAYWHGLHP

15

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W48653) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

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<HP10703> (SEQ ID NOS: 8, 18 and 28)

25

Determination of the whole base sequence of the cDNA insert of clone HP10703 obtained from cDNA library of human kidney revealed the structure consisting of a 359-bp

5'-untranslated region, a 270-bp ORF, and a 1388-bp 3'-untranslated region. The ORF encodes a protein consisting of 89 amino acid residues and there existed one putative transmembrane domain. Figure 8 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 18 kDa that was larger than the molecular weight of 10,469 predicted from the ORF.

10           The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T08343) among ESTs. However, since they are partial sequences, it can not be judged whether or not they  
15           encode the same protein as the protein of the present invention.

          <HP10711> (SEQ ID NOS: 9, 19 and 29)

          Determination of the whole base sequence of the cDNA insert of clone HP10711 obtained from cDNA library of  
20           human kidney revealed the structure consisting of a 29-bp 5'-untranslated region, a 1221-bp ORF, and a 356-bp 3'-untranslated region. The ORF encodes a protein consisting of 406 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative  
25           transmembrane domain at the N-terminus. Figure 9 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 44 kDa that was almost identical with the molecular weight of 43,836 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 58 kDa. In addition, there exist in the amino acid sequence of this protein seven sites at which N-glycosylation may occur (Asn-Ser-Thr at position 65, Asn-Trp-Ser at position 95, Asn-Val-Ser at position 134, Asn-Ile-Thr at position 159, Asn-Gly-Ser at position 187, Asn-Arg-Ser at position 230 and Asn-Leu-Thr at position 333). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamic acid at position 36.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse kidney predominant protein (Accession No. BAA92527). Table 9 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse kidney predominant protein (MM). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The

both proteins shared a homology of 79.9% in the entire region.

Table 9

5

---

HS MRGSVECTWGWGHCAPSPLLLWTLFFFAPFGLLGKTRQVSLEVIPNWLGPLQNLLHIR

\* \*\*\* .\*\*\*.\* \*\* .\*\* .\*\*\*\*\* \*\*.\*\*\*\*.\* \*\* .\*

MM MFRCWGPWGWVPCAPTPWLLSLLVCSAPFGLQGEETRQVSMEVISGWPNP-QNLLHIR

10

HS AVGTNSTLHYVWSSLGPLAVVMVATNTPHSTLSVNWSLLLSPEPDGGLMVLPKDSIQFSS

\*\*\*.\*\*\*\*\* \*\*.\*\*\*\*.\*.\*\*\*\*\*.\*.\*.\*\*\*\*\*.\*\*\*\*\*

MM AVGSNSTLHYVWSSLGPPAVVLVATNTTQSVLSVNWSLLLSPPDPAGALMVLKSSIQFSS

15

HS ALVFTRLLEFDSTNVSDTAAPLGRPYPPYSLADFSWNNITDSDPATLSATFQGHMND

\*\*\*\*\*.\*.\*.\*.\*\*\*\*\*.\*\*\*\*\*.\*.\*.\*\*\*.\*.\*\*\*.\*.\*

MM ALVFTRLLEFDSTNASE-GAQQPGKPYPPYSLAKFSWNNITNSLDLANLSADFQGRPVDD

HS PTRTFANGSLAFRVQAFSRSSRPAQPPRLLHTADTCQLEVALIGASPRGNRSLFGLEVAT

\*\* .\*\*\*\*\*.\*.\*\*\*\*\*.\*\*\*\*\*.\*\*\*\*\*.\*\*\*\*\*.\*\*\*\*\*

20

MM PTGAFANGSLTFKVQAFSRSGRPAQPPRLLHTADVCQLEVALVGASPRGNHSLFGLEVAT

HS LGQGPDCPSMQEQHSIDDEYAPAVFQLDQLLWGSLSGFAQWRPVAYSQKPGGRESALPC

\*\*\*\*\*.\*.\*.\*\*\*\*\*.\*\*\*\*\* \*\*\*\* \*.\*.\*\*\*\*\*

MM LGQGPDCPSVNERNSIDDEYAPAVFQLNQLLWGSSPSGFMQWRPVAFSEERAREALPC

25

MM QASTLHSTLASSLP HSP I VQAFFGSQNNFCAFNLTFGAPTGP GYWDQYYLCWSM L LGMGF

MM PPVDIFSPLVLGIMAVALGAPGLMFLGGGLFLLLRHRRYSEYQSIN

Determination of the whole base sequence of the cDNA insert of clone HP10712 obtained from cDNA library of human kidney revealed the structure consisting of a 52-bp 5'-untranslated region, a 579-bp ORF, and a 1064-bp 3'-untranslated region. The ORF encodes a protein consisting of 192 amino acid residues and there existed four putative transmembrane domains. Figure 10 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-

Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse calcium channel gamma 5 subunit (Accession No. CAB86387). Table 10 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse calcium channel gamma 5 subunit (MM). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 75.0% in the entire region.

Table 10

---

|    |    |   |
|----|----|---|
|    | HS | MTAVGVQQRPLGQRQPRRSFFESFIRTLIITCVALAVVLSSVSICDGHWLLAEDRLFGL   |
| 20 |    | ***.*.**.. ** ..*.*****. *.*****. **.****                     |
|    | MM | MTAIGAQAHLKLLGLKRPHRSFFESFIRTLIIVCTALAVVLSSVSICDGHWLLVEDHLFGL |
|    | HS | WHFCTTTNQSVPICFRDLGQAHVPGLAVGMGLVRSVGALAVVAAIFGLEFLMVSQLCEDK  |
|    |    | *.***. *. * * *.***.***.*****.***.*.*****. *.***.***          |
| 25 | MM | WYFCTIGNHSEPHCLRDLSQAHPGLAVGMGLARSVAAMAVVAAIFGLEMLIVSQVCEDV   |

HS HSQCKWVMGSILLVSVFLSSGGLLG FVILLRNQVT LIGFTLMFWCEFTASFLFLNAIS

. \*. \*\*. \*\* \*\*\*\*. \*. \*\*\*\*\*. \*. \*\*\*. \*\*. \*. \*\*\*\*\*. \*\*\*\* \*

MM RSRRKWAIGSYLLLVAFILSSGGLLTFIILLKNQINLLGFTLMFWCEFTASFLFLNAAS

5

HS GLHINSITHPWE

\*\*\*\*\*. \*. \*\*.

MM GLHINSLTQPWDPPAGTLAYRKRGYDGTSLI

10

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA910339) among ESTs.

15

However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03010> (SEQ ID NOS: 31, 41 and 51)

20

Determination of the whole base sequence of the cDNA insert of clone HP03010 obtained from cDNA library of human kidney revealed the structure consisting of a 97-bp 5'-untranslated region, a 1134-bp ORF, and a 320-bp 3'-untranslated region. The ORF encodes a protein consisting of 377 amino acid residues and there existed at least eight putative transmembrane domains. Figure 11 depicts the

25

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 42 kDa that was almost identical with the molecular weight of 41,462 predicted from the ORF as well as a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Arabidopsis thaliana* hypothetical protein (Accession No. AAC34490). Table 11 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Arabidopsis thaliana* hypothetical protein (AT). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 42.0% in the entire region other than the N-terminal region.

Table 11

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HP MDSALSDPHNGSAEAGGPTNSTTRPPSTPEGIALAYGSLLLMALLPIFFGALRSVRCARG

\* \* \*

25 AT MKNCERFANLALAGLTLAPLVVRVNPPLNVILTACITVYVGCFRS



HP KNASDMPETITSRDAARFPIIASCTLLGLYLFFKIFSQEYINLLSMYFFVLGILALSHT

... \*\*... \* \*\*\*... \* \*\*.\*.\*.\*.\*... \* .\*. \*\*\*\*\*.\*\*\* \*

AT VKDTPPTETMSKEHAMRFPLVGSAMLLSLFLLFKFLSKDLVNAVLTAYFFVLGIVALSAT

5

HP ISPFMNKFFPASFPNRQYQLLFTQGSGENKEEIINYEFDTKDLVCLGLSSIVGVWYLLRK

. \* ...\*.\*... .. \* .. \*\*.....\* ... .\*\* .\*

AT LLPAIRRFLPNPWNDNLIVWRF-----PYFKSLEVEFTKSQVVAGIPGTFFCAWYAWKK

10

HP HWIANNLFGLAFLSLNGVELLHLNNVSTGCILLGGLFIYDVFVWFGTNVMVTVAKSFEAPI

\*\*, \*\*.. \*\*, \*...\*, \*, \* \*.. \*\*. \*\*\*, \*\*\*, \*\*, \*\*\*\*\* \* \*\*\*, \*\*\*, \*\*\*,

AT HWLANNILGLSFCIQGIEMLSLGSFKTGAILLAGLFFYDIFWVFFTPVMVSVAKSFDAPI

HP KLVFPQDLLEKGLEANNFAMLGLGDVVIPGIFIALLLRFDISLKKNTHTYFYTSFAAYIF

15

\*\*, \*\* . ..\* . ..\*\*\*\*\*.\*\*\*\*\*. \*\* \*\*\*\*.\* ..... \*\* ..\* .\*

AT KLLFPTG---DALRP--YSMLGLGDIVIPGIFVALALRFDVSRRRQPQ-YFTSAFIGYAV

HP GLGLTIFIMHIFKHAQPALLYLPACIGFPVLVALAKGEVTEMFSYEESNPKDPAAVTES

\*, \*\*\* .\*, \*. \*\*\*\*\*.\*\*\* \*\*\* . . \*. ... ..\*\*.... \*...\*\*

20

AT GVILTIVVMNWFQAAQPALLYIVPAVIGFLASHCIWNGDIKPLLAFDESKTEE-ATTDES

HP KEGTEASASKGLEKKEK

\*...\*.. ...

AT KTSEEVNKAHDE

25

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA380429) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03576> (SEQ ID NOS: 32, 42 and 52)

Determination of the whole base sequence of the cDNA insert of clone HP03576 obtained from cDNA library of human kidney revealed the structure consisting of a 88-bp 5'-untranslated region, a 246-bp ORF, and a 1379-bp 3'-untranslated region. The ORF encodes a protein consisting of 81 amino acid residues and there existed two putative transmembrane domains. Figure 12 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 20 kDa that was larger than the molecular weight of 9,178 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human vacuolar proton ATPase 9 kDa (Accession No. NP\_003936). Table 12 shows the comparison

between amino acid sequences of the human protein of the present invention (HP) and human vacuolar proton ATPase 9 kDa (VP). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 71.2% in the entire region.

10 Table 12

HP MTAHSFALPVIIFTTFWGLVGIAGPWFVPKGPNGVVIITMLVATAVCCYLFWLIAILAQL

```
*. *. . . *. *. . . ****. **.      ****. *****.          *****
```

VP MAYHGLTVPLIVMSVFWGFVGLVPWFIPKGPNRGVIITMLVTCVCCYFLWLIAILAQL

15

HP NPLFGPQLKNETIWYVRFLWE

\*\*\*\*\*. . . \*

VP NPLFGPQLKNETIWYLYHWP

20

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W22566) among ESTs. However, since they are partial sequences, it can not be judged

whether or not they encode the same protein as the protein of the present invention.

<HP03611> (SEQ ID NOS: 33, 43 and 53)

Determination of the whole base sequence of the  
5 cDNA insert of clone HP03611 obtained from cDNA library of  
human kidney revealed the structure consisting of a 189-bp  
5'-untranslated region, a 1464-bp ORF, and a 105-bp 3'-  
untranslated region. The ORF encodes a protein consisting of  
487 amino acid residues and there existed eleven putative  
10 transmembrane domains. Figure 13 depicts the  
hydrophobicity/hydrophilicity profile, obtained by the Kyte-  
Doolittle method, of the present protein. In vitro  
translation resulted in formation of a translation product  
of high molecular weight.

15 The search of the protein database using the amino  
acid sequence of the present protein revealed that the  
protein was similar to human cystine/glutamate transporter  
(Accession No. BAA82628). Table 13 shows the comparison  
between amino acid sequences of the human protein of the  
20 present invention (HP) and human cystine/glutamate  
transporter (CG). Therein, the marks of -, \*, and .  
represent a gap, an amino acid residue identical with that  
of the protein of the present invention, and an amino acid  
residue similar to that of the protein of the present  
25 invention, respectively. The both proteins shared a homology

of 43.8% in the entire region other than the N-terminal region.

Table 13

5

HP MGD TGLRKRREDEKSIQSQEPKTTSLQKELGLISGISIIVGTIIGS  
..... \*.....\*.\*.\*\*\*.\*\*\*\*\*.

CG MVRKPVVSTISKGGYLQGNVNGRLPSLGNKEPPGQEKVQLKRKVTLLRGVSIIGTIIGA

10 HP GIFVSPKSVLSNTEAVGPCLIIWAACGVLATLGALCF AELGTMITKSGGEYPYLMEAYGP  
\*\*\*.\*\*\*.\*\* \*\*.\*.\*\*\*.\*\*\*\*.\*\*\*.\*\*\*\*\* \*.\*\*\*\*.\*.\*.\*.\*\*\*

CG GIFISPKGVLQNTGSVMSLTIWTVCGVLSLFGALSYAELGTTIKKSGGHYTYILEVFGP

```

HP IPAYLFSWASLIVIKPTSFATIICLSFSEYVCAPFYVGCKPPQIVVKLAAAAILFISTVN
15  .**.. *.**.*.*. *.**.*. *. **.. *. *.**.* **.*.* . .*.

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CG LPAFVRVWVELLIIRPAATAVISLAFGRYILEPFFIQCEIPELAIKLITAVGITVVMVLN

HP SLSVRLGSYVQNIFTAAKLIVIVAIIIIISGLVLLAQGNTKNFDNSFEGAQLSVGAISLAFY  
\*. \*\* . . . \* . . \* \*\*. . \*\*\*\*. \*. . \* . \*. \*. \*\*. . . \*. \* . \* . . . \*\*\*\*

20 CG SMSVSW SARIQIFLTFCKLTAILIIIVPGVMQLIKGQTQNFKDAFSGRDSSITRLPLAFY

HP NGLWAYDGNQLNYITEELRNPNRLPLAIIIGIPLVTACYILMNVSYFTVMTATELLQS  
\*.\*.\*.\* \*\*.\*\*\*\*. \*\* ...\*\*\*\*\* \*... \*\* \* \* \* \* \*\*\*...\*.\*\*\* \*

CG YGMYAYAGWFYLNFTVEEVENPEKTIPLAICISMAIVTIGYVLTNAVYFTTINAEELLS

HP QAVAVTFGDRVLYPASWIVPLFVAFSTIGAANGTCFTAGRLIYVAGREGHMLKVLSYISV  
 .\*\*\*\*\*.\*.\* \* \*\*.\*\*\*.\*.\* \*\*.\*...\*\*.\*\*\*.\*\*\*.\* \*\*.\*  
 CG NAVAVTFSERLLGNFSLAVPIFVALSCFGSMNGGVFAVSRLFYVASREGLPEILSMIHV

5 HP RRLTPAPAIIFYGIIATIIYIIPGDINSLVNYFSFAAWLFYGLTILGLIVMRFRKELERP  
 \*. \*\* \*\*.\* .. \* ...\*\*.\*\*\*.\*.\* \*\*.\*\*\*.\*\*\*.\* \*\*.\* \*\*.\* ..\*\*  
 CG RKHTPLPAVIVLHPLTMIMLFSGDLDSLLNFLSFARWLFGLAVAGLIYLRKCPDMHRP

HP IKVPVVIPVLMTLISVFLVLAPIISKPTWEYLYCVLFILSGLLFYFLFVHY--KFGWAQK  
 10 .\*\*\*\*. \*\*.\*.....\*.\* .. \*.\* .. ...\*.\*. \*.\*\*.\*. \*.\*.  
 CG FKVPLFIPALFSFTCLFMVALSLYSDP-FSTGIGFVITLTGVPAYYLFIIWDKKPRWFRI

HP ISKPITMHLQMLMEVVPPEEDPE  
 .\*. \*\*. \*\*.\*...\*\*\*\*.\*.  
 15 CG MSEKITRTLQIILEVVPEEDKL

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The search of the GenBank using the base sequences  
 of the present cDNA has revealed the registration of  
 20 sequences that shared a homology of 90% or more (for example,  
 Accession No. R07056) among ESTs. However, since they are  
 partial sequences, it can not be judged whether or not they  
 encode the same protein as the protein of the present  
 invention.

Determination of the whole base sequence of the cDNA insert of clone HP03612 obtained from cDNA library of human kidney revealed the structure consisting of a 153-bp 5'-untranslated region, a 1128-bp ORF, and a 269-bp 3'-untranslated region. The ORF encodes a protein consisting of 375 amino acid residues and there existed seven putative transmembrane domains. Figure 14 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 39 kDa that was somewhat larger than the molecular weight of 37,930 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human monocarboxylate transporter (Accession No. AAC70919). Table 14 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human monocarboxylate transporter (MC). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 41.7% in the N-terminal region of 192 amino acid residues.

Table 14

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|    |    |   |
|----|----|---|
|    | HP | MTPQPAGPPDGGGWVVAAAAFAINGLSYGLLRSLGLAFPDLAEHFDRSAQDTAW        |
|    |    | .*. *****.*.*.* *.**.. ..... * ..... *. . .**                 |
| 5  | MC | MPPMPSAPPVHPPDGGGWIVVGATFISIGFSYAFPKAVTVFFKEIQQIFHTTYSEIAW    |
|    | HP | ISALALAVQQAASPVGSALSTRWGARPVVMVGGVLASLGFVFSAFASGLLHLYLGLGLLA  |
|    |    | **.. *** *.**.*.* ...*.*****.***.* **.*...*.**...***.*...     |
|    | MC | ISSIMLAVMYAGGPVSSVLVNKYGSRPVVIAGLLCCLGMVLASFSSSVVQLYLTMGFIT   |
| 10 | HP | GFGWALVFAPALGTLTRYFSRRRVLAVGLALTGNGASSLLLAPALQLLLDTFGWRGALLL  |
|    |    | *.*.*. ....**.*.*.* **..**.. *** *.*.***.*.*.*.               |
|    | MC | GLGLAFNLQPALTIIGKYFYRKRPMANGLAMAGNPVFLSSLAPFNQYLFNTFGWKGSFLI  |
| 15 | HP | LGAITLHLTPCGALLPLVLPDPPAPPRSPLAALGLSLFTRRAFSIFALGTALVGGGYF    |
|    |    | **.. *. *.**.**   |
|    | MC | LGSLLLNA CVAGSLMRPLGPNQTTSKSKNKTGKTEDDSSPKIKTKKSTWEKVNKYLD FS |
|    | HP | VPYVHLAPRFRPGGIRSSAGGGRGCDGGCGRPAGLRVAGRPRLGAPPAAAGRIRGSDW    |
| 20 | MC | LFKHRGFLIYLSGNVIMFLGFFAPIIFPAPYAKDQGIDEYSAFLLSVMAFVDMFARPSV   |
|    | HP | AGAVGGGAGARGRRRELGGSPAGRGCLWAERGELRPAGFRCTPRAGRRRCGAGHRAG     |
| 25 | MC | GLIANSKYIRPRIQYFFSFAIMFNGVCHLLCPLAQDYTSVLVYAVFFGLGFGSVSSVLFE  |



HP DDADEPRGAPGPSVRLPKG

MC TLMDLVGAPRFSSAVGLVTIVECGPVLLGPPLAGKLVDLTGEYKMYMSCGAIVVAASVW

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The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI742291) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10407> (SEQ ID NOS: 35, 45 and 55)

15 Determination of the whole base sequence of the cDNA insert of clone HP10407 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 100-bp 5'-untranslated region, a 1053-bp ORF, and a 332-bp 3'-untranslated region. The ORF encodes a protein consisting of 350 amino acid residues and there existed at least four putative transmembrane domains. Figure 15 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

25 The search of the protein database using the amino acid sequence of the present protein revealed that the

protein was longer by 35 amino acid residues at the N-terminus than human hypothetical protein (Accession No. CAB43375).

Furthermore, the search of the GenBank using the  
5 base sequences of the present cDNA has revealed the registration of a clone beginning from the 117th base of the present cDNA (Accession No. AL050274).

<HP10713> (SEQ ID NOS: 36, 46 and 56)

Determination of the whole base sequence of the  
10 cDNA insert of clone HP10713 obtained from cDNA library of human kidney revealed the structure consisting of a 79-bp 5'-untranslated region, a 2004-bp ORF, and a 611-bp 3'-untranslated region. The ORF encodes a protein consisting of 667 amino acid residues and there existed nine putative  
15 transmembrane domains. Figure 16 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

20 The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse retinoic acid-responsive protein (Accession No. AAC16016). Table 15 shows the comparison between amino acid sequences of the human protein  
25 of the present invention (HP) and mouse retinoic acid-

responsive protein (MM). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 74.1% in the entire region.

Table 15

10 HP MSSQPAGNQTS PGATEDYSYGSWYIDEPQGG EELQPEGEVPSCHTSIPPGLYHACLAS

\*.\*\*\*. \*. \*.\*\*\* \*\*\*\*\*. \*\* \*.\*\*\*.\*\*\*\*\* . \* \*. . \*\*.\* \*\*\*\*\*

MM MESQASENGSQTSSGVTDAYS--SWYIEEPLGAEEVQPEGVIPLCQLTAPPALLHACLAS

HP LSILVLLLLAMLVRRRQLWPDCVRGRGPLSPVDFLAGDRPRAVPAAVFMVLLSSLCLLL

```
15      **,*****.*****.*** * .      ***** .. *****.**,*.*****
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MM LSFLVLLLALLVRRRRLWPRCGHRGLGLPSPVDFLAGDLSWTVPAAVFVVLFSNLCLLL

HP PDEDALPFLTLASAPSQDGKTEAPRGAWKILGLFYAAALYYPLAACATAGHTAAHLLGST

\*\*\*.\*\*\*\*\*.\*.\*.\*.\*.\*\*\*.\*.\*.\*\*\*.\*\*\*.\*.\*.\*\*\*.\*\*\*\*\*.\*\*\* \*\* \*\*\*,

20 MM PDENPLPFLNLTAASSPDGEMETSRGPWKLLALLYYPALYYPLAACASAGHQA AFL LGTV

HP LSWAHLGVQVWQRAECPQVPKIYKYYSLLASLPLLLGLGFLSLWYPVQLVRSFSRRTGAG

\*\*\*\*\*

MM LSWAHFGVQVWQKA ECPQDPKIYKHYSLLASLPLLLGLGFLSLWYPVQLVQSLRHRTGAG



. \*\*\*\*\*. \*\*. \*\*\*\*\* \*\*\*\*\* . . \*. \*\*\*\*\*. \*\*. \*\*\*.

MM PPLAPQDSLRLPAEEEEGMQLLQTKDLMAKGAGHKGSQSRARWGLAYTLLHNPSLQAFRKA

HP ALLGANGAQP

5        \*\*. \*. .

MM ALTSAKANQTQP

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10        The search of the GenBank using the base sequences  
of the present cDNA has revealed the registration of  
sequences that shared a homology of 90% or more (for example,  
Accession No. AI760170) among ESTs. However, since they are  
partial sequences, it can not be judged whether or not they  
encode the same protein as the protein of the present  
15        invention.

<HP10714> (SEQ ID NOS: 37, 47 and 57)

20        Determination of the whole base sequence of the  
cDNA insert of clone HP10714 obtained from cDNA library of  
human umbilical cord blood revealed the structure consisting  
of a 82-bp 5'-untranslated region, a 1395-bp ORF, and a  
1820-bp 3'-untranslated region. The ORF encodes a protein  
consisting of 464 amino acid residues and there existed a  
putative secretory signal at the N-terminus. Figure 17  
depicts the hydrophobicity/hydrophilicity profile, obtained  
25        by the Kyte-Doolittle method, of the present protein. In

vitro translation resulted in formation of a translation product of 49 kDa that was somewhat smaller than the molecular weight of 52,340 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 52 kDa. In addition, there exist in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Ala-Thr at position 164 and Asn-Asp-Ser at position 320). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from threonine at position 22.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA861134) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10716> (SEQ ID NOS: 38, 48 and 58)

Determination of the whole base sequence of the cDNA insert of clone HP10716 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 60-bp 5'-untranslated region, a 1413-bp ORF, and a 653-bp 3'-untranslated region. The ORF encodes a protein consisting of 470 amino acid residues and there existed one

putative transmembrane domain at the N-terminus. Figure 18 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 61 kDa that was larger than the molecular weight of 52,086 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human hypothetical protein CGI-90 (Accession No. AAD34085). Table 16 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human hypothetical protein CGI-90 (CG). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 32.4% in the entire region.

Table 16

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HP MSRLGALGGARAGLGLLLGTAAGLGFLCLLYSQRWKRTQRHGRSQSLPNSLDYTQTSDPG

HP RHVMLLRAPGGAGDASVLPSPREGQEKVLDRLDFVLTSLVALRREVEELRSSLRGLAG

HP EIVGEVRCHMEENQRVARRRRFPFVRERSDSTGSSSVYFTASSGATFTDAESEGGYTTAN

CG

MALAARLWRLLPFRRGAAPGSRLPA

5 HP AESDNERDSKESEDGEDEVSCETVKMGRKDSLDEEEAASGASSALEAGGSSGLEDVLP

. \*. . . . \*

CG GPSGSRGIAAPARFRGFVGMNPGTFNRGLLLSALSYLGFETYQVISQAAVVHATAKVEE

HP LLQQADELHRGDEQGKREGFQLLLNNKL VYGSRQDFLWRLARAYSDMCELT-EEVSEKKS

10 . \*. \*\*\* \*. . . \* . \* . \*\*\* . \* . . . . \*\*\*\*\* . \*. . \*. . . \*\*\*

CG ILEQADYLYESGETEK--LYQLLTQYK--ESED AELLWRLARASRDVAQLSRTSEEEKKL

HP YALDGKEEAEEAALEKGDDESADCHLWYAVLCGQLAEHESIQRRIQSGFSFKEHVDKAIALQ

. . . \* \*. \*\*\*\*. . . \* . \* . \*\*\*. . . . . \*. \*. . \*. . . . \*\*\* . \*\*\*. \*.

15 CG LVYEALEYAKRALEKNESSFASHKWYAICLSDVGDYEGIKAKIANAYIIKEHFKAIELN

HP PENPMAHFLLGRWCYQVSHLSWLEKKTATALLSPLSATVEDALQSFLKAEELQPGFSKA

\*. . . . \* . \* \*\*\* . . . . \* . . . . \*. \*. . . . \* . \* . \* . \* . \* . \* . \* . \*

CG PKDATSIHLMGIWCYTFAEMPWYQRRIAKMLFATPPSSTYEKALGYFHRAEQVDPNPFYSK

20

HP GRVYISKCYRELGKNSEARWWMKLALELPDVTKEDLAIQKDLEELEVLIRD

. . . . \* . \* . \* . . . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \*

CG NLLLLGKTYLKLHNKKLA AFWLMKAKDYPAHTEEDKQIQTEAAQLLTSFSEKN



The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA852295) among ESTs. However, since they are  
5 partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10717> (SEQ ID NOS: 39, 49 and 59)

Determination of the whole base sequence of the  
10 cDNA insert of clone HP10717 obtained from cDNA library of human kidney revealed the structure consisting of a 73-bp 5'-untranslated region, a 732-bp ORF, and a 976-bp 3'-untranslated region. The ORF encodes a protein consisting of 243 amino acid residues and there existed two putative  
15 transmembrane domains. Figure 19 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 36 kDa that was larger than the molecular weight of  
20 26,270 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI478174) among ESTs. However, since they are  
25 partial sequences, it can not be judged whether or not they

encode the same protein as the protein of the present invention.

<HP10718> (SEQ ID NOS: 40, 50 and 60)

Determination of the whole base sequence of the  
5 cDNA insert of clone HP10718 obtained from cDNA library of  
human umbilical cord blood revealed the structure consisting  
of a 86-bp 5'-untranslated region, a 813-bp ORF, and a 889-  
bp 3'-untranslated region. The ORF encodes a protein  
consisting of 270 amino acid residues and there existed  
10 three putative transmembrane domains. Figure 20 depicts the  
hydrophobicity/hydrophilicity profile, obtained by the Kyte-  
Doolittle method, of the present protein. In vitro  
translation resulted in formation of a translation product  
of 28 kDa that was smaller than the molecular weight of  
15 31,116 predicted from the ORF.

The search of the protein database using the amino  
acid sequence of the present protein revealed that the  
protein was similar to *Caenorhabditis elegans* hypothetical  
protein Y53C10A (Accession No. CAA22139). Table 17 shows the  
20 comparison between amino acid sequences of the human protein  
of the present invention (HP) and *Caenorhabditis elegans*  
hypothetical protein Y53C10A (CE). Therein, the marks of -,  
\*, and . represent a gap, an amino acid residue identical  
with that of the protein of the present invention, and an  
25 amino acid residue similar to that of the protein of the

present invention, respectively. The both proteins shared a homology of 54.8% in the entire region other than the N-terminal region.

## 5 Table 17

---

|    | HP   | MAGAEDWPGQ |
|----|--|------------|
|    | CE MTSSSAASSSTTTSTMPDENECLKKEEERFKSPDPAPTLDEEVDIDTLPSMLEDDPNG    |            |
| 10 | HP QLELDEDEASCCRWGAQHAGARELAALYSPGKRLQEWCSVILCFSLIAHNLVHLLLLARW  |            |
|    | ***.*****..**..** .***** *.. . *.. ... ***. *                    |            |
|    | CE NVVECDLGFKGPRWGPQHAGAKKLASMYSKEKRLQEKVSLFAAIFLFSIVFIN-LLLS-W  |            |
| 15 | HP EDT--PLVILGVVAGALIADFLSGLVHWGADTWGSVELPIVGKAFIRPFREHHIDPTAIT  |            |
|    | *.. *....* * ..*** *****.***.***** . *..*****.*****              |            |
|    | CE ESSIWVSVLVSAVLGIMTADFASGLVHWAADTFGSVE-TWFGRSFIRPFREHHVDPTAIT  |            |
|    | HP RHDFIETNGDNCLVTLLPLLNMAYKFRTHSPEALEQ--LYPWEFCVFCLIIFGTFTNQIH  |            |
| 20 | ***..*.*****.. . *** . *. *. ..*..* ..* ... * *. ..*****         |            |
|    | CE RHDIVEVNGDNCMLCVGPLLWILYQQMTYQRDAITQWATFWH--YILLGLGIYVALTNQIH |            |
|    | HP KWSHTYFGLPRWVTLLQDWHVILPRKHHRHHVSPHETYFCITTGWLNYPLEKIGFWRRL   |            |
|    | ***** **..**.. *.****.***.***.***. *.*****.*** *****.            |            |
| 25 | CE KWSHTYFGLPTWVFLQKAHIILPRSHHKIHHISPHACYYCITTGWLNPLEYIGFWRKM    |            |

HP EDLIQGLTGKPRADDMKWAQKIK

\* .. ..\*\* .\*\*.\*.\*\*\* \*..

CE EWVVTTVTGMQPREDDLKWATKLQ

5

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA176107) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention. In addition, the region from position 466 to position 778 of the cDNA of the present invention matched with the region from position 2 to position 314 of human ubiquitin-conjugating enzyme E2 variant 1 (Accession NO. NM\_003349) although no match was observed in another region.

20 <HP03745> (SEQ ID NOS: 61, 71 and 81)

Determination of the whole base sequence of the cDNA insert of clone HP03745 obtained from cDNA library of human kidney revealed the structure consisting of a 99-bp 5'-untranslated region, a 1170-bp ORF, and a 107-bp 3'-untranslated region. The ORF encodes a protein consisting of 389 amino acid residues and there existed at least nine

25

putative transmembrane domains. Figure 21 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product  
 5 of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human solute carrier family 7 (Accession No. NP\_003974). Table 18 shows the comparison  
 10 between amino acid sequences of the human protein of the present invention (HP) and human solute carrier family 7 (SC). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that  
 15 of the protein of the present invention, respectively. The both proteins shared a homology of 36.0% in the N-terminal region of 397 amino acid residues.

Table 18

20

---

|       |  |
|-------|--|
| HP    | MDRGEKIQLKRVFGYWWGTSFLLINIIG                                 |
|       | . * . * * . . . * . * . . * . * *                            |
| SC    | MEAREPGRPTPTYHLVPNTSQSQVEEDVSSPPQRSSETMQLKKEISLLNGVSLVVGNMIG |
| 25 HP | AGIFVSPKGVLAYSCMNVGVSVCVWAGCAILAMTSTLCSAEISISFPCSGAQYYFLKRYF |

\*\*\*\*\*... . \*.\*\* \*\*\* .....\*\* \*\*..... \*\*\* \* .. \*  
 SC SGIFVSPKGVLYHT-ASYGMSLIVWAIGGLFSVVGALCYAELGTTITKSGASYAYILEAF  
  
 HP GSTVAFNLWTSFLGSGVVAG-QALLAEYSIQPFFPSCSVPKLPKKCLALAMLWIVGI  
 5       \*. \*\*..\*\*..\*\*.. . . . . \*. .\*. \* \*\*\* \*\*\*\*. \* \*. . \*\* \* . ....  
 SC GGFIAFIRLWVSLLVVEPTGQAIITFANYIIQPSFPCDPPYLACRLAAACICLLTF  
  
 HP LTRGVKEVTWLQIASSVLKVSILSFISLTGVVFLIRGKKENVERFQNAFDAELPDISHL  
 ... \*\* \*..\* . . \*\* \* \* . \*. \* \* . \* . \*.\*\*.\*..\* . ...\*  
 10       SC VNCAYVKWGTRVQDTFTYAKVVALIAIIVMGLVKLCQG---HSEHFQDAFEGSSWDMGNL  
  
 HP IQAIFQGYFAYSG-----ELKKPRTTIPKCIFTALPLVTVVYLLVNISYLTVLTTPR  
 \*.. . \*.\*\*\*               \*.\*. \* ..\* \* ...\*.\*\*..\*.\*.\*.\*\*\*. .  
 SC SLALYSALFSYSGWDTLNFVTEEIKNPERNLPLAIGISMPIVTLIYILTNAVYYTVLNIS  
 15  
 HP EILSSDAVAITWADRAFPSLAWIMPFAISTSLFSNLLISIFKSSRPIYLASQEGQLPLLF  
 ..\*\*\*\*\*.\*.\*.\*. \* ..\*.\*.\*. \* \*..\* \*\*\* \*\* ..\*.\*.\*.\*.  
 SC DVLSSDAVAITFADQTFGMFSWTIPIAVALSCFGGLNASIFASSRLFFVGSREGHLPDLL  
  
 20       HP NTLNSHS-SPFTAVLLLVTGLSLAIILTSIDLINIFYFTGSLWSILLMIGILRRRYQEP  
 . . . . .\*.\*.\*. \*.. . \*.\*\*\*\*\*. \* . . \* ..\* \* \*..\*\*  
 SC SMIHIERFTPIPALFNCTMALIYLVEDVFQLINIFYFSFYWFFVGLSVVGQLYLRWKEP  
  
 HP NLSIPYKVKLDF  
 25       . . \* \*..\* . \*

SC KRPRPLKLSVFFPIVFCICSVFLVIVPLFTDTINSLIGIGIALSGVPPFYFMGVYLPESRR

---

<HP03747> (SEQ ID NOS: 62, 72 and 82)

5           Determination of the whole base sequence of the  
cDNA insert of clone HP03747 obtained from cDNA library of  
human umbilical cord blood revealed the structure consisting  
of a 21-bp 5'-untranslated region, a 1047-bp ORF, and a  
1324-bp 3'-untranslated region. The ORF encodes a protein  
10           consisting of 348 amino acid residues and there existed a  
putative secretory signal at the N-terminus and one putative  
transmembrane domain at the C-terminus. Figure 22 depicts  
the hydrophobicity/hydrophilicity profile, obtained by the  
Kyte-Doolittle method, of the present protein. In vitro  
15           translation resulted in formation of a translation product  
of 40 kDa that was almost identical with the molecular  
weight of 39,685 predicted from the ORF. Application of the  
(-3,-1) rule, a method for predicting the cleavage site of  
the secretory signal sequence, allows to expect that the  
20           mature protein starts from proline at position 39.

          The search of the protein database using the amino  
acid sequence of the present protein revealed that the  
protein was similar to human endoplasmic reticulum  
glycoprotein (Accession No. NP\_006807). Table 19 shows the  
25           comparison between amino acid sequences of the human protein

of the present invention (HP) and human endoplasmic  
reticulum glycoprotein (ER). Therein, the marks of -, \*,  
and . represent a gap, an amino acid residue identical with  
that of the protein of the present invention, and an amino  
5 acid residue similar to that of the protein of the present  
invention, respectively. The both proteins shared a homology  
of 54.1% in the entire region.

Table 19

10

---

HP MAATLGPLGSWQ-QW-RRCLSARD-----GSRMLLLLLLLGSGQGPQQVGAGQTFEYLK

\*. \* \*\*\*\*. .. \*. \*.\*\*\*\* \* .....\*.. \*.\*\*

ER MAAEGWIWRWGWGRRCLGRPGLLGPGPGPTTFLLLL-LGSVTADITDGNS-EHLK

15

HP REHSLSKPYQGVGTGSSSLWNLGMNAMVMTQYIRLTPDMQSKQGALWNRVPCFLRDWELQ

\*\*\*\*\* \*\*\*\*\*. \* .\*\*.. \*..\* .\*\*..\*\*\*\*\* .\*\*.\*..\*\*.. \*\*\*\*.\*\*\*..

ER REHSLIKPYQGVGSSSMPLWDFQGSTMLTSQYVRLTPDERSKEGSIWNHQPCLKDWEMH

HP VHFKIHGQGKKNLHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDTPNEEKQQERVF

20

\*\*\*\*. \*\* \*\*\*\*\*. \*.\*\*\*. \*\*. \*\*\*\*\*. \*. \* \*\*..\*. \*\*\*\*\*. \*. \*\*\*\*

ER VHFKVHGTGKKNLHGDGIALWYTRDRLVPGPVFGSKDNFHLAIFLDTPNDET-TERVF

HP PYISAMVNNGSLSYDHERDGRPTELGGCTAIVRNLYHDTFLVIRYVKRHLTIMMDIDGKH

\*\*\*\*. \*\*\*\*\*. \*\*\* \*\*..\*\*\*\* \*\* ..\*\*\*\*..\*\* . .\*\*.\* \*...\*

25

ER PYISVMVNNGSLSYDHSKDGRWTELAGCTADFRNRDHDFTLAVRYSRGRLTVMTDLEDKN



HP EWRDCIEVPGVRLPRGYFGTSSITGDLSDNHDVISLKLFEITVERTPEEEKLHRDVFLP

\*\*. \*\*... \*\*\*\*\* \*\*\*,\*. \*\*\*\*\*. \*\*, \*\*\*,\* \*\*, \*\*, \*\*,..... . \*

ER EWKNCIDITGVRLPTGYFGASAGTGDLSNDHIISMKLFQLMVEHTPDEESIDWTKIEP

5

HP SVDNMKLP-----EMTAPL--PPLSGLALFLIVFFSLVFSVFAIVIGIILYNKWQEQRK

\*\*. . \* \* . \*. . \*\*. \* . \*\*... . \*. \* \* \* . . . \*. \*\*.. \*

ER SVNFLKSPKDNVDDPTGNFRSGPLTGWRVFLLLLCALLGIVVCAVVGAVVFQKRQERN-K

10 HP RFY

\*\*\*

ER RFY

15                   Furthermore, the search of the GenBank using the  
base sequences of the present cDNA has revealed the  
registration of sequences that shared a homology of 90% or  
more (for example, Accession No. AA262924) among ESTs.  
However, since they are partial sequences, it can not be  
20 judged whether or not they encode the same protein as the  
protein of the present invention.

<HP10719> (SEQ ID NOS: 63, 73 and 83)

Determination of the whole base sequence of the  
cDNA insert of clone HP10719 obtained from cDNA library of  
25 human kidney revealed the structure consisting of a 54-bp

5'-untranslated region, a 786-bp ORF, and a 576-bp 3'-untranslated region. The ORF encodes a protein consisting of 261 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 23 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 33 kDa that was larger than the molecular weight of 27,435 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from asparagine at position 19.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse endomucin (Accession No. AAD05208). Table 20 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse endomucin (MM). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 47.9% in the entire region.

Table 20

```

HP MELLQVTIL-FLLP-SIC-SSNSTGVL-EAANNSLVVTTTKPSITTPNTESLQKNVVTPT
    * *.*,*.* ***,*.* *.....* .. .. ..***.*.*.*..*..*..*.
5  MM MRLLQATVLFLLSNSLCHSEDGKDVQNDSIPTPAETSTTKASVTIPGIVSV-TNPNKPA

HP TGTPPKGITITNELLKMSLMSTATFLTSTKDEGLKATTTDVRKNDISIISNVTVTSVTLPNVA
    .**.*.*..... . **..* . **, .. . **.. .*.* . ..**..... **
MM DGTPEGTTKSDVSQTSLSVTTINSLTTPKHEVGTTTEGPLRNESSTMKITVPNTPTSNAN
10 HP STLQSSPKKTETQSSIKTTEIPGSVLQPDASPSKTGTLTSIPVTIPENTSQSQVIGTEGG
    ***,*.* *..** . . . . .*,** . . . . . * . . **.
MM STLPGSQNKITTQ-----LLDALPKITATPS-----ASLTTAHTMSLLQDTEDR

15 HP KNASTSATRSYSSIILPVVIALIVITLSVFVLVGLYRMCWKADPGTPENGNDQPQSDKE
    * *,*.*.*.*****.***** **,*****.*** *****
MM KIATTPSTTPSYSSIILPVVIALVVITLLVFTLVGLYRICWKRDPGTPENGNDQPQSDKE

HP SVKLLTVKTISHESGEHSAQGKTKN
20 *****

MM SVKLLTVKTISHESGEHSAQGKTKN

```

The search of the GenBank using the base sequences  
25 of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example, Accession No. AA486620) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10720> (SEQ ID NOS: 64, 74 and 84)

Determination of the whole base sequence of the cDNA insert of clone HP10720 obtained from cDNA library of human kidney revealed the structure consisting of a 25-bp 5'-untranslated region, a 669-bp ORF, and a 653-bp 3'-untranslated region. The ORF encodes a protein consisting of 222 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 24 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 28 kDa that was somewhat larger than the molecular weight of 25,219 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 35 kDa. In addition, there exist in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Val-Thr at position 76 and Asn-His-Thr at position 93). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to

expect that the mature protein starts from glutamic acid at position 15.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI792241) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

10           <HP10721> (SEQ ID NOS: 65, 75 and 85)

Determination of the whole base sequence of the cDNA insert of clone HP10721 obtained from cDNA library of human kidney revealed the structure consisting of a 74-bp 5'-untranslated region, a 552-bp ORF, and a 1658-bp 3'-untranslated region. The ORF encodes a protein consisting of 183 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 25 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 23 kDa that was somewhat larger than the molecular weight of 19,989 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 22 kDa. Application of the (-3,-1) rule, a method for predicting the

15

20

25

cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamic acid at position 25.

The search of the GenBank using the base sequences  
5 of the present cDNA has revealed the registration of  
sequences that shared a homology of 90% or more (for example,  
Accession No. R27187) among ESTs. However, since they are  
partial sequences, it can not be judged whether or not they  
encode the same protein as the protein of the present  
10 invention.

<HP10725> (SEQ ID NOS: 66, 76 and 86)

Determination of the whole base sequence of the  
cDNA insert of clone HP10725 obtained from cDNA library of  
human kidney revealed the structure consisting of a 235-bp  
15 5'-untranslated region, a 789-bp ORF, and a 713-bp 3'-  
untranslated region. The ORF encodes a protein consisting of  
262 amino acid residues and there existed one putative  
transmembrane domain. Figure 26 depicts the  
hydrophobicity/hydrophilicity profile, obtained by the Kyte-  
20 Doolittle method, of the present protein. In vitro  
translation resulted in formation of a translation product  
of high molecular weight.

The search of the GenBank using the base sequences  
of the present cDNA has revealed the registration of  
25 sequences that shared a homology of 90% or more (for example,

Accession No. A1127782) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

5                   <HP10727> (SEQ ID NOS: 67, 77 and 87)

Determination of the whole base sequence of the cDNA insert of clone HP10727 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 102-bp 5'-untranslated region, a 507-bp ORF, and a 947-  
10 bp 3'-untranslated region. The ORF encodes a protein consisting of 168 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 27 depicts the hydrophobicity/hydrophilicity profile, obtained by the  
15 Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 24 kDa that was larger than the molecular weight of 17,822 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 23 kDa.  
20 Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from lysine at position 29.

The search of the GenBank using the base sequences  
25 of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example, Accession No. R80316) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10728> (SEQ ID NOS: 68, 78 and 88)

Determination of the whole base sequence of the cDNA insert of clone HP10728 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 221-bp 5'-untranslated region, a 732-bp ORF, and a 902-bp 3'-untranslated region. The ORF encodes a protein consisting of 243 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 28 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 30 kDa that was larger than the molecular weight of 26,534 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H23535) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.



<HP10730> (SEQ ID NOS: 69, 79 and 89)

Determination of the whole base sequence of the cDNA insert of clone HP10730 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 27-bp 5'-untranslated region, a 1287-bp ORF, and a 1216-bp 3'-untranslated region. The ORF encodes a protein consisting of 428 amino acid residues and there existed one putative transmembrane domain. Figure 29 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 50 kDa that was somewhat larger than the molecular weight of 48,992 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. C19105) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10742> (SEQ ID NOS: 70, 80 and 90)

Determination of the whole base sequence of the cDNA insert of clone HP10742 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 231-bp 5'-untranslated region, a 852-bp ORF, and a 828-

bp 3'-untranslated region. The ORF encodes a protein consisting of 283 amino acid residues and there existed two putative transmembrane domains. Figure 30 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 30 kDa that was smaller than the molecular weight of 31,629 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T35949) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03800> (SEQ ID NOS: 91, 101 and 111)

Determination of the whole base sequence of the cDNA insert of clone HP03800 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 67-bp 5'-untranslated region, a 1431-bp ORF, and a 135-bp 3'-untranslated region. The ORF encodes a protein consisting of 476 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 31 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In

vitro translation resulted in formation of a translation product of 55 kDa that was almost identical with the molecular weight of 54,110 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 58 kDa. In addition, there exist in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Lys-Thr at position 81, Asn-Met-Thr at position 132, Asn-Val-Thr at position 307 and Asn-Gln-Thr at position 346). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from leucine at position 23.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mosquito vitellogenic carboxypeptidase (Accession No. P42660). Table 21 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mosquito vitellogenic carboxypeptidase (VC). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 44.5% in the entire region. In addition, the C-terminal portion beginning from alanine at position 182 matched with

human probable carboxypeptidase (Accession No. AAC23787)  
except one amino acid residue.

Table 21

5

HP MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPK-GDSGQPLFLTPYIEAGKIQKG

... \* \*. \*\* \* \*\* \*\*\*\*\* ... \*\*\*...

VC MVKFHLLVLIAFTCYTCSDATLWNPYKKLMRGSASPPRPGESGEPLFLTPLLQDGKIEEA

10

HP RELSLVGPPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSM

\*. . \*. . . . \*\*. \*\*. \*\*. . . \*\*\*\*\*. \*\*. . . \*. \*\*. . . \*\*\*\*\*. \*\*.

VC RNKARVNHMLSSVESYSGFMTVDAKHNSNLFFWYVPAKNNREQAPILVWLQGGPGASSL

HP FGLFVEHGPPYVVTSNMTLRDRDFPWTTL SMLYIDNPVGTGFSFTDDTHGYAVNEDDVAR

15

\*\*\* \* \*\* . . \* . . . . \* . . \* . \* . \*\*\*\*\* . . \*\* . \*\* . \*

VC FGMFEENGPFHIHRNKS VKQREYSWHQNHMMIYIDNPVGTGFSFTDSDEGYSTNEEHVGE

HP DLYSALIQFFQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHS LNPVREVKINLNGIAIGD

. \* . \*\*\* . \*\* . . \*\* . \*\*\*\*\* . \*\* . \*\*\* . . \*\* \* . . \*\*\*\*\* . \* . \*\*\*\*\*

20

VC NLMKFIQQFFVLFPNLLKHPFYISGESYGGKFVPAFGYAIH--NSQSQPKINLQGLAIGD

HP GYSDPESIIGGYAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGD

\*\*\* \*\* . . . \* \* \*\* . \*\* \* . . \* \* . . . \* . . . . \* . . . \* \*\*

VC GYTDPLNQL-NYGEYLYELGLIDLNGRKKFDEDTAAAIACAERKDMNSANRLIQGLFDG-

VC LDGQESYFKKVTGFSSYYNFIKGDEESKQDSVLMEFLSNPEVRKGIHVGELPFHDS DGHN

VC KVAEMLSEDTLDTVAPWVSKLLSHYRVLFYNGQLDIICAYPMTVDFLMKMPFDGDSEYKR

VC ANRE---IYRVDGEIAGYKKRAGRLQEVLI RNAGHMVPRDQPKWAFDMITSFTHKNYL

15

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA095665) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

Determination of the whole base sequence of the  
25 cdna insert of clone HP03831 obtained from cdna library of

human kidney revealed the structure consisting of a 191-bp 5'-untranslated region, a 681-bp ORF, and a 223-bp 3'-untranslated region. The ORF encodes a protein consisting of 226 amino acid residues and there existed four putative transmembrane domains. Figure 32 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human claudin-10 (Accession No. NP\_008915). Table 22 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human claudin-10 (CD). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 76.2% in the entire region. The C-terminal region downstream from glycine at position 72 completely matched with that sequence.

Table 22

120

HP MSRAQIWALVSGVGGFGALVAATTSNEWKVTTTRASSVITATWVYQGLWMNCAGNALGS

..\* \*.. ..\* . . . . . \*\*\*.\* ...\*\*\*.. ...\*\*..\*.... \*

CD MASTASEIIAFMVSISGWLVSSLTPTDYWKVSTIDGTVITTATYWANLWKACVTDSTGV

5 HP FHCRPHFTIFKVAGYIQACRGLMIAAVSLGFFGSIFALFGMKCTKVGGSDKAKAKIACLA

.\*. ... ..\*\*\*\*\*

CD SNCKDFPSMLALDGYIQACRGLMIAAVSLGFFGSIFALFGMKCTKVGGSDKAKAKIACLA

HP GIVFILSGLCSMTGCSLYANKITTEFFDPLFVEQKYELGAALFIGWAGASLCIIGGVIFC

10 \*\*\*\*\*

CD GIVFILSGLCSMTGCSLYANKITTEFFDPLFVEQKYELGAALFIGWAGASLCIIGGVIFC

HP FSISDNNKTPRYTYNGATSVMSRRTKYHGGEDFKTTNPSKQFDKNAYV

\*\*\*\*\*

15 CD FSISDNNKTPRYTYNGATSVMSRRTKYHGGEDFKTTNPSKQFDKNAYV

---

Furthermore, the search of the GenBank using the  
base sequences of the present cDNA has revealed the  
20 registration of sequences that shared a homology of 90% or  
more (for example, Accession No. N41613) among ESTs. However,  
since they are partial sequences, it can not be judged  
whether or not they encode the same protein as the protein  
of the present invention.

25 &lt;HP03879&gt; (SEQ ID NOS: 93, 103 and 113)

Determination of the whole base sequence of the cDNA insert of clone HP03879 obtained from cDNA library of human kidney revealed the structure consisting of a 33-bp 5'-untranslated region, a 918-bp ORF, and a 651-bp 3'-untranslated region. The ORF encodes a protein consisting of 305 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 33 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 34 kDa that was almost identical with the molecular weight of 34,073 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human NADH-cytochrome b5 reductase (Accession No. Y09501). Table 23 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human NADH-cytochrome b5 reductase (CT). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 63.5% in the entire region other than the N-terminal region.



Table 23

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|    |    |  |  |
|----|----|--|--|
|    | HP | MGIQTSPVLLASLGVGLVTLLGLAVGSYLVRSSRRPQVTLLDPNEKYLLRLLDKTTVSHN |  |
|    |    |  | * . ** * . ** . * . ** *** . * . . . ** .  |
| 5  | CT | MGAQLSTLGHMVLFPVWFLYSLMKLFQRS-TPAITLESPDIKYPLRLIDREIISHD     |  |
|    | HP | TKRFRFALPTAHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQGYVDLVIKVYLKG  |  |
|    |    |  | * . ***** . . * . ***** . ***** . ***** . ** . ***** . ** . * . * . ***** . *          |
|    | CT | TRRFRFALPSPQHILGLPVGQHIYLSARIDGNLVVRPYTPISSDDDKGFVDLVIKVYFKD |  |
| 10 |    |  |  |
|    | HP | VHPKFPEGGKMSQYLDLKVGDVVEFRGPSGLLTYTGKGFNIQPNKKSPPPEPRVAKKLG  |  |
|    |    |  | . ***** . ***** . * . . ** . ***** . * *** . * . * . *** * * . . * . *                 |
|    | CT | THPKFPAGGKMSQYLESMQIGDTIEFRGPSGLLVYQGKGKFAIRPDKKSNIIRTVKSVG  |  |
|    |    |  |  |
| 15 | HP | MIAGGTGITPMLQLIRAILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFLW  |  |
|    |    |  | ***** . ***** . **** . * * . * * ***** . ** . **** . . . . *****                       |
|    | CT | MIAGGTGITPMLQVIRAIMKDPDDHTVCHLLFANQTEKDILLRPELEELRNKHSARFKLW |  |
|    |    |  |  |
|    | HP | FTLDHPPKDWAYSKGFVTADMIREHLPAPGDDVLVLLCGPPPMVQLACHPNLDKLGYSQK |  |
| 20 |    |  | . *** . * . * . * . *** . . . . *** . *** . * . . . *** . ***** . * ** ***** . * . . . |
|    | CT | YTLDRAPEAWDYGQGFVNEEMIRDHLPPEEEPLVLMCGPPPMIQYACLPNLDHVGHPT   |  |
|    |    |  |  |
|    | HP | MRFTY  |  |
|    |    |  | . * . .  |
| 25 | CT | RCFVF  |  |

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The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. F06459) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

10                   <HP03880> (SEQ ID NOS: 94, 104 and 114)

Determination of the whole base sequence of the cDNA insert of clone HP03880 obtained from cDNA library of human kidney revealed the structure consisting of a 98-bp 5'-untranslated region, a 684-bp ORF, and a 115-bp 3'-untranslated region. The ORF encodes a protein consisting of 227 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 34 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 28 kDa that was somewhat larger than the molecular weight of 25,717 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 27 kDa. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to

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20

25

expect that the mature protein starts from aspartic acid at position 23.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to rat phosphatidylethanolamine-binding protein (Accession No. P31044). Table 24 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and rat phosphatidylethanolamine-binding protein (RN). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 37.6% in the region of 133 amino acid residues other than the N-terminal region.

Table 24

---

|    |  |
|----|--|
| 20 | HP MGWTMRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKV |
|    | RN MAADISQWAGPLSLQEVDEPPQHALRVDYGGVTV                          |
|    | HP VPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFRHWLVTDIKG |
|    | ... * * *.**..***** .*. * *.**..**                             |
| 25 | RN DELGKVLTPQVMNRPSSISWDGLDPGKLYTLVLTDPDAPSRKDPKFREWHHFLVVMKG  |

HP ADLKKGKIQQQELSA YQAPSPPAHSGFHRYQFFVYLQEGKV---ISLLP-KENKTRGSWK  
 . \* . . \* .        \*\* . \* . . . \*\* . . \* . \*\*\* . . \*\* \*\* . . . . \* . \* . . . \*\* . \*  
 RN NDISSGTV----LSEYVGS GPPKDTGLHRYVWL VYEQEQLNCDEPILSNKSGDNRGKFK

5

HP MDRFLNRFHLGEPEASTQFMTQNYQDSPTLQAPRERASEPKHKNQAEIAAC  
... \* ... \*\*\*. \* \*. \* \* .. .. \*. \*.  
RN VESFRKKYHLGAPVAGTCFQAEWDDSVPKLHDQLAGK

10

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H83784) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10704> (SEQ ID NOS: 95, 105 and 115)

Determination of the whole base sequence of the  
20 cDNA insert of clone HP10704 obtained from cDNA library of  
human kidney revealed the structure consisting of a 141-bp  
5'-untranslated region, a 1326-bp ORF, and a 399-bp 3'-  
untranslated region. The ORF encodes a protein consisting of  
441 amino acid residues and there existed eight putative  
25 transmembrane domains. Figure 35 depicts the

25

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

5           The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human unknown gene product (Accession No. AAC27544). Table 25 shows the comparison between amino acid sequences of the human protein of the present invention  
10       (HP) and human unknown gene product (UP). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins  
15       shared a homology of 39.1% in the entire region.

Table 25

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|    |  |
|----|--|
| HP | MAIHKALVMCLGLPLFLFPG-AWAQGHVPPGCSQGLNPLYYNLCDRSGAWGIVLE        |
| 20 | * **.... * ... ..** . * * * .*** .. ****.*                     |
|    | UN MFVASERKMRAHQVLTFLLLFVITSVASENASTSRGCGDLLPQYVSLCDLDAIWGIVVE |
|    | HP AVAGAGIVTTFVLTIILVASLPFVQDTKKRSLGTQVFLLGTLGLFCLVFACVVKPDFS  |
|    | ***** ..*..* .**...***.....*.* * . ***** *..** ... * .         |
| 25 | UN AVAGAGALITLLLMLILLVRLPFIKEKEKSPVGLHFLFLLGTLGLFGLTFAFIIQEDET |

127

HP TCASRRFLFGVLFALCFSCLAHVFAFNFLARKNHGPRGWVIFTVALLTLVEVIINTEW

. \*. \*\*\*\*. \*\*\*\*. \*\*\*\*. .... .. \*. \*.. \*\* \*\* . . . \*\* \* \*\*. \*\*\*\*. \*\*

UN ICSVRRFLWGVLFALCFSCLLSQAWRVRLVRHGTGPAGWQLVGLALCLMLVQVIIAVEW

5

HP LIITLVRGSGEGGPQGNSSAGWAVASPCAIANMDFVMALIYVMLLLLGAFLGAWPALCGR

\*. \*. \* .. .. \*\* . \*\*\*\*\* \*. \*\*.. .. \* . \*\*\*\*.

UN LVLTVLR-----DT-----RPACAYEPMDFVMALIYDMVLLVVTGLALFTLCGK

10

HP YKRWRKHGVFVLLTTATSVAIWVWVIVMYTYGN-KQHNSPTWDDPTLAIALAANAWAFVL

. \*\*\*\*. \*. \*. \*. \*. \*\* \*\*\*\*. \*. \*\* . \*\* \* ... . \*. \*\*\*\*\*. \*\*\*\*. \*. \*\*.

UN FKRWKLNGAFLITAFLSVLIWVAWMTMYLFGNVKLQQGDAWNDPTLAITLAASGWVFVI

HP FYVIPEVSQVTKSSPEQSYQGDMYPTRGVGY-ETILKEQ-KGQSMFVENKAFSMDEPVAA

15

\*. \*. \*\*\*\*. . \* .. \*. . . \*. \*\* .. \*. . . . \*\*\*\*\*. \*\*

UN FHAIPEI-HCTLLPALQENTPNYFDTSQPRMRETAFEEDVQLPRAYMENKAFSMDEHNAA

HP KRPVS-PYSGYNGQLLTSVYQPTMALMHKVPSEGAYDIILPRATANSQVMGSANSTLRA

\*. . . \* . . . . \*. . . . . \* . . . . \* . \* . . . . . \*

20

UN LRTAGFPNGSLGKRPSGLGKRPSAPFRSNVYQPTMAVVLNGGTIPTAPPSHTGRHLW

HP EDMYSAQSHQAATPPKDGKNSQVFRNPYVWD

of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA346702) among ESTs. However, since they are partial sequences, it can not be judged whether or not they  
5 encode the same protein as the protein of the present invention.

<HP10715> (SEQ ID NOS: 96, 106 and 116)

Determination of the whole base sequence of the cDNA insert of clone HP10715 obtained from cDNA library of  
10 human umbilical cord blood revealed the structure consisting of a 49-bp 5'-untranslated region, a 798-bp ORF, and a 1351-bp 3'-untranslated region. The ORF encodes a protein consisting of 265 amino acid residues and there existed two putative transmembrane domains. Figure 36 depicts the  
15 hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 43 kDa that was larger than the molecular weight of 29,217 predicted from the ORF.

20 The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI381750) among ESTs. However, since they are partial sequences, it can not be judged whether or not they  
25 encode the same protein as the protein of the present

invention.

<HP10724> (SEQ ID NOS: 97, 107 and 117)

Determination of the whole base sequence of the cDNA insert of clone HP10724 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 68-bp 5'-untranslated region, a 627-bp ORF, and a 1485-bp 3'-untranslated region. The ORF encodes a protein consisting of 208 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 37 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 24 kDa that was almost identical with the molecular weight of 23,850 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T78035) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10733> (SEQ ID NOS: 98, 108 and 118)

Determination of the whole base sequence of the cDNA insert of clone HP10733 obtained from cDNA library of human umbilical cord blood revealed the structure consisting



of a 102-bp 5'-untranslated region, a 1203-bp ORF, and a 222-bp 3'-untranslated region. The ORF encodes a protein consisting of 400 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 38 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 50 kDa that was larger than the molecular weight of 43,151 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 54 kDa. In addition, there exist in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Leu-Thr at position 52, Asn-Ala-Ser at position 131, Asn-Ile-Thr at position 145 and Asn-Leu-Ser at position 343). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from arginine at position 33.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Drosophila melanogaster* GOLIATH protein (Accession No. Q06003). Table 26 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Drosophila melanogaster*

GOLIATH protein (DM). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 35.0% in the entire region.

Table 26

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|    |  |
|----|--|
| 10 | HP MAWRRREASVGARGVLALALLALALCVPGARGRALEWFSAVVNIEYVDPQTNLTVWSVSE  |
|    | HP SGRFGDSSPKEGAHGLVGVPWAPGGDLEGCAPDTRFFVPEPGGRGAAPWVALVARGGCTF  |
|    | HP KDKVLVAARRNASAVVLYNEERYGNITLPM SHAGTGNIVVIMISYPKGREILEL-VQKGI   |
| 15 | <div style="display: flex; justify-content: space-between;"> <div> DM </div> <div> *   *... .. *.*..   .*. * ..** </div> </div> <div style="display: flex; justify-content: space-between; margin-top: 10px;"> <div> DM </div> <div> MQLEKMQIKGKTRNIAAVITYQNIGQDLSLTDKGY </div> </div> |
|    | HP PVTMTIGVGTRHVQEF--ISGQSVVFVAIAFITMMIISLAWLIFYYIQRFLY-TGSQIGS  |
|    | <div style="display: flex; justify-content: space-between;"> <div> **..*   * * *... ..   **. **. *.**   .   * ***** *   ...   * </div> </div>  |
| 20 | DM NVTISIIIEGRRGVRTISSLNRTSVLFVSISFI--VDDILCWLIFYYIQRFRYMQAQDQQS   |
|    | HP QSHRKETKKVIGQLLLHTVKHGEKGIDVDAENCAVCIENFKVKDIIRILPCKHIFHRICI  |
|    | <div style="display: flex; justify-content: space-between;"> <div> ..   .   **. * ..   . * * ..   . *.*..   **. **. *.*   . *. ***** **   ** </div> </div>   |
|    | DM RNLC SVTKKAIMKIPTKTGKFSD-EKDLSDCCAICIEAYKPTDTIRILPCKHEFHKNCI  |

HP DPWLLDHRTCPMCKLDVIKALGYWGEPGDVQEMPAPESPGRDPAANLSLALPDDGGSDE

\*\*\*\*..\*\*\*\*\*.\* \*\* ... . \*. \* . . . . .

DM DPWLVHRTCPMCKLDVLFYGY-VVGDQIYQTPSPQHTAPIASIEEVPVIVVAVPHGPQ

5 HP SSPPSASPAESEPQCDPSFKGDAGENTALLEAGRSDSRHGGPIS

. . \* . . . \* . . . \* . . . . .

DM PLQPLQASNMSSFAPSHYFQSSRSPSSSVQQQLAPLTYQHPQQAASERGRRNSAPATMP

10                   The search of the GenBank using the base sequences  
of the present cDNA has revealed the registration of  
sequences that shared a homology of 90% or more (for example,  
Accession No. AI286184) among ESTs. However, since they are  
partial sequences, it can not be judged whether or not they  
15 encode the same protein as the protein of the present  
invention.

<HP10734> (SEQ ID NOS: 99, 109 and 119)

Determination of the whole base sequence of the  
cDNA insert of clone HP10734 obtained from cDNA library of  
20 human umbilical cord blood revealed the structure consisting  
of a 124-bp 5'-untranslated region, a 579-bp ORF, and a  
1202-bp 3'-untranslated region. The ORF encodes a protein  
consisting of 192 amino acid residues and there existed one  
putative transmembrane domain. Figure 39 depicts the  
25 hydrophobicity/hydrophilicity profile, obtained by the Kyte-

Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human sodium channel  $\beta 2$  subunit (Accession No. AAD47196). Table 27 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human sodium channel  $\beta 2$  subunit (SC). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 26.3% in the N-terminal region of 152 amino acid residues.

Table 27

---

|    |   |
|----|---|
| HP | MFCPLKLILLPVLLDYSLGLNDLNVS-PELTVHVGDSALMGCVFQS--TEDK            |
| 20 | ...*. *..... ....*. *.*** *.** . *.** * ..                      |
| SC | MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNH    |
| HP | CIFKIDWTLSPGEHAKDE-YVLYYYSNLSVPIGRFQNRVHLMGDNLCNDGSLLLQDVQEA    |
|    | *...** .. ..* .. . ....**.*. *. * ..*..** .                     |
| 25 | SC KQFSLNWTYQECNNCSEEMFLQFRMKIINLKLRFQDRVEFSGNPSKYDVSVMRLRNVQPE |

HP DQGTYICEIRLKGESQVFKKAVVLHVLPEEPKELMVHVGGGLIQMGCVFQSTEVKHAVTKVE

\*.\*.\*.\*.\* ... .\*.\*\* \*\*\* \* \*. ..

SC DEGIYNCYIMNPPDRHRGHGKIHLQVLMEEPPERDFTVAVIVGASVGGFLAVVILVLMVV

5

HP WIFSGRRRAKVTRRKHHCVREGSG

SC KCVRRKKEQKLSTDDLKTEEEGKTDGEGNPDDGAK

10

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. C03216) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10756> (SEQ ID NOS: 100, 110 and 120)

Determination of the whole base sequence of the cDNA insert of clone HP10756 obtained from cDNA library of human kidney revealed the structure consisting of a 49-bp 5'-untranslated region, a 783-bp ORF, and a 166-bp 3'-untranslated region. The ORF encodes a protein consisting of 260 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 40 depicts the

25

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was almost identical with the molecular weight of 27,356 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AW027769) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03670> (SEQ ID NOS: 121, 131 and 141)

Determination of the whole base sequence of the cDNA insert of clone HP03670 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 77-bp 5'-untranslated region, a 1014-bp ORF, and a 531-bp 3'-untranslated region. The ORF encodes a protein consisting of 337 amino acid residues and there existed at least seven putative transmembrane domains. Figure 41 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human hypothetical protein KIAA0260

(Accession No. BAA13390). Table 28 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human hypothetical protein KIAA0260 (KI). Therein, the marks of -, \*, and . represent

5 a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 57.6% in the entire region other than the N-terminal region. In

10 addition, the C-terminal region beginning from leucine at position 77 matched with human putative Sqv-7-like protein (Accession No. AJ005866) except one amino acid residue.

Table 28

15

HP

MTAGGQAEAEAGAGGEPG

KI NSWSPLGAAAAGPRAARPRRQATAAAAAAMAEVHRRQHARVKGEAPAKSSTLRDEEELGMA

20

HP AARLPSRVARLLSALFYGTCSFLIVLVNKAALLTTYGFPSPIFLGIGQMAATIMILYVSKL

. \*\*. \* \*\*\*. . \*\*\*\*\*. \*\*\*. . \*\*. \* \*\*\*. . . \*. \*\*\*. \*\*. . \*. \*. \*

KI SAETLTVFLKLLAAGFYGVSSFLIVVVNKSFLTNYRFPSSLCVGLGQMVATVAVLWVGKA

HP NKIIHFPDFDKKIPVKLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLETI

25

.... \*\*\*. \*. . . \* \* \*\*\*\*\* \*\*\*. \*. \*\* \*\*\*. \*\*\*. \*\*\*\*\*. \*. \* \*. \*.. \*..

KI LRVVKFPDLDRNVPRKTFPLPLLYFGNQITGLFSTKKLNLPMFTVLRRFSILFTMFAEGV

HP ILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLNDIFTAANGVYTKQKMDPK

. \* \* . \* . \* . . \* \* \* . \* . \* \* \* . \* \* . \* \* \* \* . \* . . \* \* . \* . \* \* \* . \* . \*

5 KI LLKKTFSWGIKMTVFAMIIGAFVAASSDLAFDLEGYAFILINDVLTAAANGAYVKQKLDISK

HP ELGKYGVLFYNACFMIIPTLIISVSTGDLQQATEFNQWKNVVFILQFLLSCFLGFLLMYS

\* \* \* \* \* . \* . \* \* \* \* \* . \* \* \* \* \* . \* . \* \* \* . \* . \* \* \* . \* . \* \* \* . \* . \* \* \* .

KI ELGKYGLLYYNALFMILPTLAIAYFTGDAQKAVEFEGWADTLFLLQFTLSCVMGFILMYA

10

HP TVLCSYNSALTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRYSFRTL

\* \* \* \* \* . \* \* \* \* \* . \* \* \* \* \* . \* \* \* \* \* . \* \* \* \* \* . \* \* \* \* \* . \* \* \* \* \* . \* \* \* \* \* .

KI TVLCTQYNSALTTTIVGCIKNILITYIGMVFGGDYIFTWTNFIGLNISIAGSLVYSYITF

15 HP SSQLKPKPVGEENICLDLKS

. . . . \* . \* . \* \* \* . \*

KI TEEQLSKQ-SEANNKLDIKGKAV

20

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R24922) among ESTs. However, since they are partial sequences, it can not be judged whether or not they

25 encode the same protein as the protein of the present



invention.

<HP03688> (SEQ ID NOS: 122, 132 and 142)

Determination of the whole base sequence of the cDNA insert of clone HP03688 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 35-bp 5'-untranslated region, a 711-bp ORF, and a 1729-bp 3'-untranslated region. The ORF encodes a protein consisting of 236 amino acid residues and there existed five putative transmembrane domains. Figure 42 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Caenorhabditis elegans* hypothetical protein W02D9 (Accession No. CAB03470). Table 29 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Caenorhabditis elegans* hypothetical protein W02D9 (CE). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 50.8% in the entire region other than the N-terminal

region.

Table 29

---

|    |    |  |
|----|----|--|
| 5  | HP | MAEAEE   |
|    | CE | MEILNLSSKFSLSDKPCQKFIFSLFSAVQNSRFKIISFPEIHQKPLPQEEMNSFGNASVD |
|    | HP | SPGDPGTASPRPLFAGLSDISISQDIPVEGEITIPMRSRIREFDSSTLNESVRNTIMRDL |
| 10 |    | **. . . **. *. *. *. *. **.                                  |
|    | CE | IDMLEQEMAAEQTANLSGNIAGMSAPKSSSNRRGPMQEVDLDAEFDTLLEPVWDTVKRDV |
|    | HP | KAVGKKFMHVLYPR-KSNTLLRDWDLWGPLICVTLALMLQRDSADSEKDGGPQFAEVFV  |
|    |    | . ** ** *. . . . *****. **. ***. **. . . . . ***. **.        |
| 15 | CE | LTVGAKFTHVVLPHGDKQQLLRDWDWGLFICVGLALLQH---NGGTESAPQFTQVFT    |
|    | HP | IWFAGVTITLNSKLLGGNISFFQSLCVLGYCILPLTVAMLICRLVLLADPGPVNFMVRL  |
|    |    | *. **. *. * * *****. ***. ** ** .. *. * . * . . * . **       |
|    | CE | ITFFGSVIVTANIKLLGGNISFFQSLCVIGYCLPPFVAAVLCSL-FLHGI---AFPLRL  |
| 20 | HP | FVVIVMFAWSIVASTAFLADSQPPNRRALAVYPVFLFYFVISWMILTFTPQ          |
|    |    | ... . *. **. ** . ***. ** .. * *. *****. ****..              |
|    | CE | LITSIGFVWSTYASMGFLAGCQPDKKRLVIYPVFLFYFVVSWMIIISHS            |

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Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T51465) among ESTs. However, 5 since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03825> (SEQ ID NOS: 123, 133 and 143)

Determination of the whole base sequence of the 10 cDNA insert of clone HP03825 obtained from cDNA library of human kidney revealed the structure consisting of a 20-bp 5'-untranslated region, a 1683-bp ORF, and a 36-bp 3'-untranslated region. The ORF encodes a protein consisting of 560 amino acid residues and there existed seven putative 15 transmembrane domains. Figure 43 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 56 kDa that was smaller than the molecular weight of 20 64,047 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Mycobacterium tuberculosis* hypothetical protein Rv0235c (Accession No. CAB07001). 25 Table 30 shows the comparison between amino acid sequences

of the human protein of the present invention (HP) and Mycobacterium tuberculosis hypothetical protein Rv0235c (MT). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 41.7% in the entire region other than the N-terminal region. In addition, the region from alanine at position 293 to proline at position 502 matched with human putative novel protein c360B4.1 (Accession No. CAB56180).

Table 30

---

|    |  |                             |
|----|--|-----------------------------|
| 15 | HP MAAPAESLRRRKTYGSDPEPESPPAPGRGPAGSPAHLHTGTFWLTRIVLLKALAFVYFVA  |                             |
|    |  | . . . **. *. * . . *. *. *  |
|    | MT   | MGWFSAPYWLGRLLALERGTAIIYLIA |
|    | HP FLVAFHQNKQLIGDRGLLPCRVLKKNFQQYFQDRTSWEVFSYMPITLWMDWSDMNSNLD   |                             |
| 20 | *. *. * . ***. *. ** . . * . * . . . . . *. * . . . * . . . *    |                             |
|    | MT FVAAAQQFRPLIGEHGMLPVPRYLAG-QSFWRTPSIFH-FRYSDRVFAGVCW--LGAVLS  |                             |
|    | HP LLALLGLGISSFVLITGCANMLLMAALWGLYMSLVNVGHVWYSFGWESQLLETGFLGIFL  |                             |
|    | * . * . *** . *. **. . ** *. *. ****. ***** ***** ***            |                             |
| 25 | MT --AAVVAGAASFVPLW--ATMLIWLTLWVLYLSIVNVGQAWYSFGWESLLLLETGFLMIFL |                             |

HP CPLWLSRLPQHPTSRIVLWGFRWLIFRIMLGAGLIKIRGDRCDRLTCMDPHYETQPM

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, *.
, *
***, **,
*****, ****, ****, ****,
*, *****

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MT GNERT-----APPILTLLA-RWLLFRVEFGAGLIKMRGDSCWRSLTCLYYHHETQPM

5

HP PNPVAYYLHHSPWWFHRFETLSNHFIELLVPFFLFLGRRACIIHGVLQILFQAVLIVSGN

\*.\*.....\*\* \* .\*\*.\*. .\*\*\*.\*.\*\*\*\* \*\* ..\* \* .....\* \*.\*\*\*

MT PGPLSWFFHHLPKPLHRIEVAGNHFAQLVVPFGLFTPQPAASIAAAIIVVTQLWLVASGN

10 HP LSFLNWLTMVPSLACFDDATLGFLFPSGPGSLKDRVLMQQRDIRGARPEPRFGSVVRRRAA

. \*.\*\*\*\*\*. \*\*\* . . . . . \* . . . \* \*.\*. . . \* ..\*..\* .

MT FSWLNWLTIL--LAC---SAID--TSS-AAAL----LPMPAQPALSAAPPQWFAGLV---V

HP NVSLGVLLAWLSVPVVLNLLSSRQVMNTHFNSLHIVNTYGAFGSITKERAEVILQGTASS

```
15      . .***  **      .  *****.* **  **.*.*.***** ..* **...**..*
```

MT VFTAAVLL--LSYWPARNLLSSHQRMMMSFNPFLVNTYGAFGSICRTRREVVIEGTDES

HP NASAPDAMWEDYEFKCKPGDPSRRPCLISPYHYRLDWLMWFAAFQTYEHNDWI IHLAGKL

. . . . \* . \*\*\*\*\* \*\*\*\*\* \* \* . \*\*\*\* \*\*\*\*\* . . \* . . . . \*

20 MT -PITEQTVWKAYEFKKGKPGDPRRLPRQWAPYHLRLDWLMWFAAISPGYALPWMTPLNRL

HP LASDAEALSLLAHNPFAGRPPPRWVRGEHYRYKFSRPGGRHAAEGKWWVRKRIGAYFPPL

\* . \* . . \* . \*\* \*\*\*\*\* . . . \*\*\* . \*\*\* . . \* . \* . \* . . . . . . . . . \*\*\* \* . \*\* \* \*\* \*

MT LRNDPATLKLLRHNPFP-QSPPRYVRAQLYQYRFTTVAELRRDRA-WWHRTLIGRYVPPM

25

HP SLEELRPYFRDRGWPLPGPL

\*\* ..

MT SLRKVASPPAD

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5

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA019047) among ESTs. However, since they are  
10 partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03877> (SEQ ID NOS: 124, 134 and 144)

Determination of the whole base sequence of the  
15 cDNA insert of clone HP03877 obtained from cDNA library of human kidney revealed the structure consisting of a 106-bp 5'-untranslated region, a 1221-bp ORF, and a 678-bp 3'-untranslated region. The ORF encodes a protein consisting of 406 amino acid residues and there existed four putative  
20 transmembrane domains. Figure 44 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 49 kDa that was somewhat larger than the molecular weight  
25 of 46,208 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Caenorhabditis elegans* hypothetical protein Y37D8A (Accession No. CAA21543). Table 31 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Caenorhabditis elegans* hypothetical protein Y37D8A (CE). Therein, the marks of -, \*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 50.2% in the intermediate region of 329 amino acid residues.

Table 31

| HP  | MAENG                               |
|---|-------------------------------------|
| CE MAKKQKKSTSEKSTVEFKEPPK PANSEERLVSTRQFLAKIGQKKLIKVKKNFRFSKKT    |                                     |
| HP KNC DQRRVAMNKEHHNGNFTDPSSVNEKKRREREERQNI VLWRQPLITLQYFSLEILVIL |                                     |
|   | . * ** . ** . ** . * * . . * . ** . |
| CE FIDFFSENQKKNCRLKPAGRGMKPSQSNTLNRMERETIVFWRRPHIVIPYALMEIAHLA    |                                     |
| HP KEWTSKLWHRQSIVVSFLLLLAVLIATYYVEGVHQYVQRIEKQFLLYAYWIGLGILSSV    |                                     |

\* \* . . . . . \* . \*.\*\*.\* \*\*\*. \* . . \*. \*\*.\*\*\*.

CE VELFFKILAHKTVLLLT AISIGLAVYGYHAPGAHQEHVQTIEKHILWWSWWVLLGVLSSI

5           \*\*\*, \*\*\*\*\*, \*\*\*\*\*, \*\*, \*\*\*\*\*, \*, \*\*, \*\*\*\*\*, \* \*\*, . . . . . \* \*, .

HP KVRIEACMWGIGTAIGELPPYFMARAARLSGAEPDDEEYQEFEEML—EHAESAQDFA—

\*\*\*. \*. \*\* \*\*\*\*. \*\*\*\*\*. \*\*, \*\*\*\*\*. \*\* \*. . . . \*

HP -SRAKLAVQKL VQKVGFFGILACASIPNPLFDLAGITCGHFLVPFWTFFGATLIGKAIK

```
. ***      *..   .... **  ***      ****
```

15

HP MHIQKIFVIITFSKHIVEQMVAFIGAVPGIGPSLQKPFQEYLEAQRQKLHHKSEMGTPOG

**\*\*.\*. \*\*\*.\*.\*.\*. \*.\*.\*. \*.\*\*.\*. \*.\*\*.\*. \*.\*\*.\*. \***

CE MHVQMGFVILAFSDHHAENFVKILEKIPAVGPYIRQPISDLLEKQRKALHKTPGEHSEQD

20 HP ENWLSWMFEKL VVVMVCYFILSIINSMAQSYAKRIQQRLNSEETK

CE LIDEENQSFEIEEEEEAVTPPSSCPLLLSDGFEGVVVKK



of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T18977) among ESTs. However, since they are partial sequences, it can not be judged whether or not they  
5 encode the same protein as the protein of the present invention.

<HP10765> (SEQ ID NOS: 125, 135 and 145)

Determination of the whole base sequence of the cDNA insert of clone HP10765 obtained from cDNA library of  
10 human umbilical cord blood revealed the structure consisting of a 30-bp 5'-untranslated region, a 1362-bp ORF, and a 166-bp 3'-untranslated region. The ORF encodes a protein consisting of 453 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative  
15 transmembrane domain in the inner portion. Figure 45 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 48 kDa that was almost identical with the molecular  
20 weight of 47,724 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI792834) among ESTs. However, since they are  
25 partial sequences, it can not be judged whether or not they

encode the same protein as the protein of the present invention.

<HP10766> (SEQ ID NOS: 126, 136 and 146)

Determination of the whole base sequence of the  
5 cDNA insert of clone HP10766 obtained from cDNA library of  
human kidney revealed the structure consisting of a 150-bp  
5'-untranslated region, a 180-bp ORF, and a 675-bp 3'-  
untranslated region. The ORF encodes a protein consisting of  
59 amino acid residues and there existed two putative  
10 transmembrane domains. Figure 46 depicts the  
hydrophobicity/hydrophilicity profile, obtained by the Kyte-  
Doolittle method, of the present protein. In vitro  
translation resulted in formation of a translation product  
of 10 kDa or less that was almost identical with the  
15 molecular weight of 6,098 predicted from the ORF.

The search of the GenBank using the base sequences  
of the present cDNA has revealed the registration of  
sequences that shared a homology of 90% or more (for example,  
Accession No. T85491) among ESTs. However, since they are  
20 partial sequences, it can not be judged whether or not they  
encode the same protein as the protein of the present  
invention.

<HP10770> (SEQ ID NOS: 127, 137 and 147)

Determination of the whole base sequence of the  
25 cDNA insert of clone HP10770 obtained from cDNA library of

human kidney revealed the structure consisting of a 150-bp 5'-untranslated region, a 633-bp ORF, and a 186-bp 3'-untranslated region. The ORF encodes a protein consisting of 210 amino acid residues and there existed two putative transmembrane domains. Figure 47 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was larger than the molecular weight of 22,156 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI792771) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10772> (SEQ ID NOS: 128, 138 and 148)

Determination of the whole base sequence of the cDNA insert of clone HP10772 obtained from cDNA library of human kidney revealed the structure consisting of a 19-bp 5'-untranslated region, a 498-bp ORF, and a 724-bp 3'-untranslated region. The ORF encodes a protein consisting of 165 amino acid residues and there existed four putative transmembrane domains. Figure 48 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

5           The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. F11871) among ESTs. However, since they are partial sequences, it can not be judged whether or not they  
10       encode the same protein as the protein of the present invention.

<HP10773> (SEQ ID NOS: 129, 139 and 149)

Determination of the whole base sequence of the cDNA insert of clone HP10773 obtained from cDNA library of  
15       human kidney revealed the structure consisting of a 186-bp 5'-untranslated region, a 489-bp ORF, and a 499-bp 3'-untranslated region. The ORF encodes a protein consisting of 162 amino acid residues and there existed four putative transmembrane domains. Figure 49 depicts the  
20       hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

          The search of the GenBank using the base sequences  
25       of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example, Accession No. N33828) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10776> (SEQ ID NOS: 130, 140 and 150)

Determination of the whole base sequence of the cDNA insert of clone HP10776 obtained from cDNA library of human kidney revealed the structure consisting of a 207-bp 5'-untranslated region, a 666-bp ORF, and a 139-bp 3'-untranslated region. The ORF encodes a protein consisting of 221 amino acid residues and there existed three putative transmembrane domains. Figure 50 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 30 kDa that was larger than the molecular weight of 24,883 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI929639) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

## INDUSTRIAL APPLICABILITY

The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs and eukaryotic cells expressing these DNAs. Since all of the proteins of the present invention are secreted or exist in the cell membrane, they are considered to be proteins controlling the proliferation and/or the differentiation of the cells. Accordingly, the proteins of the present invention can be employed as pharmaceuticals such as carcinostatic agents which act to control the proliferation and/or the differentiation of the cells, or as antigens for preparing antibodies against these proteins. The DNAs of the present invention can be utilized as probes for the genetic diagnosis and gene sources for the gene therapy. Furthermore, the DNAs can be utilized for expressing these proteins in large quantities. Cells into which these genes are introduced to express these proteins can be utilized for detection of the corresponding receptors or ligands, screening of novel small molecule pharmaceuticals and the like. The antibody of the present invention can be utilized for the detection, quantification, purification and the like of the protein of the present invention.

The present invention also provides genes

corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include  
5 contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements.  
10 The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate  
15 genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

Organisms that have enhanced, reduced, or modified  
20 expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and  
25 Morris, 1994, Trends Pharmacol. Sci. 15(7): 250-254;

Lavarosky et al., 1997, Biochem. Mol. Med. 62(1): 11-22; and Hampel, 1998, Prog. Nucleic Acid Res. Mol. Biol. 58: 1-39; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, Bioessays 14(9): 629-633; Zwaal et al., 1993, Proc. Natl. Acad. Sci. USA 90(16): 7431-7435; Clark et al., 1994, Proc. Natl. Acad. Sci. USA 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination,



preferably detected by positive/negative genetic selection strategies (Mansour et al., 1988, Nature 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are  
5 incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development  
10 of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s). Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such  
15 forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known  
20 techniques for determination of such domains from sequence information.

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and  
25 most preferably at least 75%) of the length of a disclosed

protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide, as determined by those of skill in the art. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is,

naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous, or related to that encoded by the polynucleotides.

5           The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

          The present invention also includes polynucleotides capable of hybridizing under reduced  
10           stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for  
15           example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 32

| Stringency Condition | Poly-nucleotide Hybrid | Hybrid Length (bp) <sup>1</sup> | Hybridization Temperature and Buffer <sup>1</sup> | Wash Temperature and Buffer <sup>1</sup> |
|----------------------|------------------------|---------------------------------|---|--|
| A                    | DNA : DNA              | ≥50                             | 65°C; 1×SSC -or- 42°C; 1×SSC, 50% formamide       | 65°C; 0.3×SSC                            |
| B                    | DNA : DNA              | <50                             | T <sub>B</sub> *; 1×SSC                           | T <sub>B</sub> *; 1×SSC                  |
| C                    | DNA : RNA              | ≥50                             | 67°C; 1×SSC -or- 45°C; 1×SSC, 50% formamide       | 67°C; 0.3×SSC                            |
| D                    | DNA : RNA              | <50                             | T <sub>D</sub> *; 1×SSC                           | T <sub>D</sub> *; 1×SSC                  |
| E                    | RNA : RNA              | ≥50                             | 70°C; 1×SSC -or- 50°C; 1×SSC, 50% formamide       | 70°C; 0.3×SSC                            |
| F                    | RNA : RNA              | <50                             | T <sub>F</sub> *; 1×SSC                           | T <sub>F</sub> *; 1×SSC                  |
| G                    | DNA : DNA              | ≥50                             | 65°C; 4×SSC -or- 42°C; 4×SSC, 50% formamide       | 65°C; 1×SSC                              |
| H                    | DNA : DNA              | <50                             | T <sub>H</sub> *; 4×SSC                           | T <sub>H</sub> *; 4×SSC                  |
| I                    | DNA : RNA              | ≥50                             | 67°C; 4×SSC -or- 45°C; 4×SSC, 50% formamide       | 67°C; 1×SSC                              |
| J                    | DNA : RNA              | <50                             | T <sub>J</sub> *; 4×SSC                           | T <sub>J</sub> *; 4×SSC                  |
| K                    | RNA : RNA              | ≥50                             | 70°C; 4×SSC -or- 50°C; 4×SSC, 50% formamide       | 67°C; 1×SSC                              |
| L                    | RNA : RNA              | <50                             | T <sub>L</sub> *; 2×SSC                           | T <sub>L</sub> *; 2×SSC                  |
| M                    | DNA : DNA              | ≥50                             | 50°C; 4×SSC -or- 40°C; 6×SSC, 50% formamide       | 50°C; 2×SSC                              |
| N                    | DNA : DNA              | <50                             | T <sub>N</sub> *; 6×SSC                           | T <sub>N</sub> *; 6×SSC                  |
| O                    | DNA : RNA              | ≥50                             | 55°C; 4×SSC -or- 42°C; 6×SSC, 50% formamide       | 55°C; 2×SSC                              |
| P                    | DNA : RNA              | <50                             | T <sub>P</sub> *; 6×SSC                           | T <sub>P</sub> *; 6×SSC                  |
| Q                    | RNA : RNA              | ≥50                             | 60°C; 4×SSC -or- 45°C; 6×SSC, 50% formamide       | 60°C; 2×SSC                              |
| R                    | RNA : RNA              | <50                             | T <sub>R</sub> *; 4×SSC                           | T <sub>R</sub> *; 4×SSC                  |

‡ : The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

† : SSPE (1×SSPE is 0.15M NaCl, 10mM NaH<sub>2</sub>PO<sub>4</sub>, and 1.25mM EDTA, pH7.4) can be substituted for SSC (1×SSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

\*T<sub>B</sub> - T<sub>R</sub> : The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T<sub>m</sub>) of the hybrid, where T<sub>m</sub> is determined according to the following equations. For hybrids less than 18 base pairs in length, T<sub>m</sub>(°C)=2(#of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T<sub>m</sub>(°C)=81.5 + 16.6(log<sub>10</sub>[Na<sup>+</sup>]) + 0.41 (%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na<sup>+</sup>] is the concentration of sodium ions in the hybridization buffer ([Na<sup>+</sup>] for 1×SSC=0.165M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and Current Protocols in Molecular Biology, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

## CLAIMS

1. A protein comprising any one of an amino acid  
sequence selected from the group consisting of SEQ ID NOS: 1  
5 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130.

2. An isolated DNA encoding the protein according to  
Claim 1.

3. An isolated cDNA comprising any one of a base  
sequence selected from the group consisting of SEQ ID NOS:  
10 11 to 20, 41 to 50, 71 to 80, 101 to 110 and 131 to 140.

4. The cDNA according to Claim 3 consisting of any  
one of a base sequence selected from the group consisting of  
SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141  
to 150.

15 5. An expression vector that is capable of expressing  
the DNA according to any one of Claim 2 to Claim 4 by in  
vitro translation or in eukaryotic cells.

6. A transformed eukaryotic cell that is capable of  
expressing the DNA according to any one of Claim 2 to Claim  
20 4 and of producing the protein according to Claim 1.

7. An antibody directed to the protein according to  
Claim 1.

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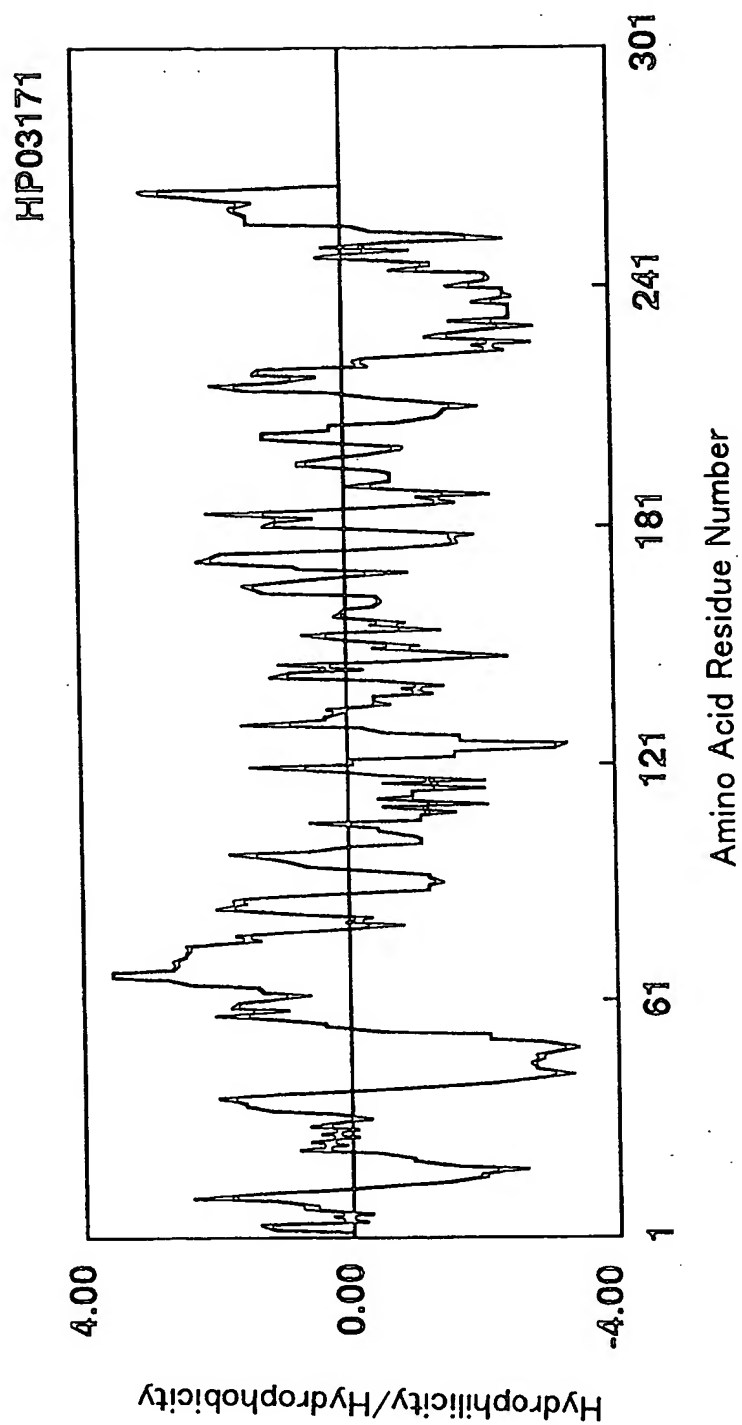


Fig.1



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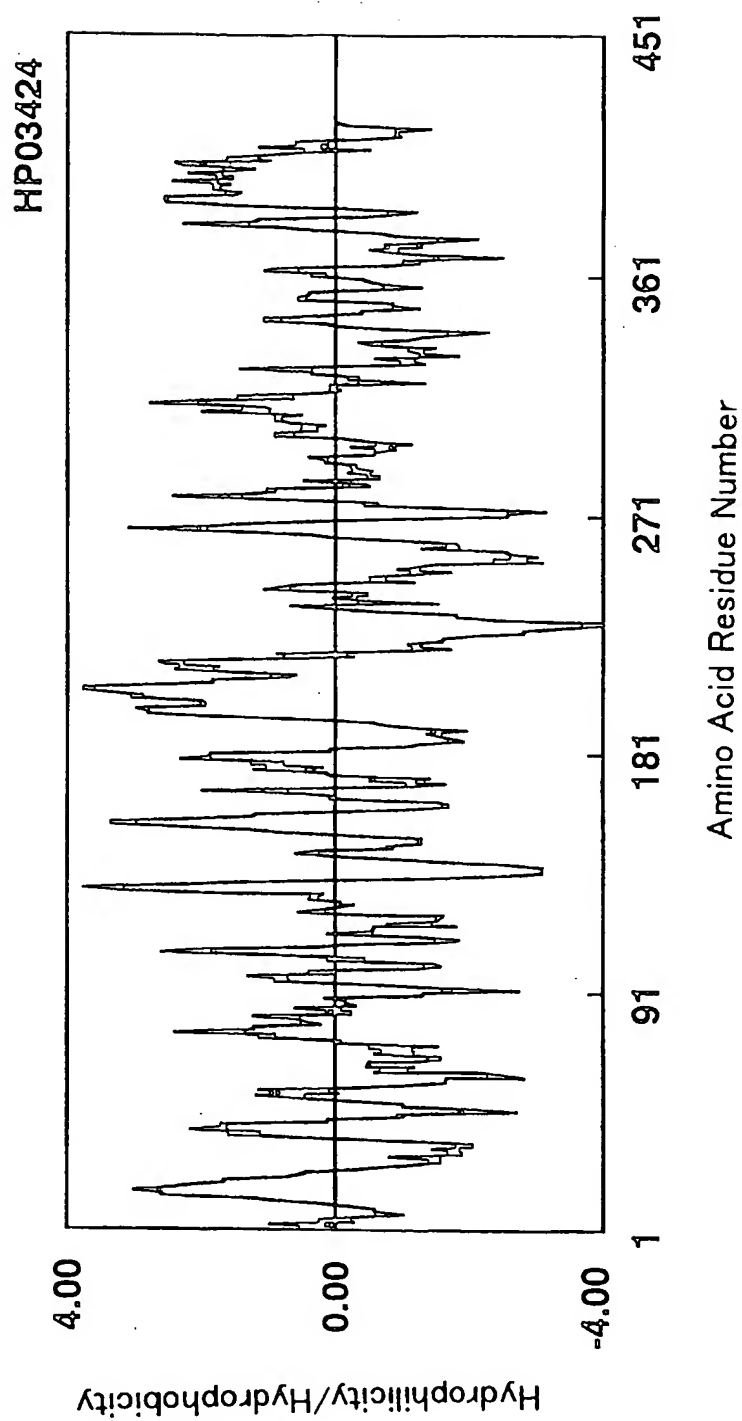


Fig.2

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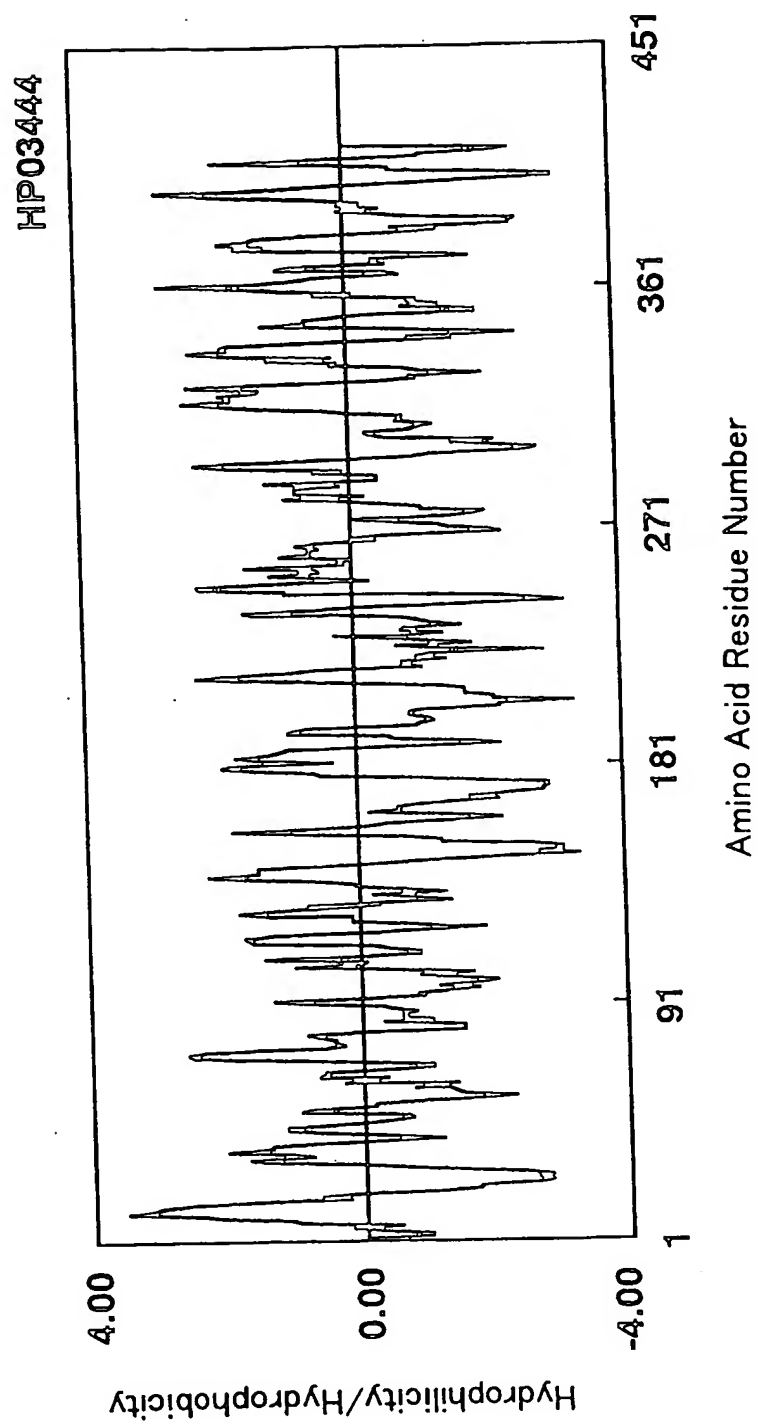


Fig.3

4/50

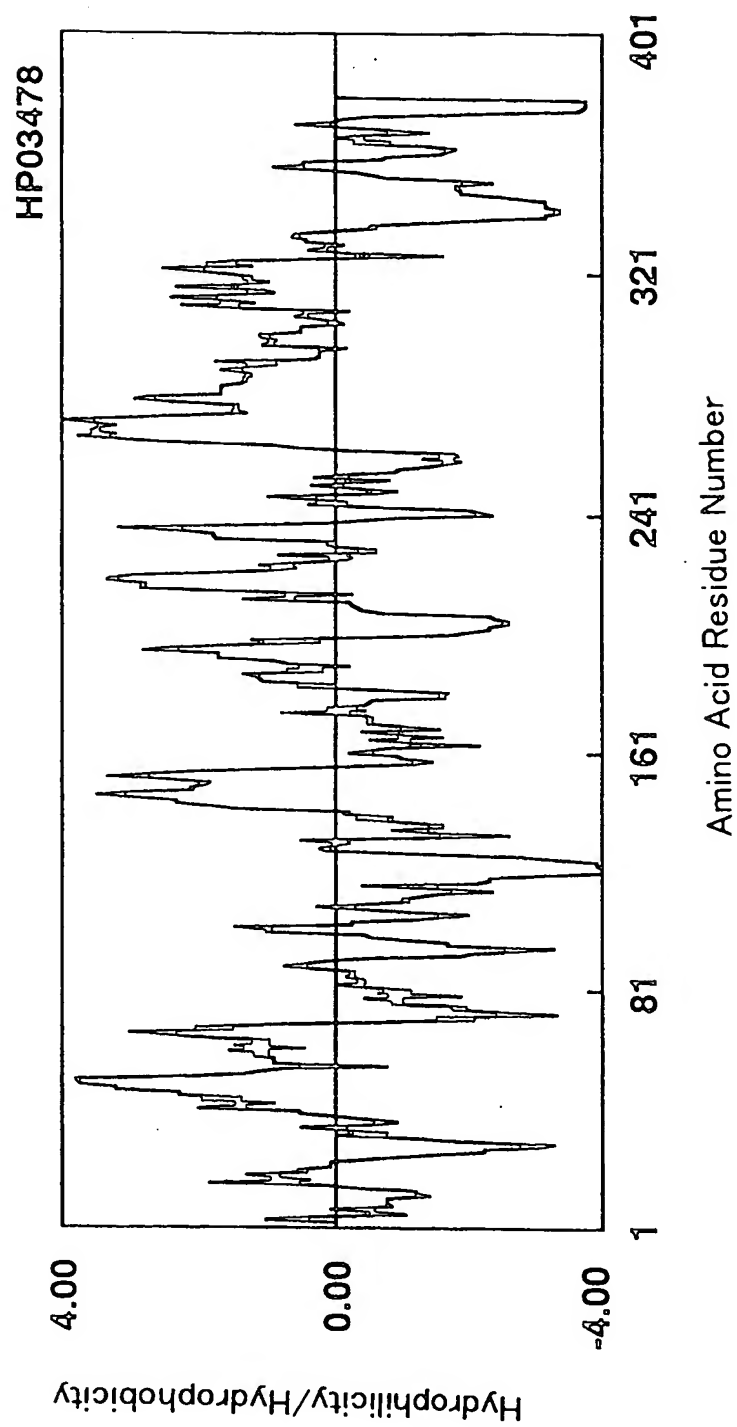


Fig.4

5/50

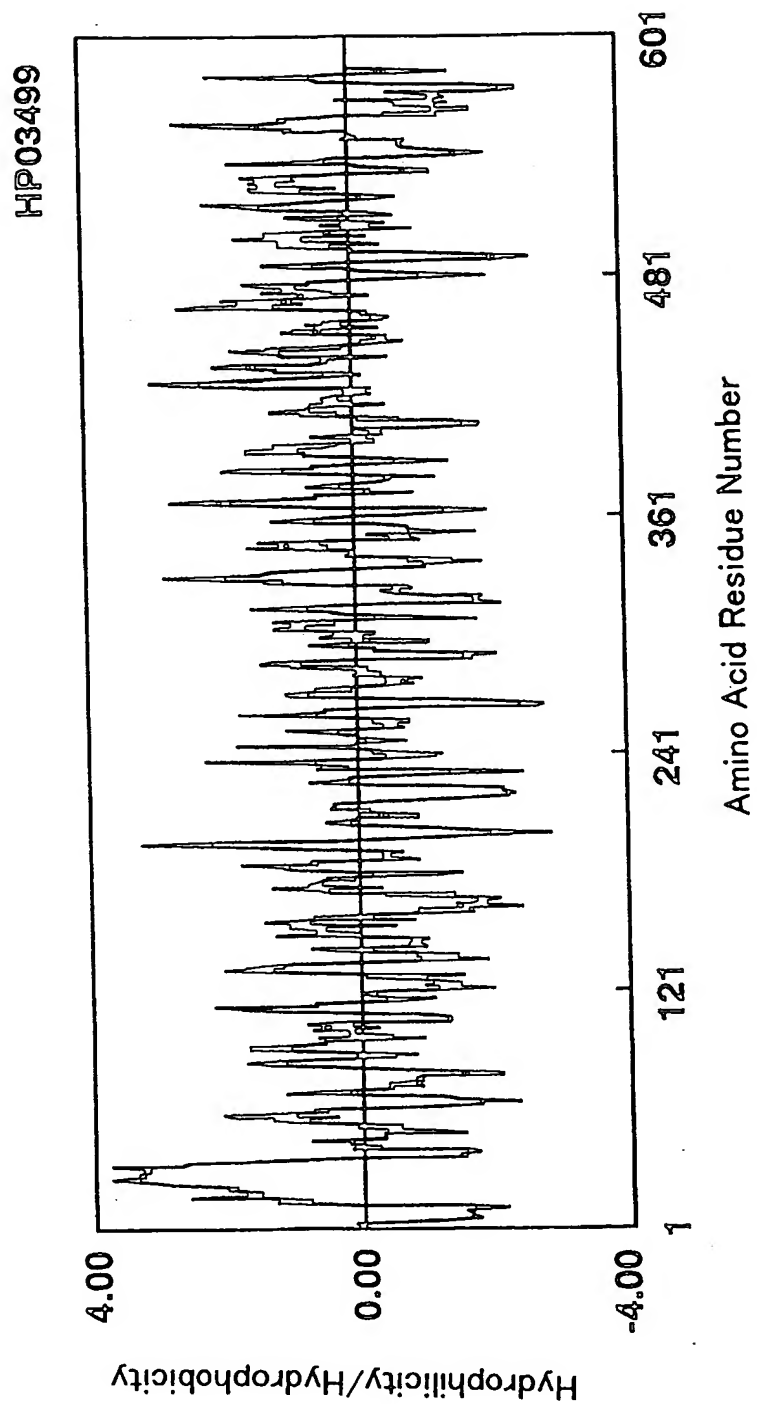


Fig.5

6/50

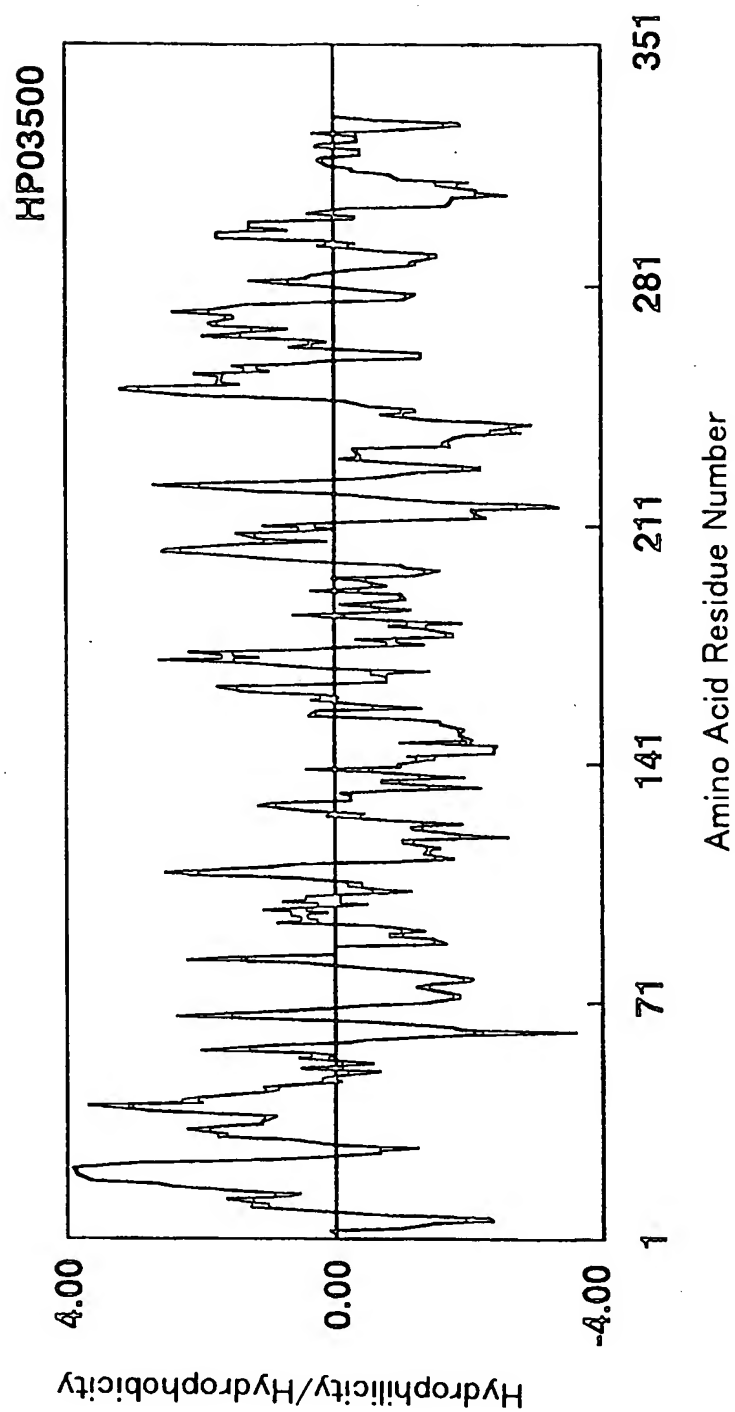


Fig.6

7/50

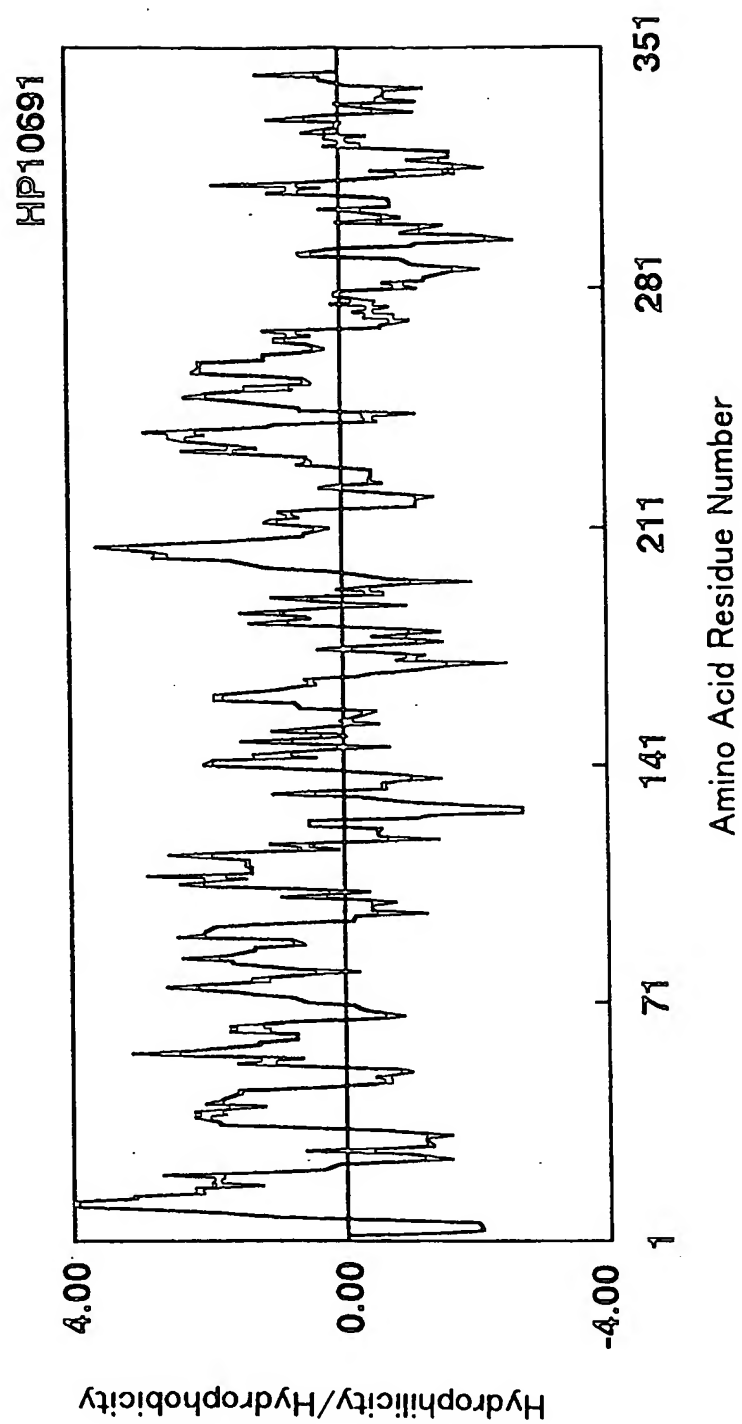


Fig.7

8/50

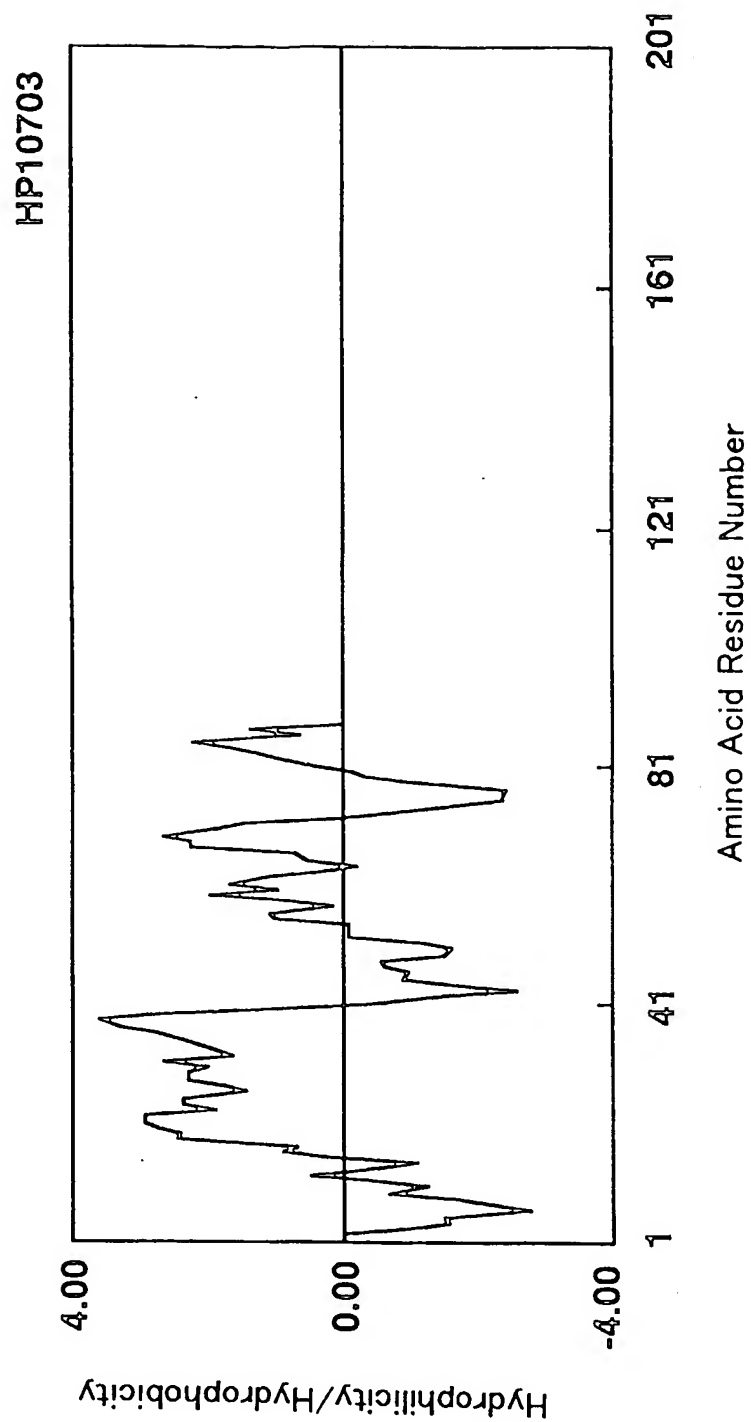


Fig.8

9/50

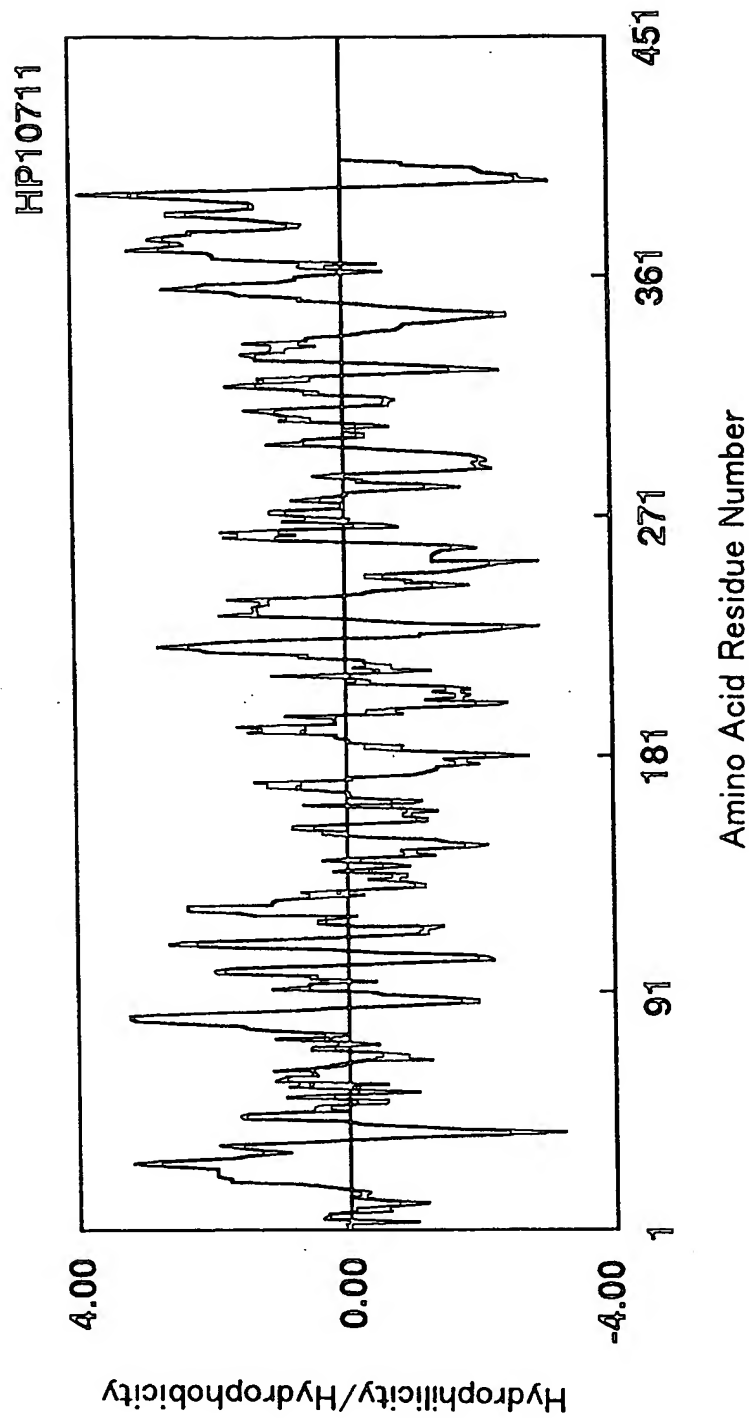


Fig.9



10/50

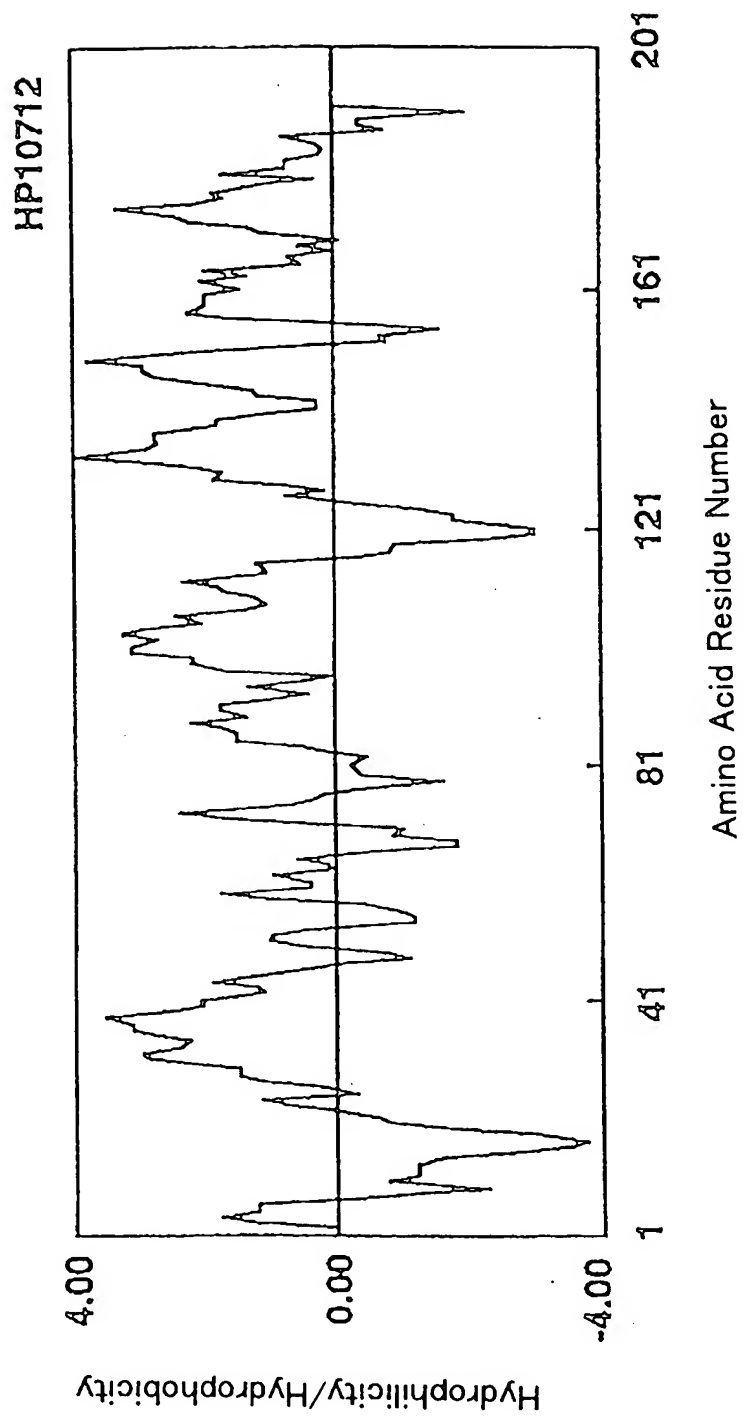


Fig.10

11/50

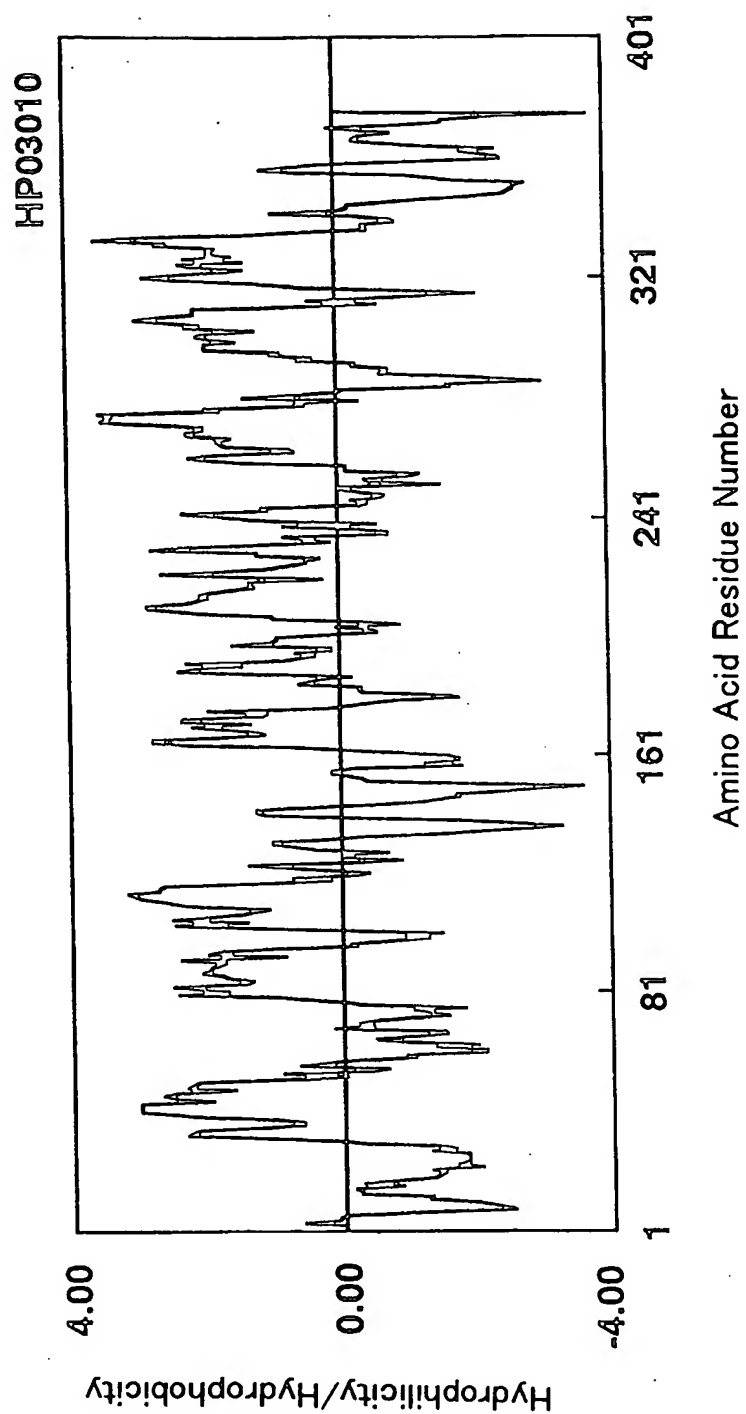


Fig.11

12/50

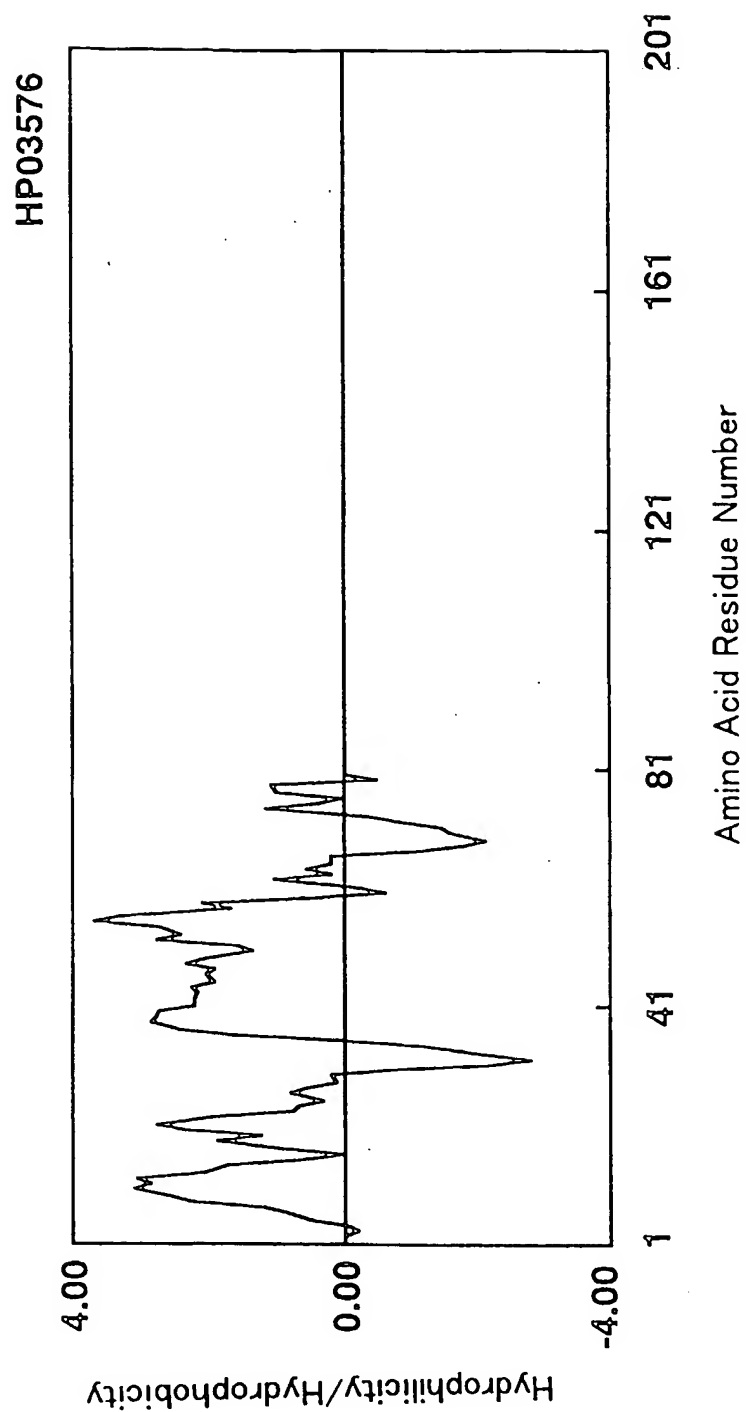


Fig.12

13/50

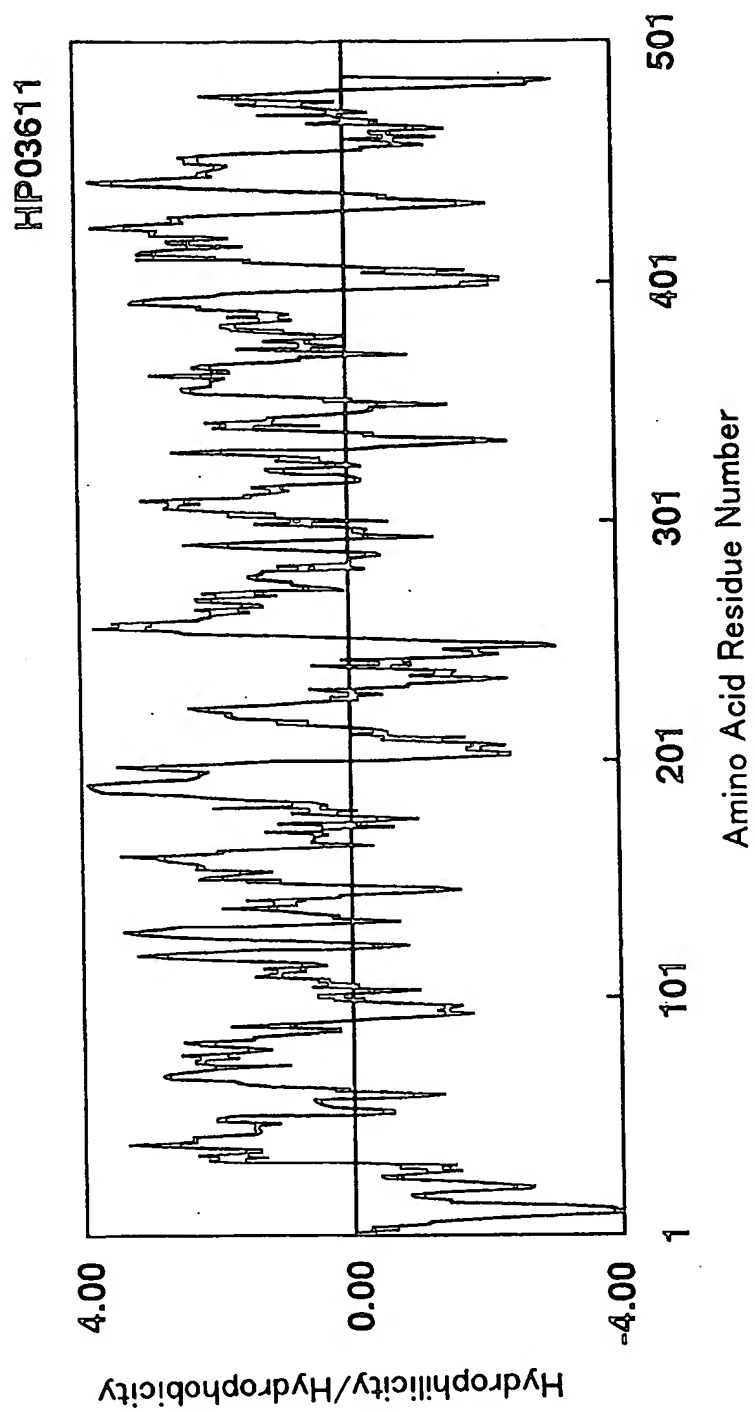


Fig.13

14/50

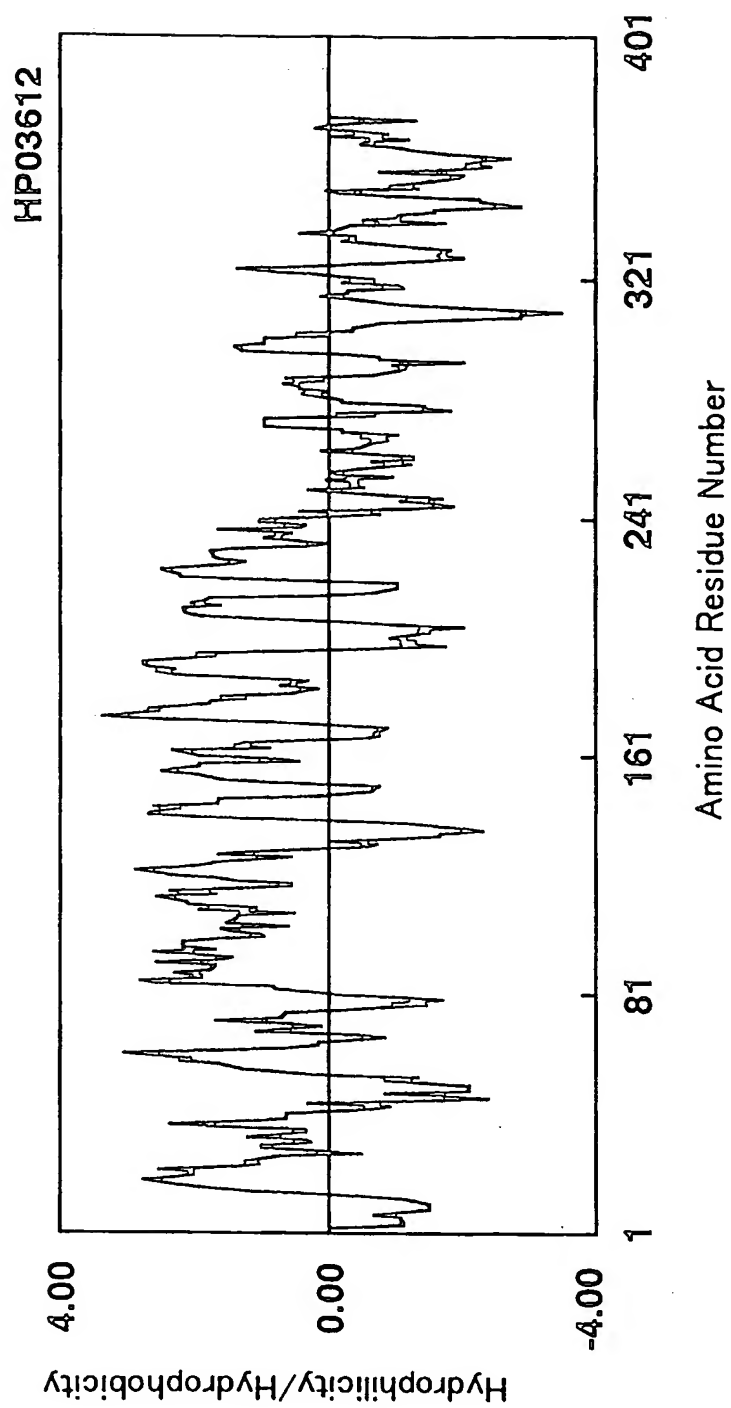


Fig.14

15/50

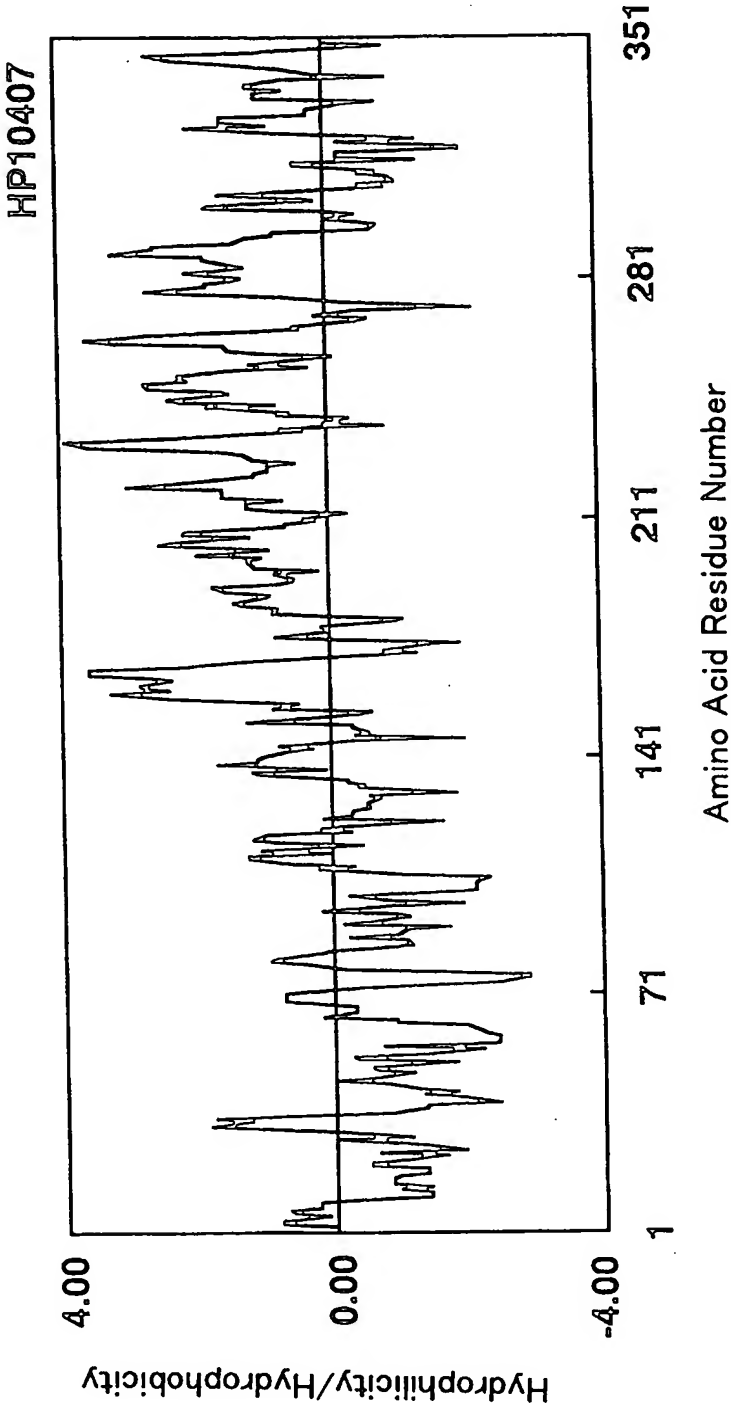


Fig.15

16/50

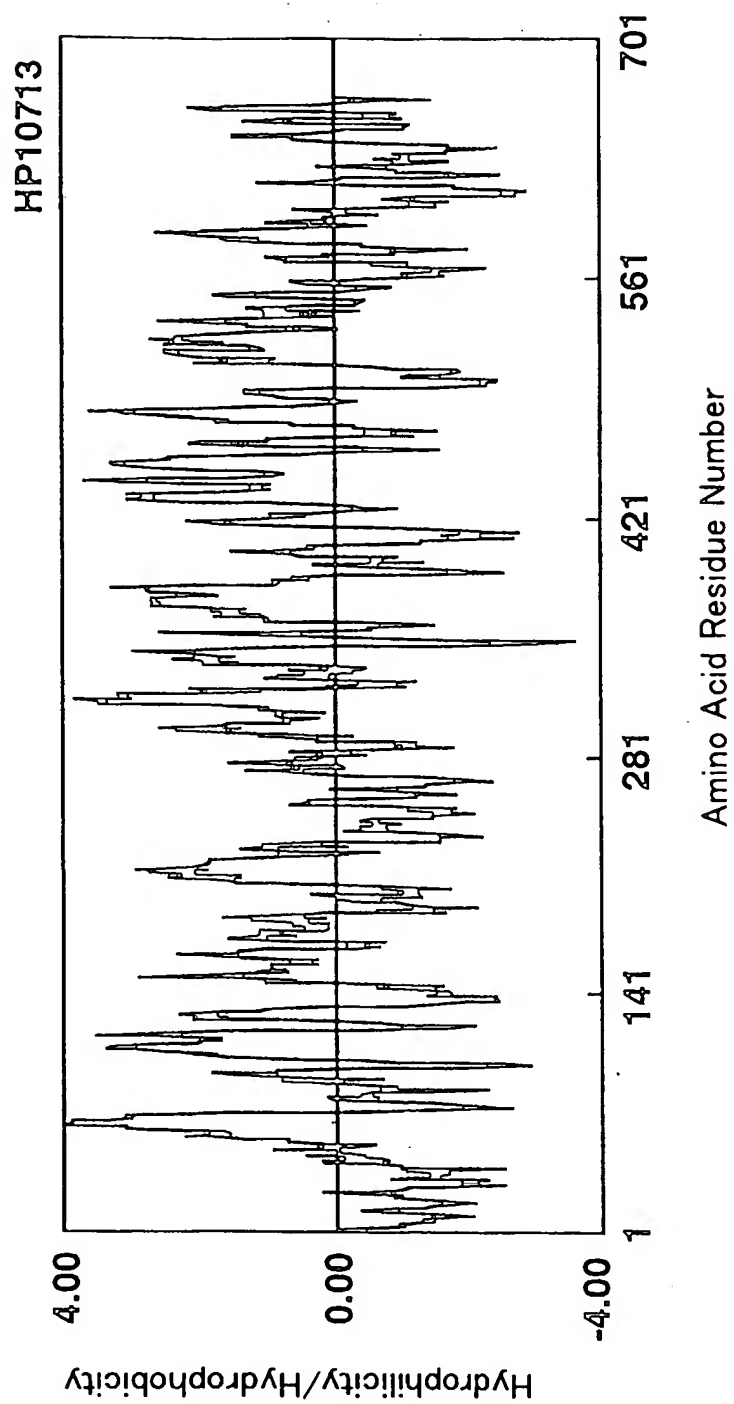


Fig.16

17/50

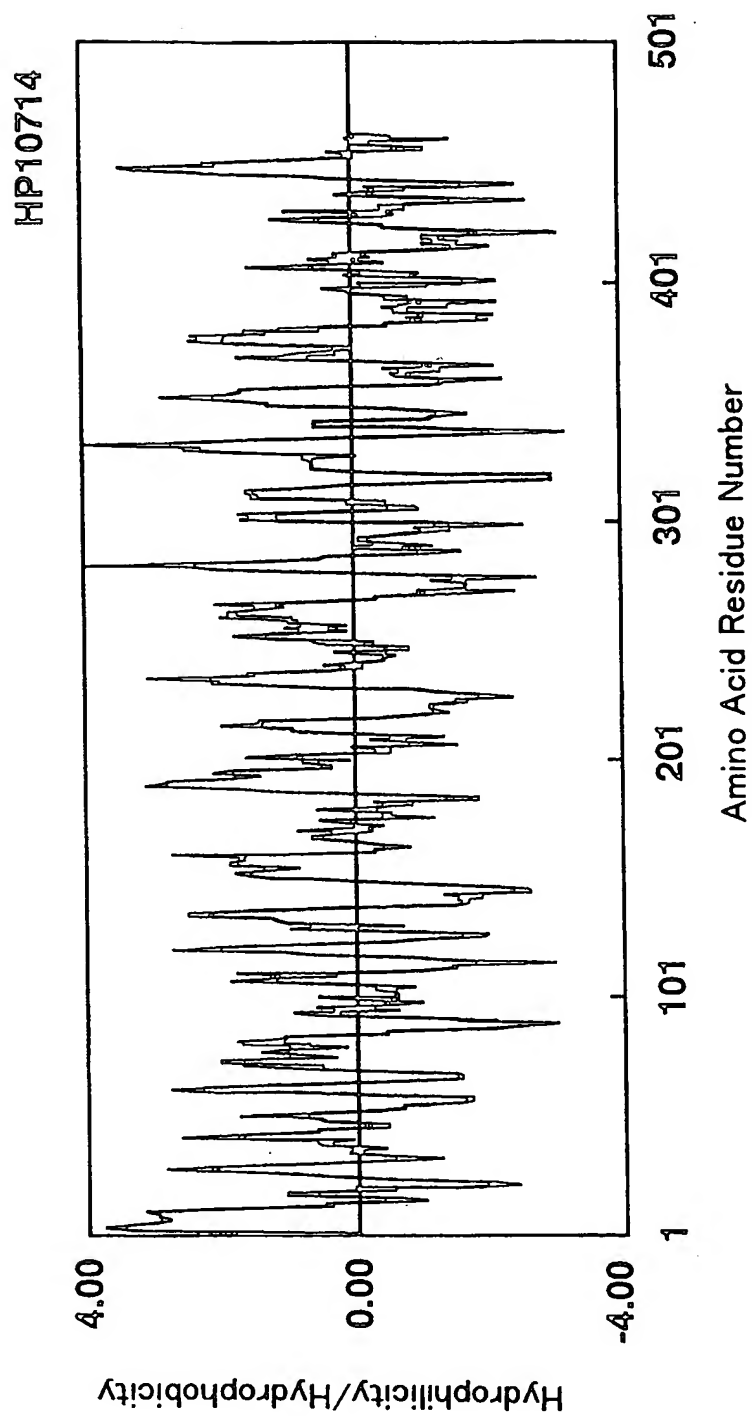


Fig.17



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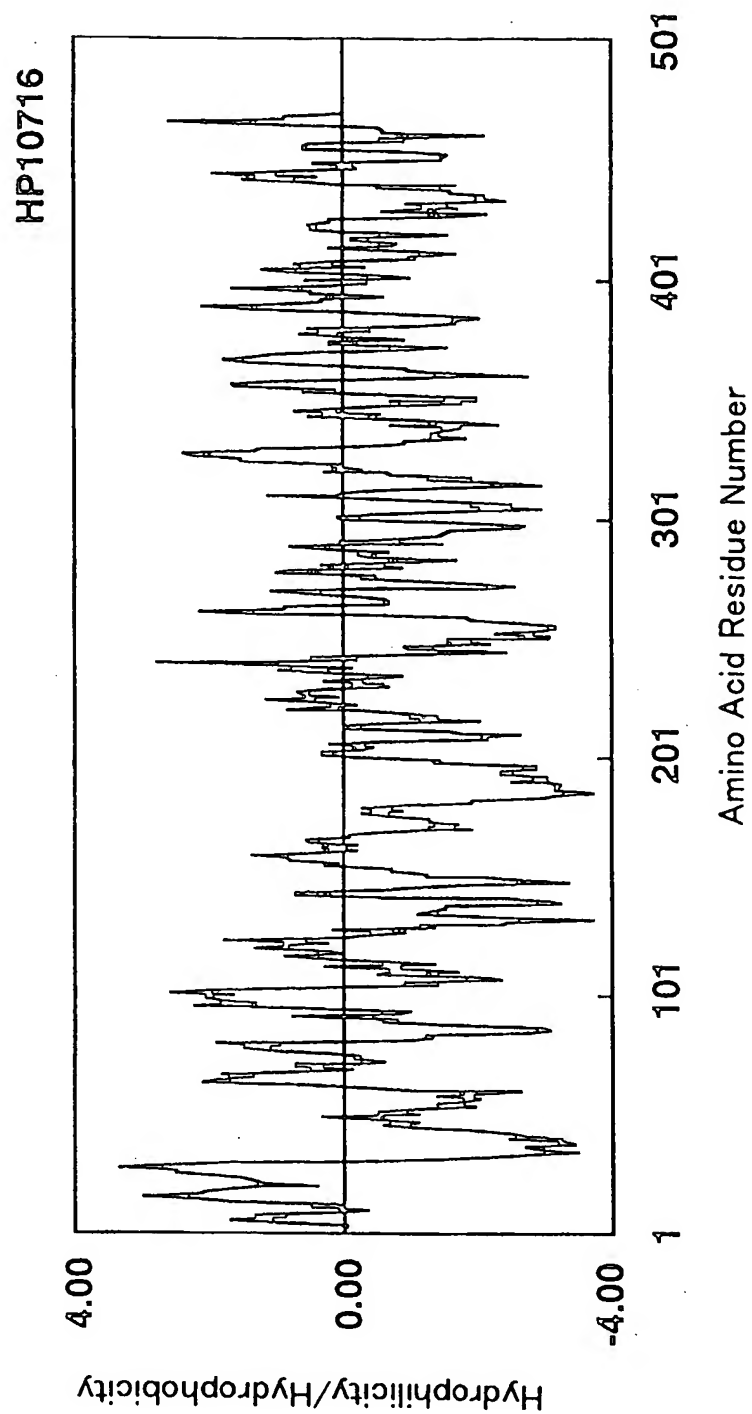


Fig.18

19/50

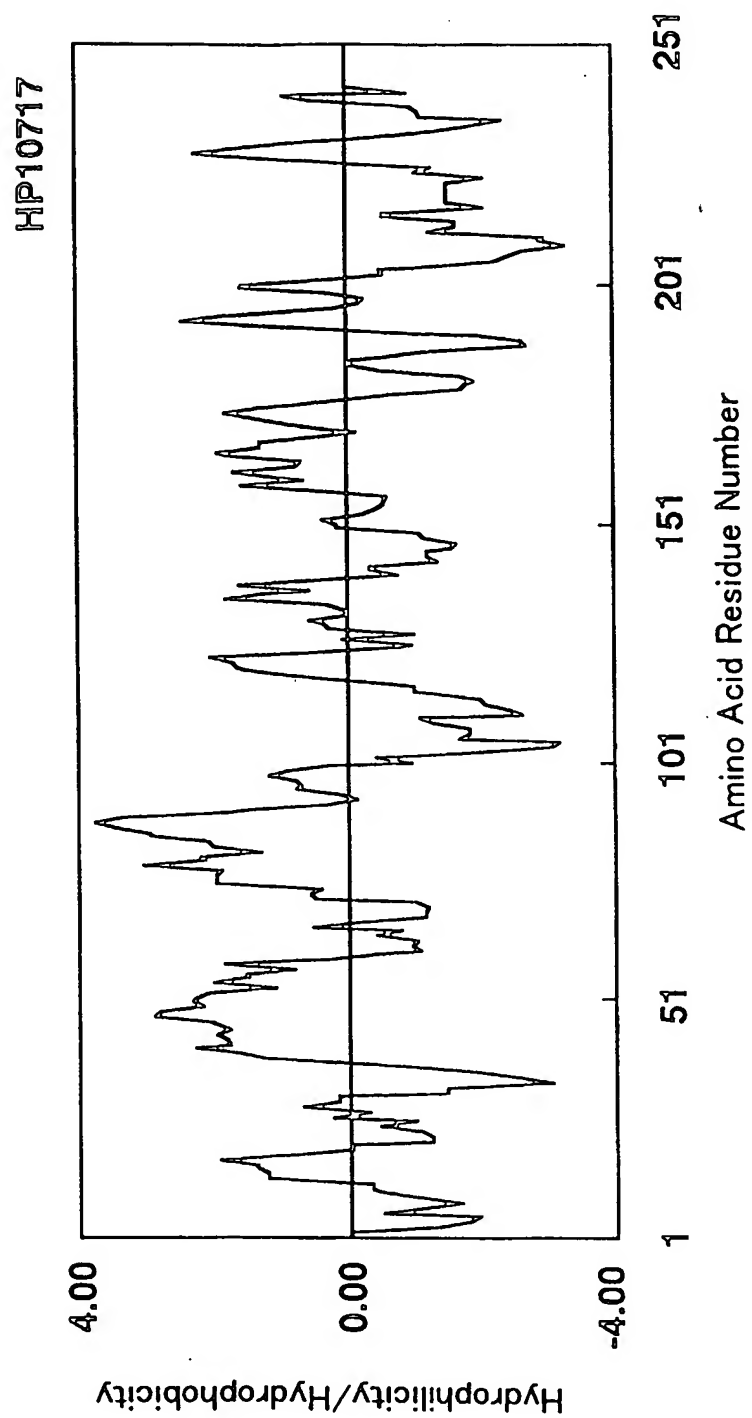


Fig.19

20/50

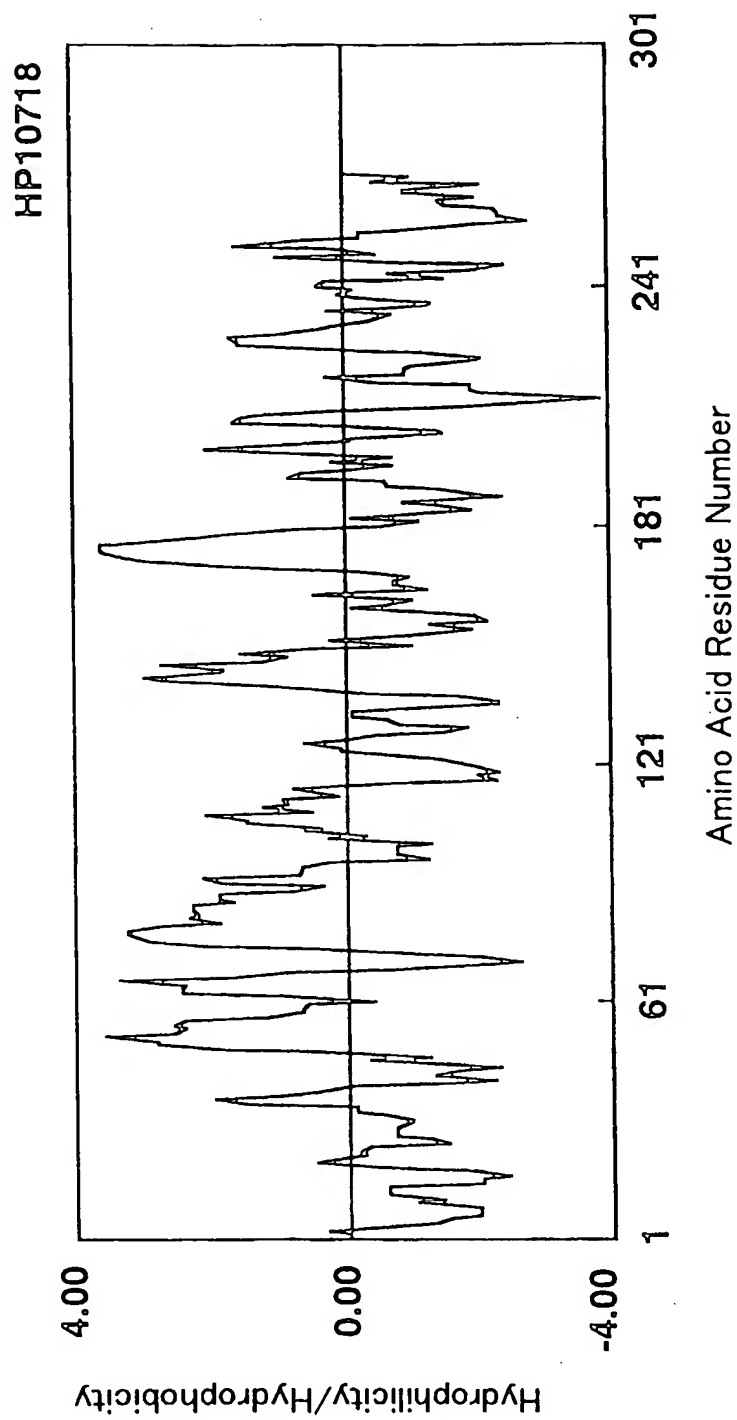


Fig.20

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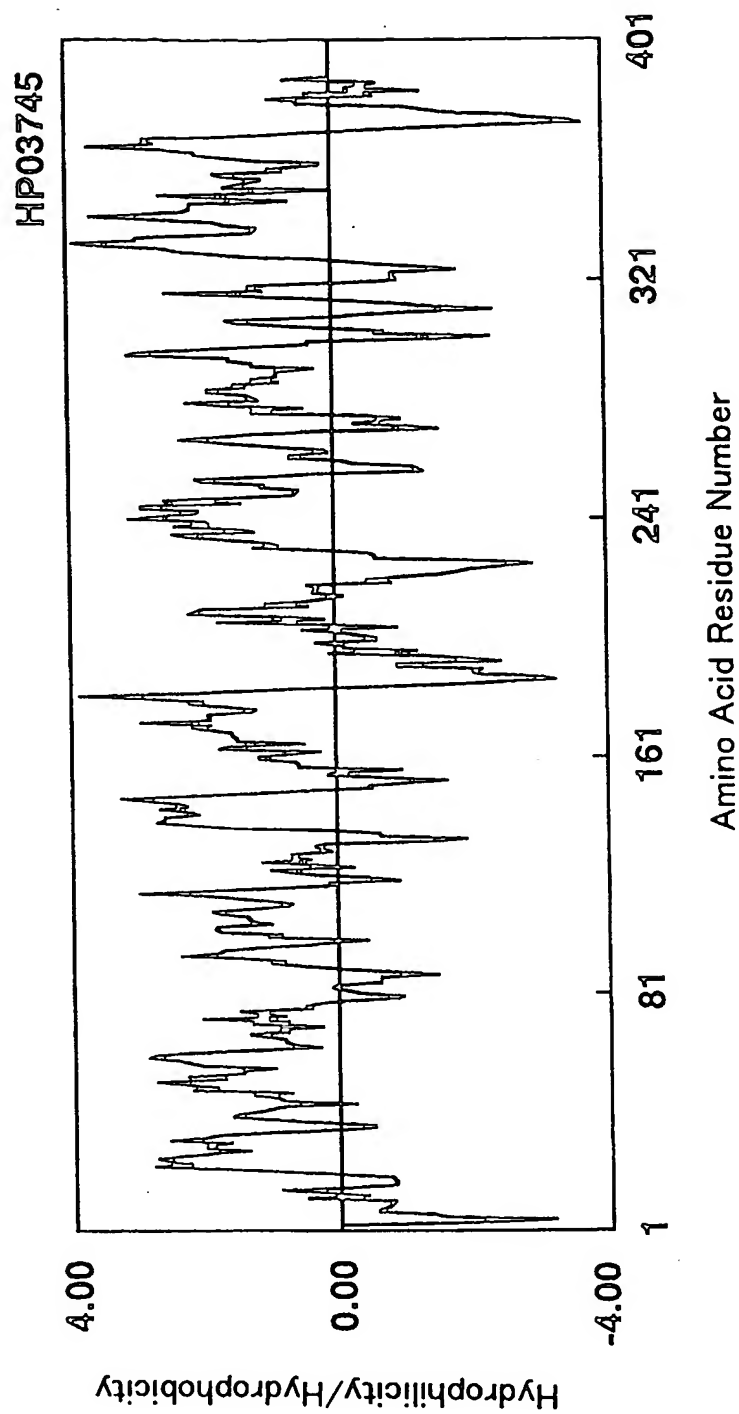


Fig.21

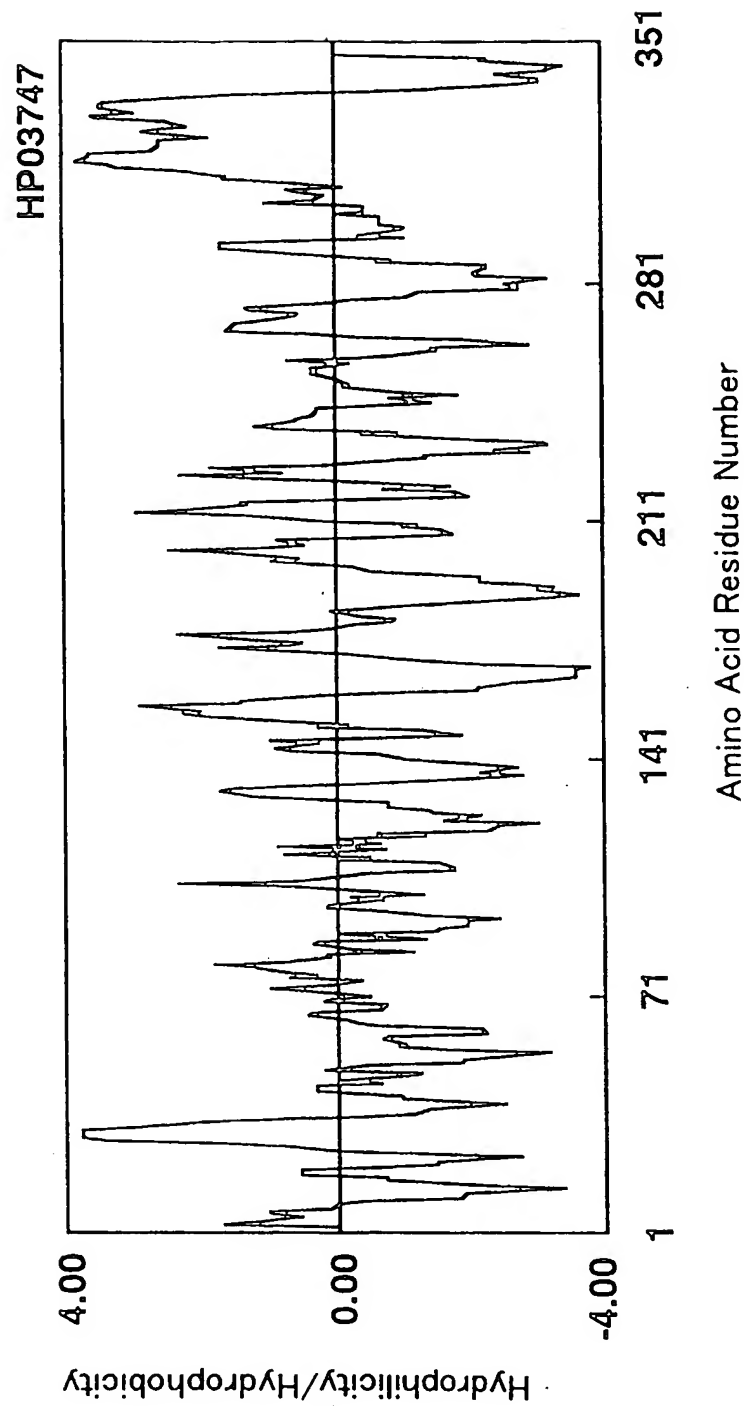


Fig.22

23/50

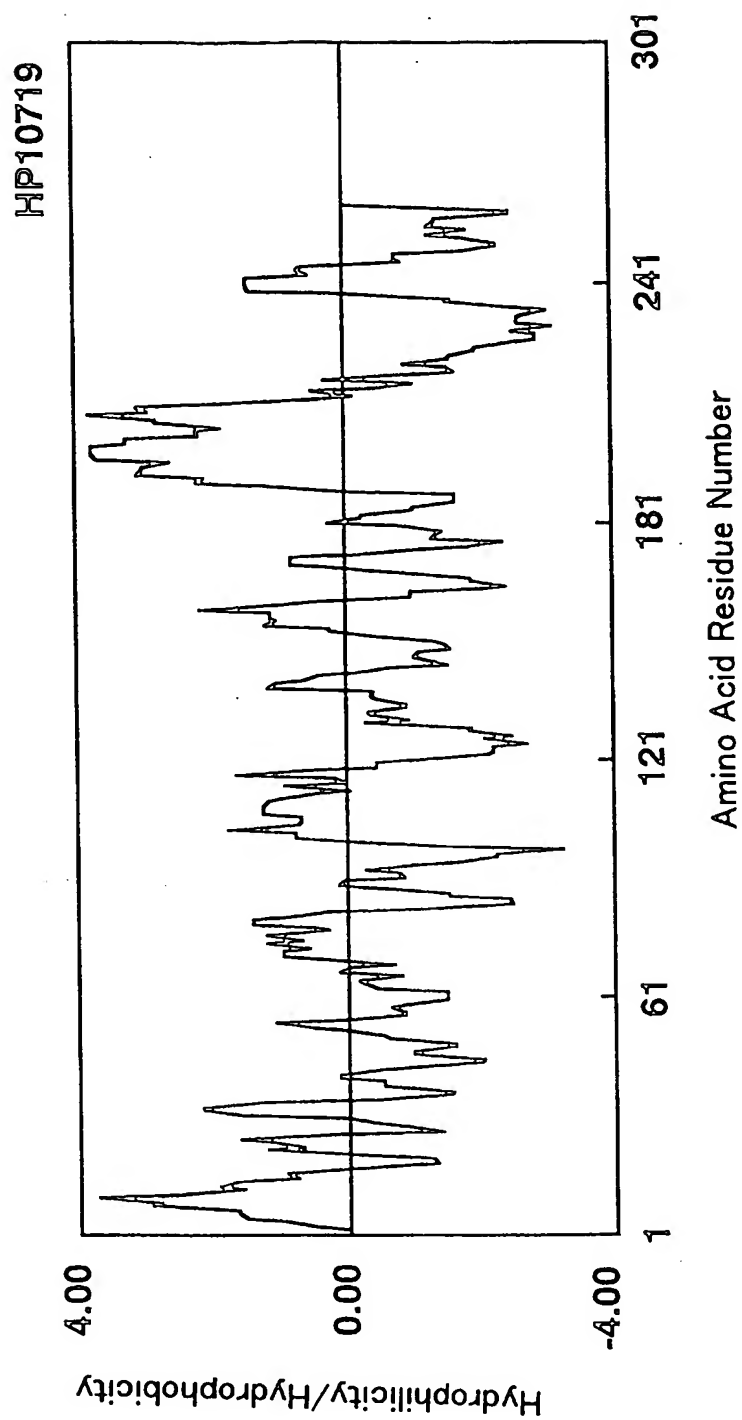


Fig.23

24/50

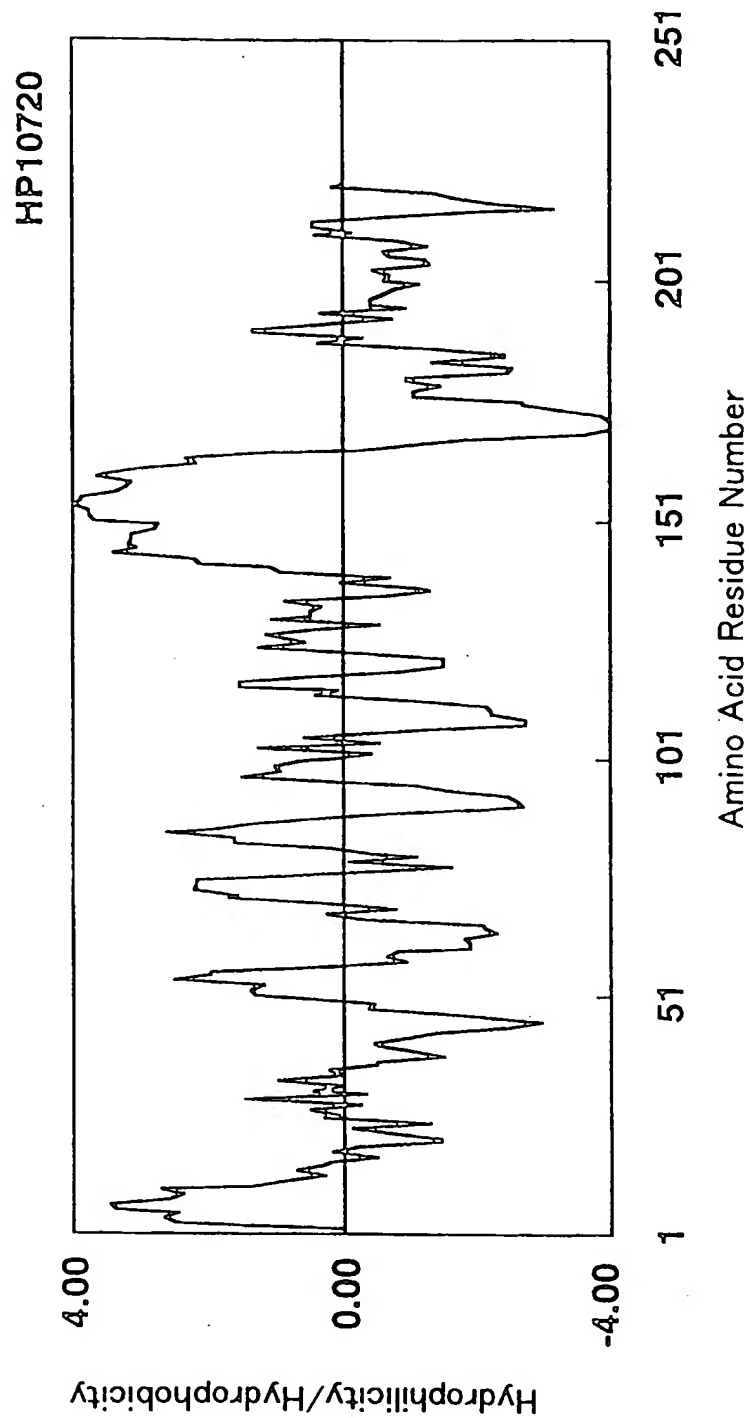


Fig.24

25/50

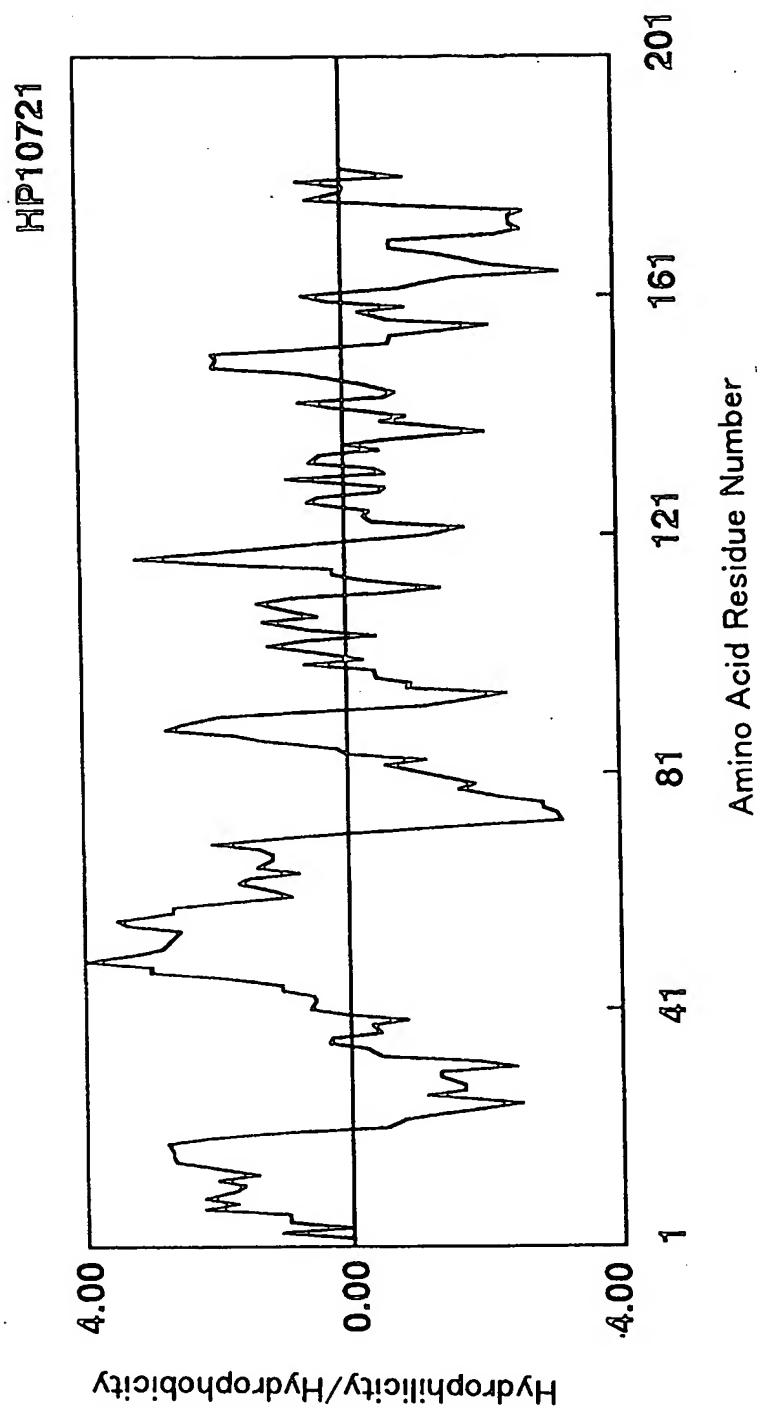


Fig.25



26/50

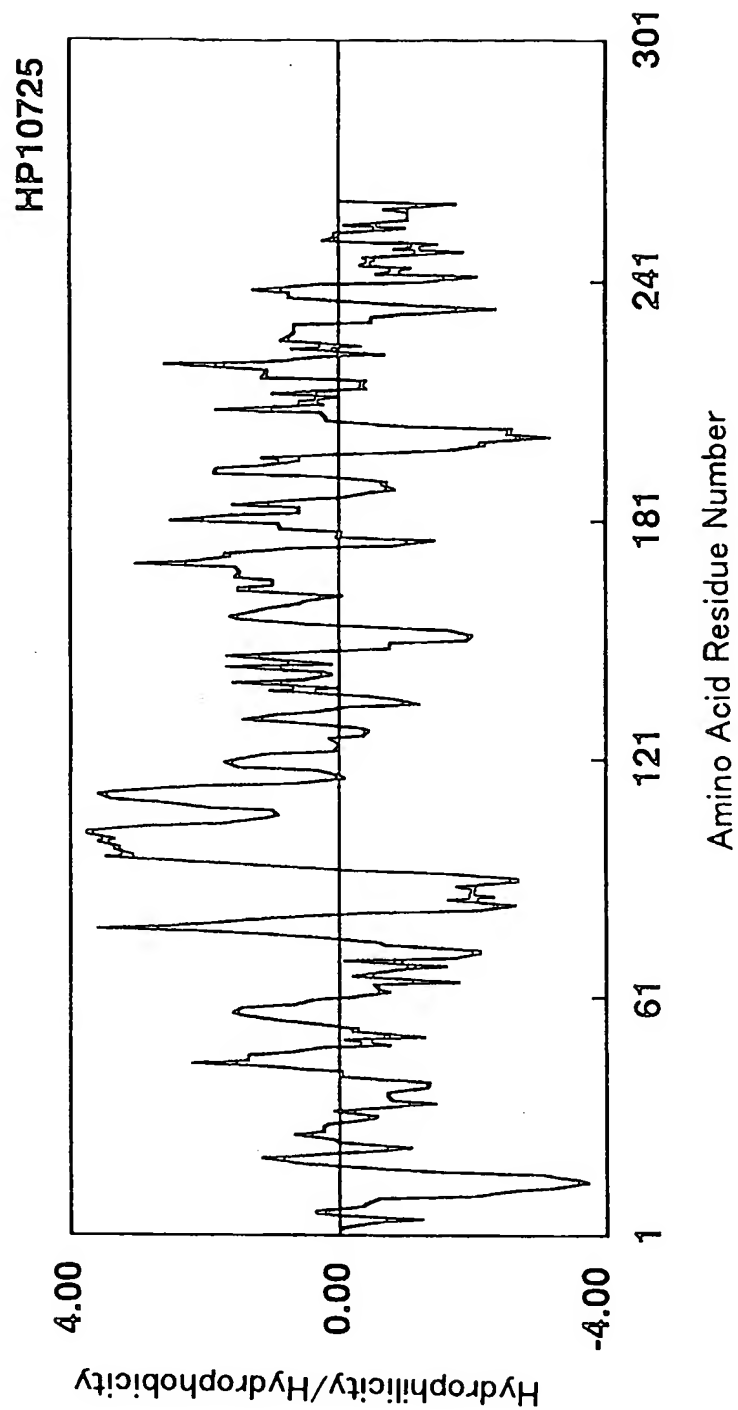


Fig.26

27/50

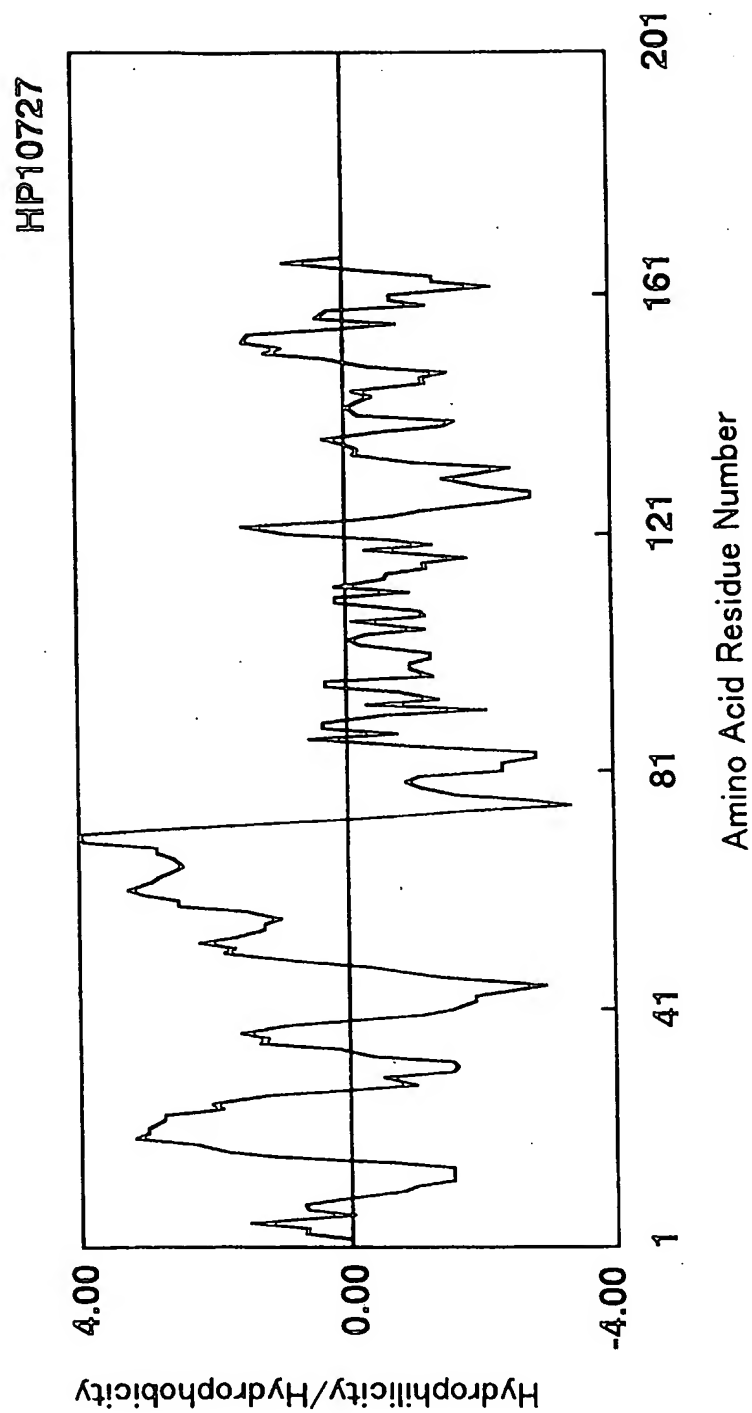


Fig.27

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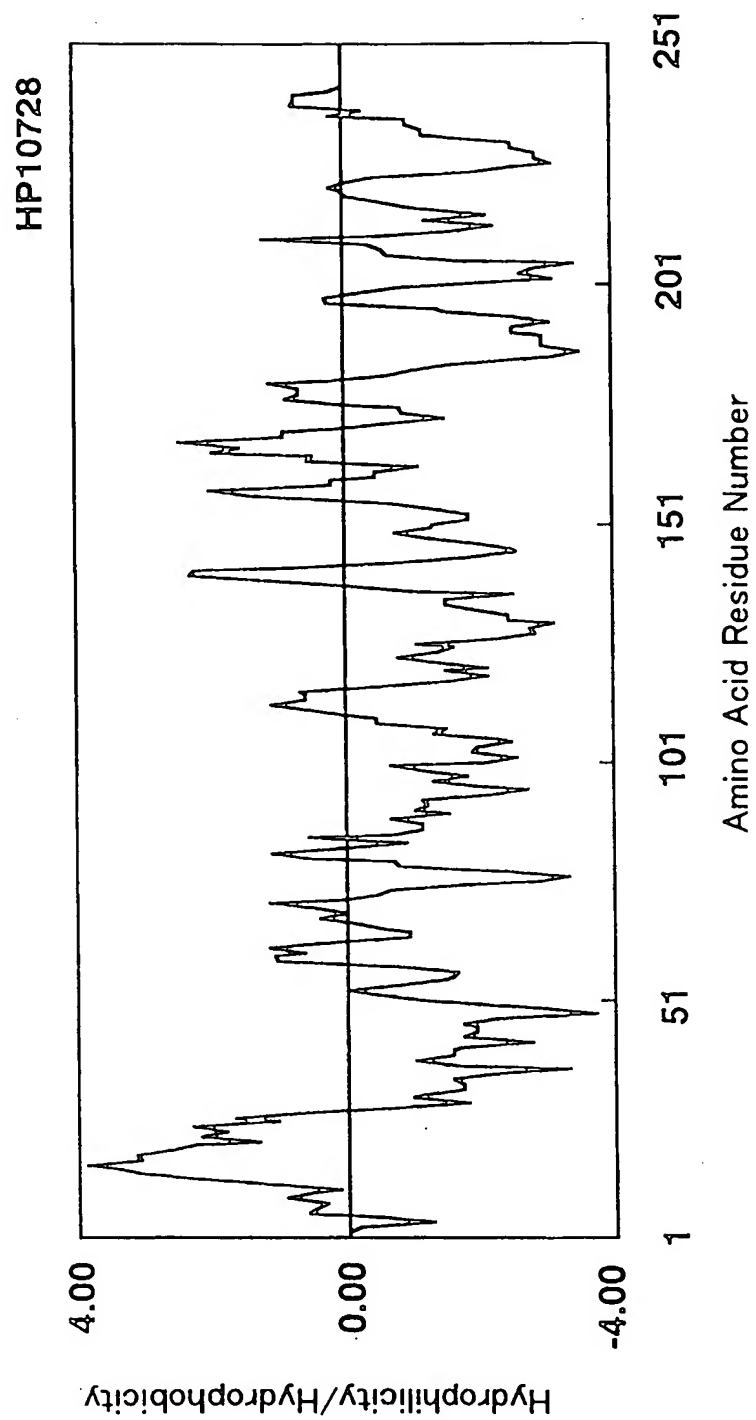


Fig.28

29/50

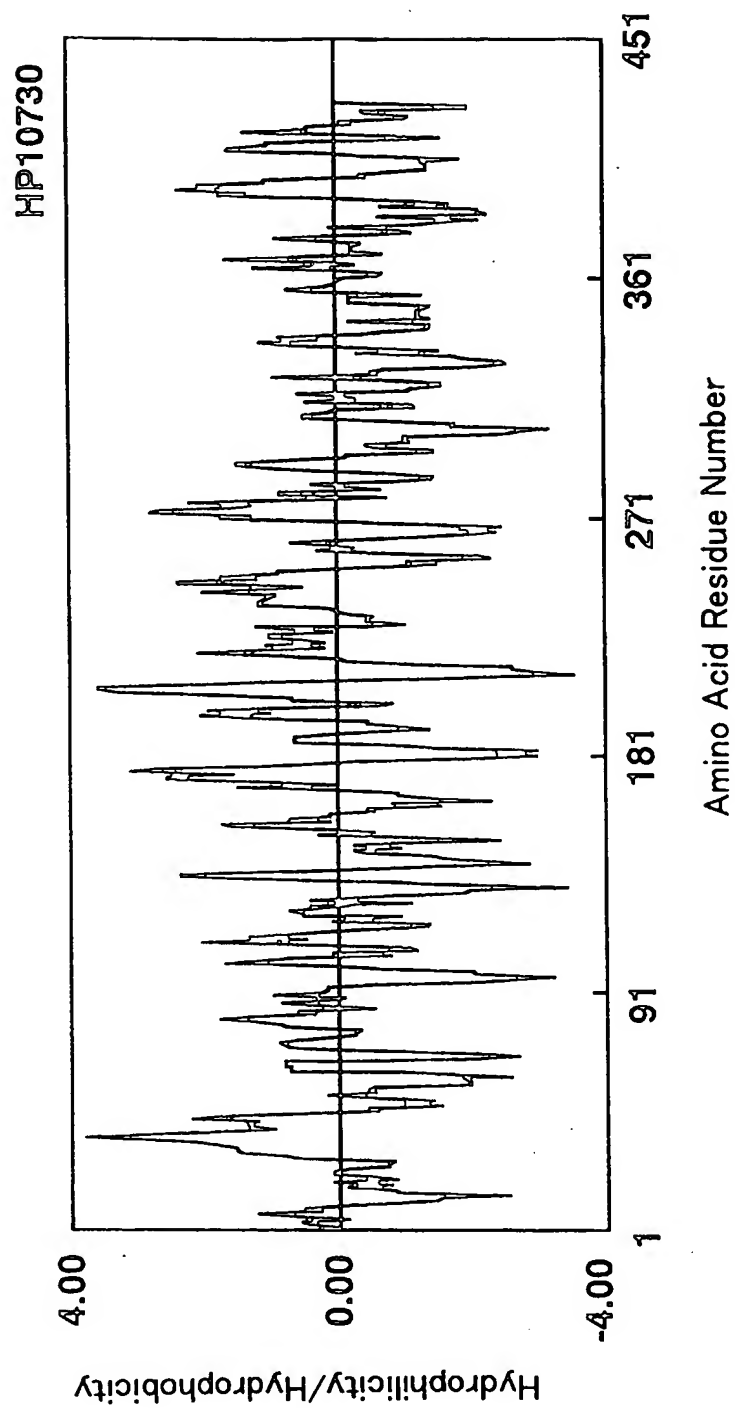


Fig.29

30/50

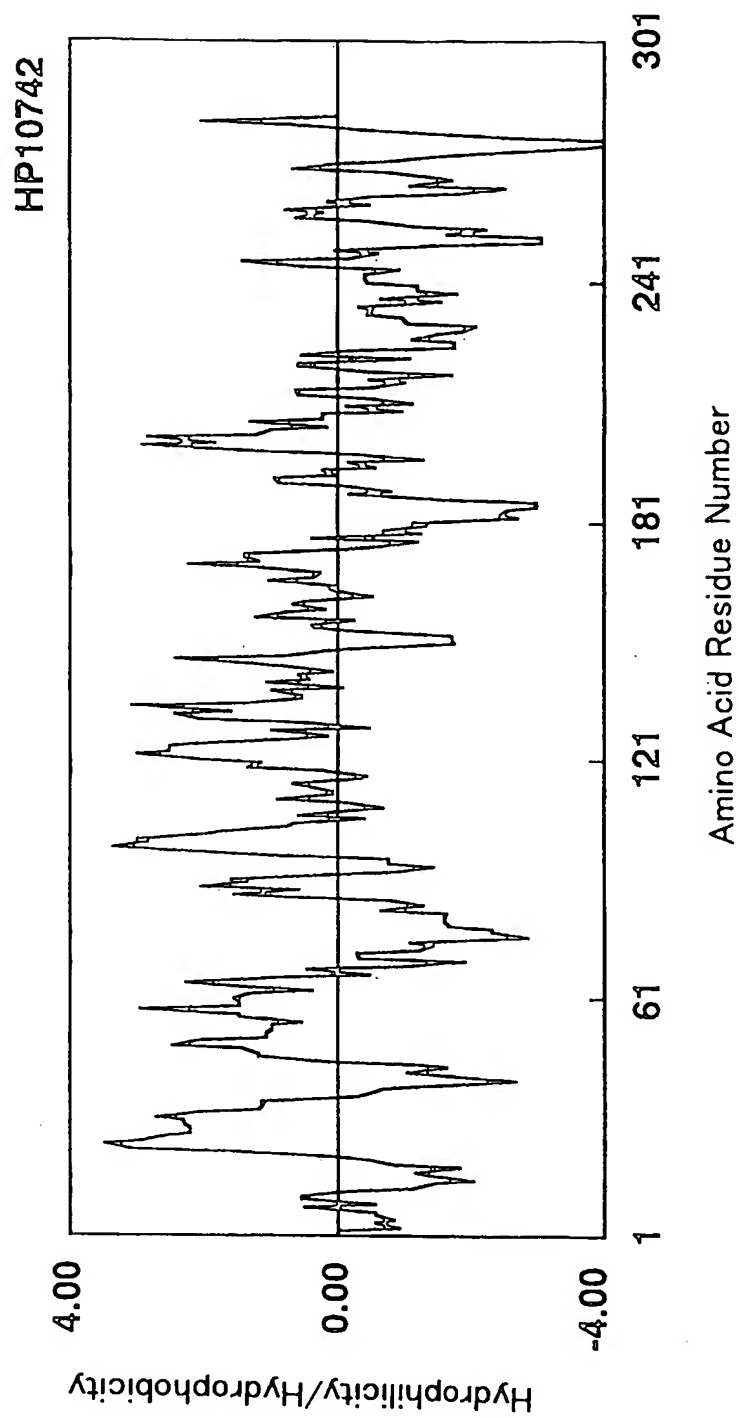


Fig.30

31/50

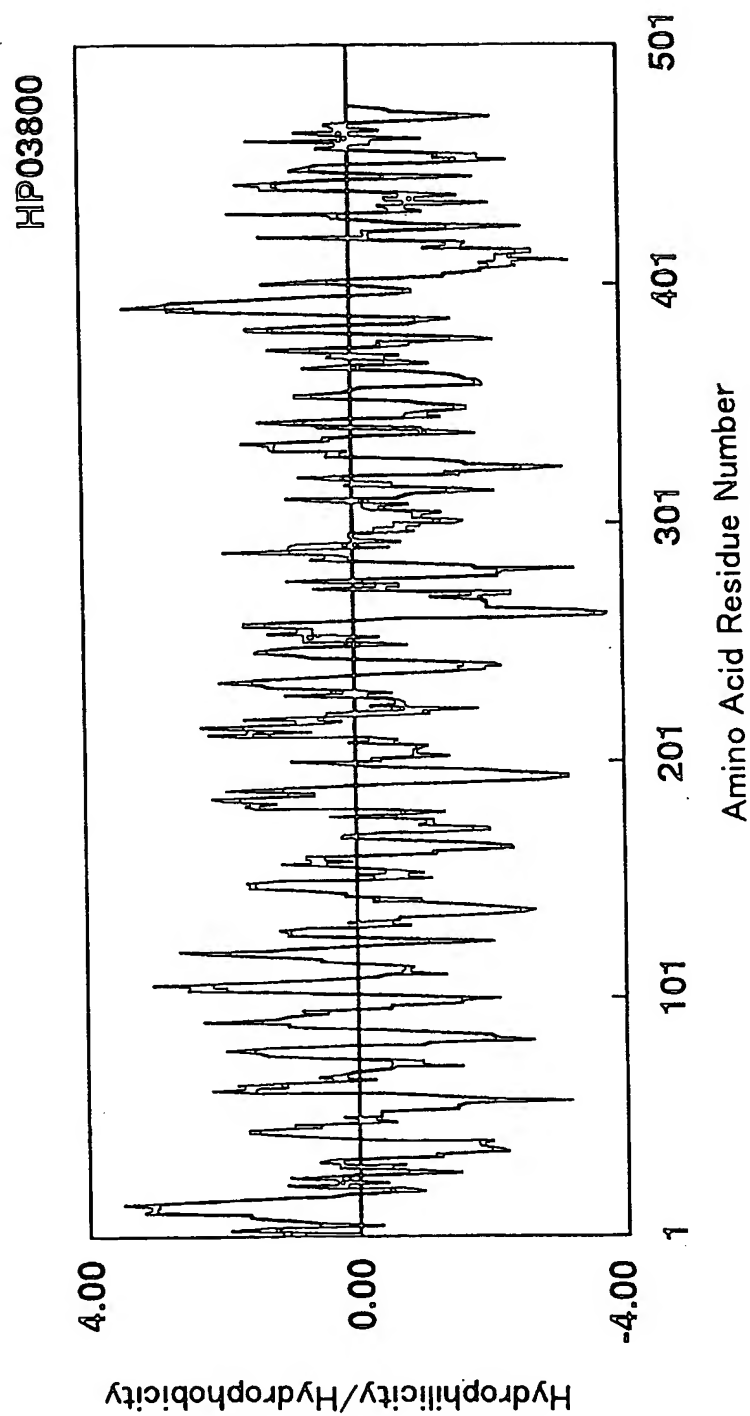


Fig.31

32/50

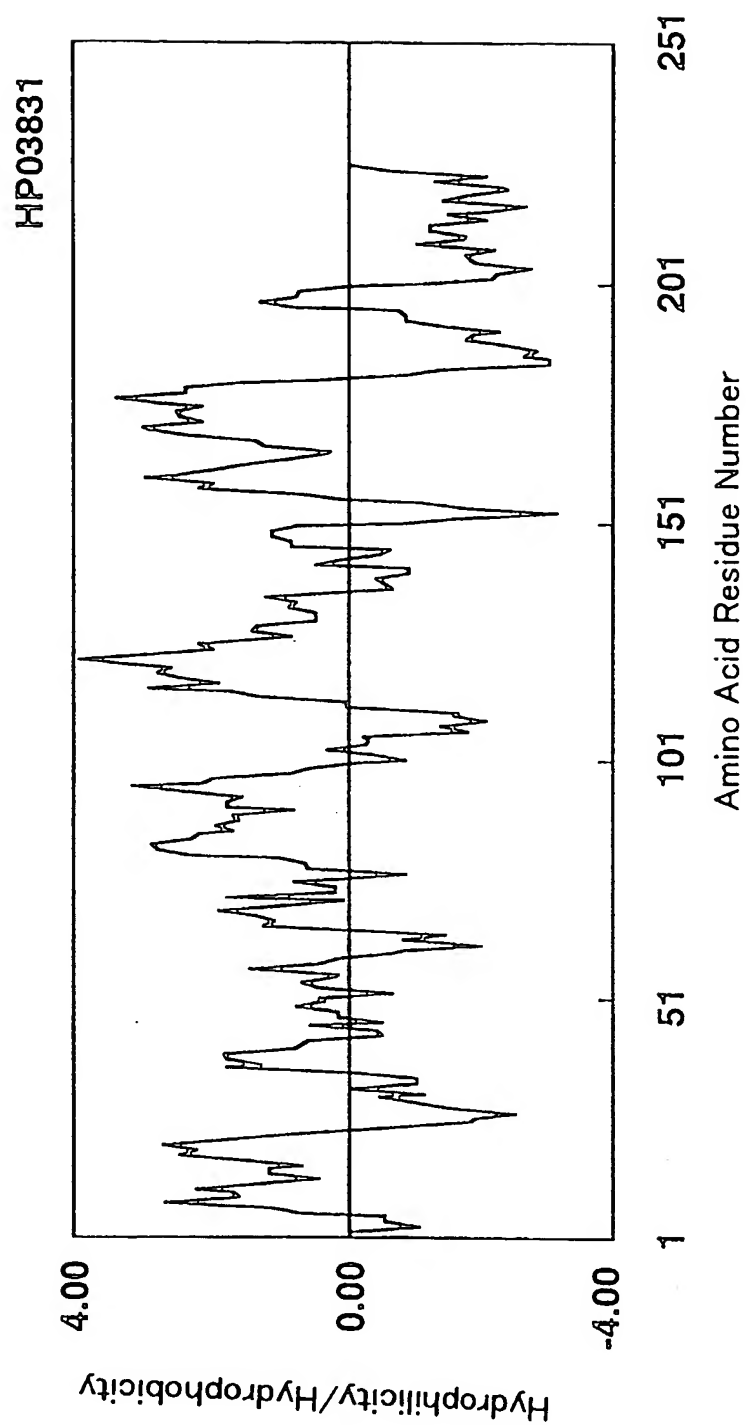


Fig.32

33/50

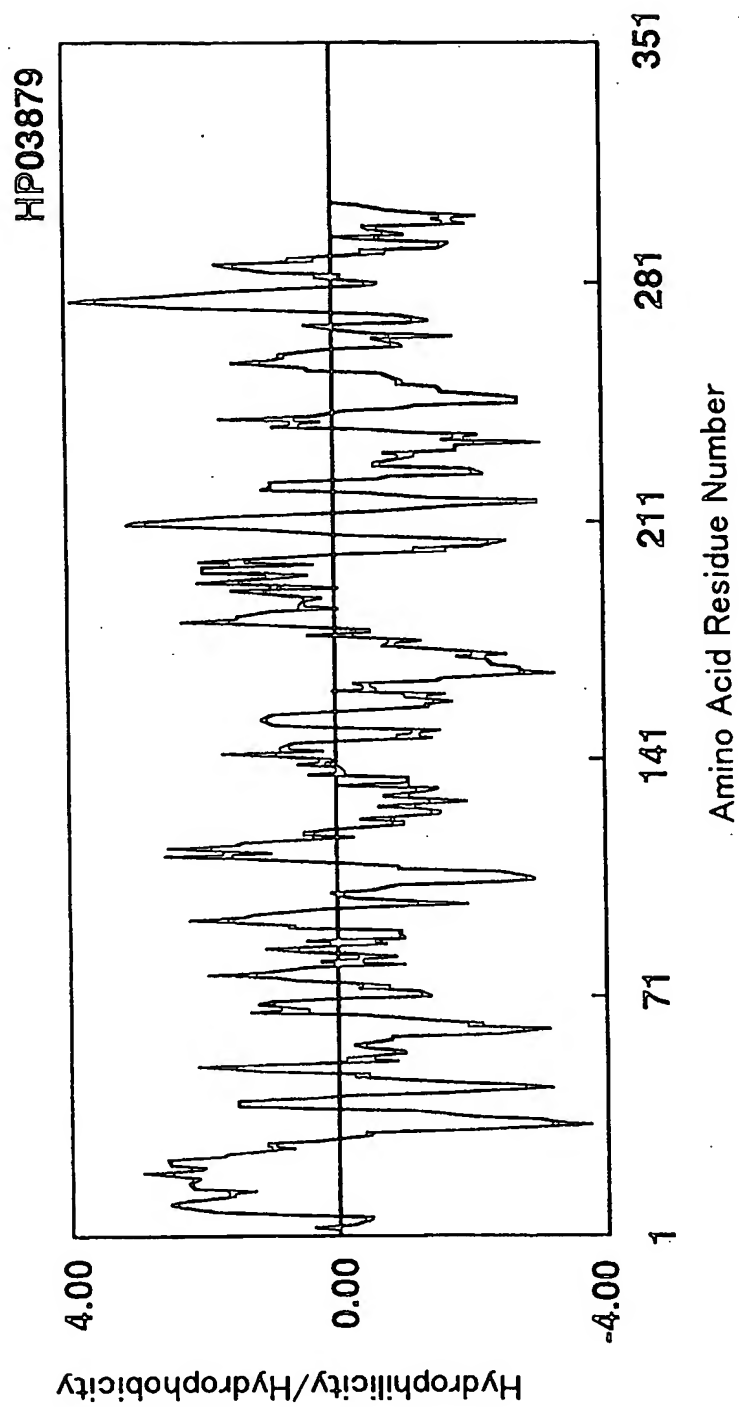


Fig.33



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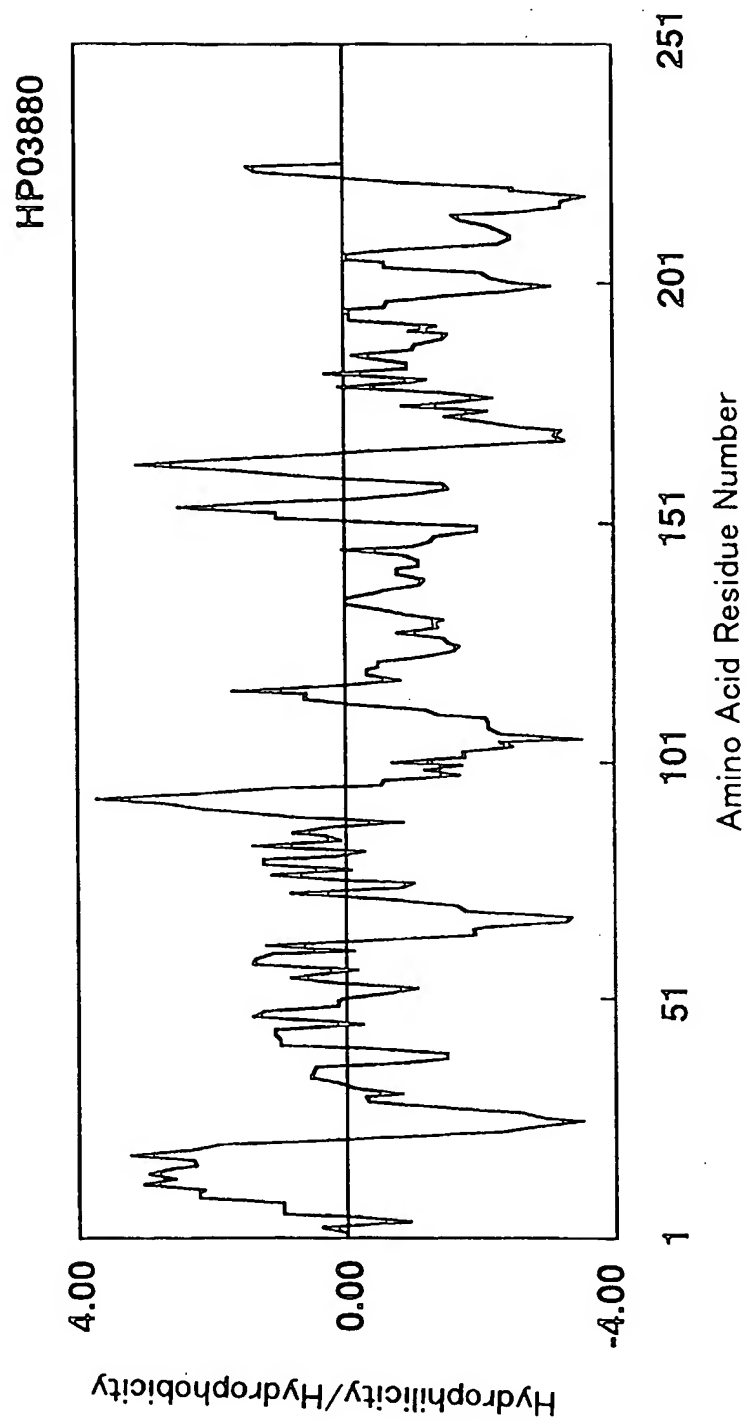


Fig.34

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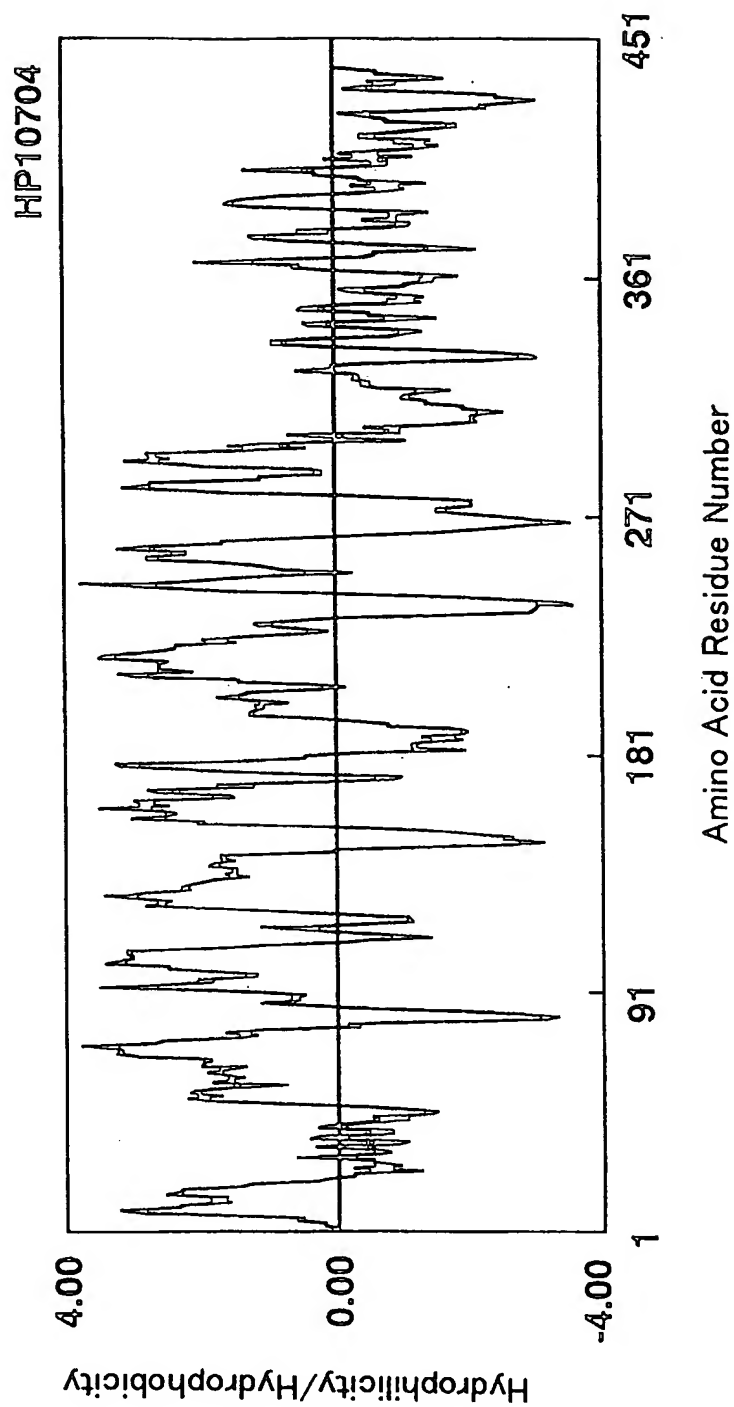


Fig.35

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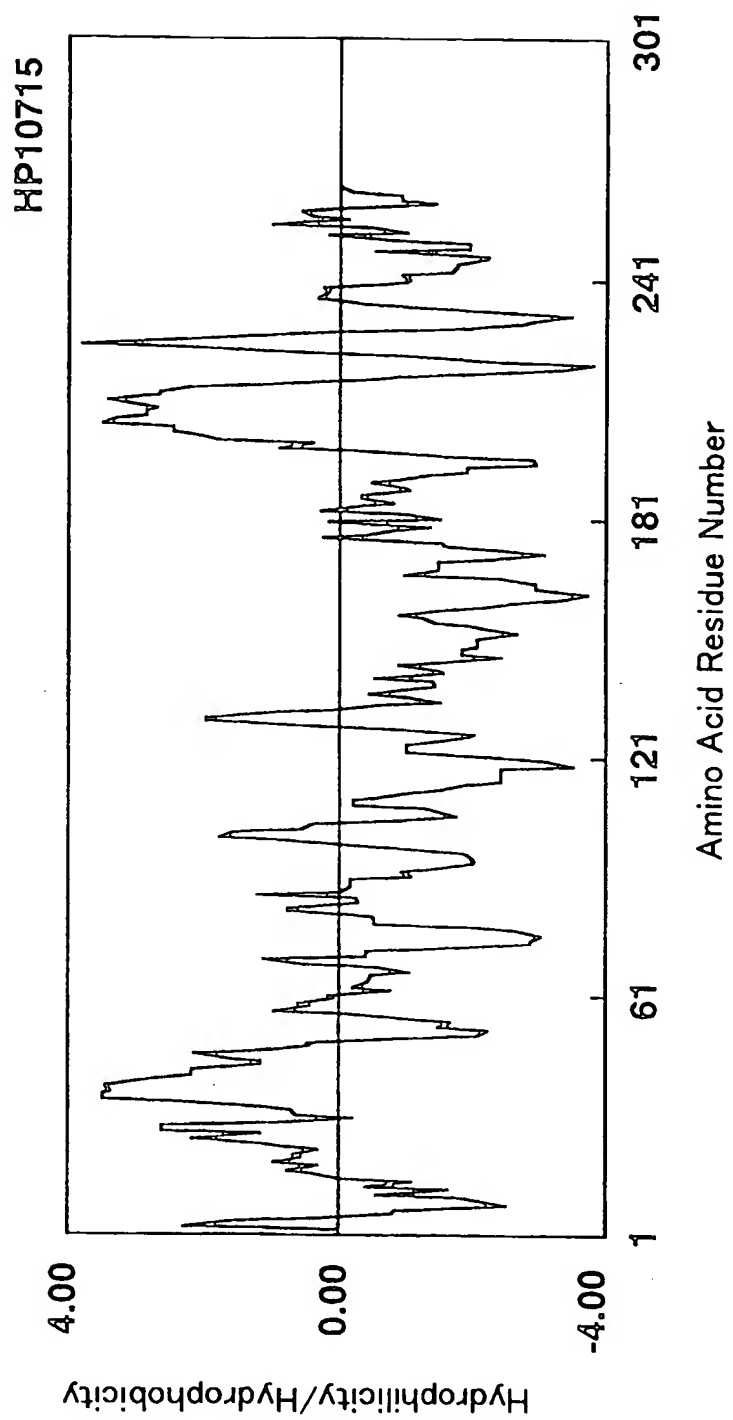


Fig.36

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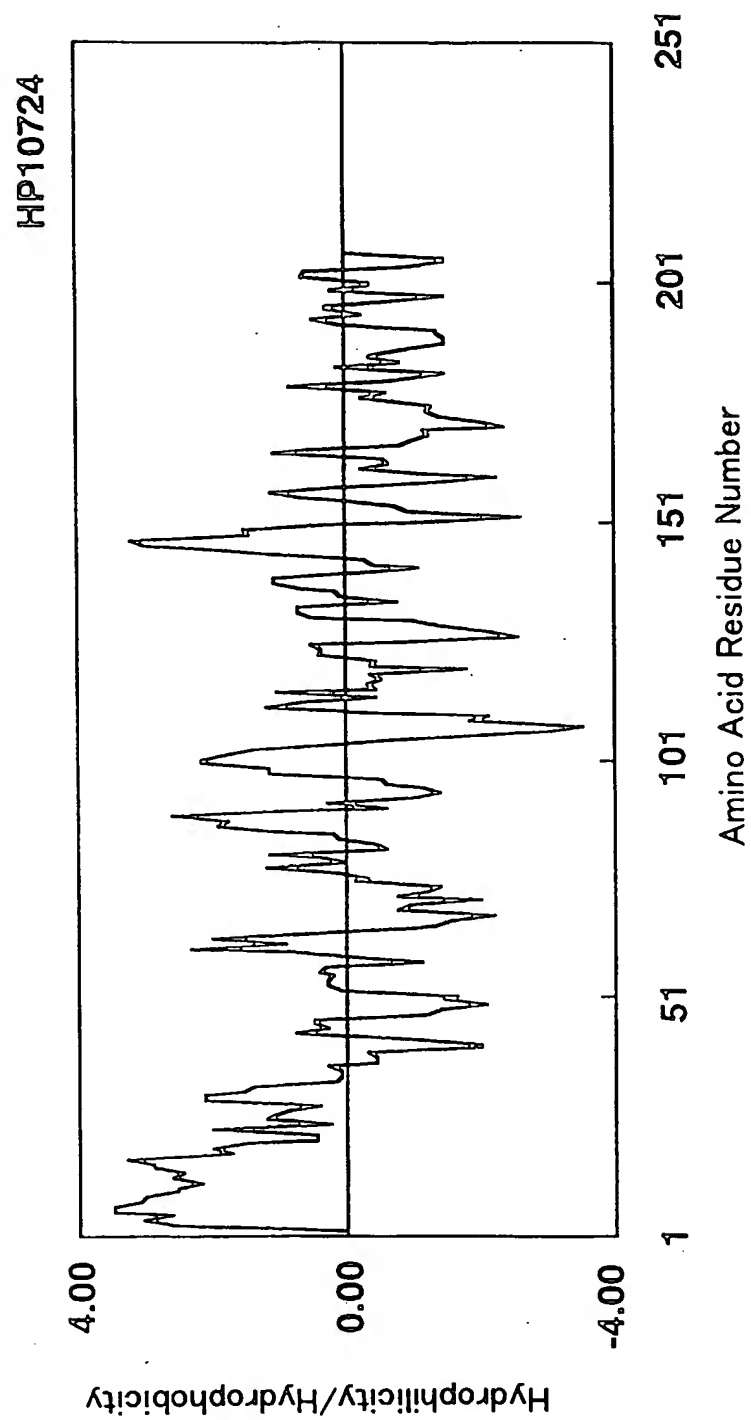


Fig.37

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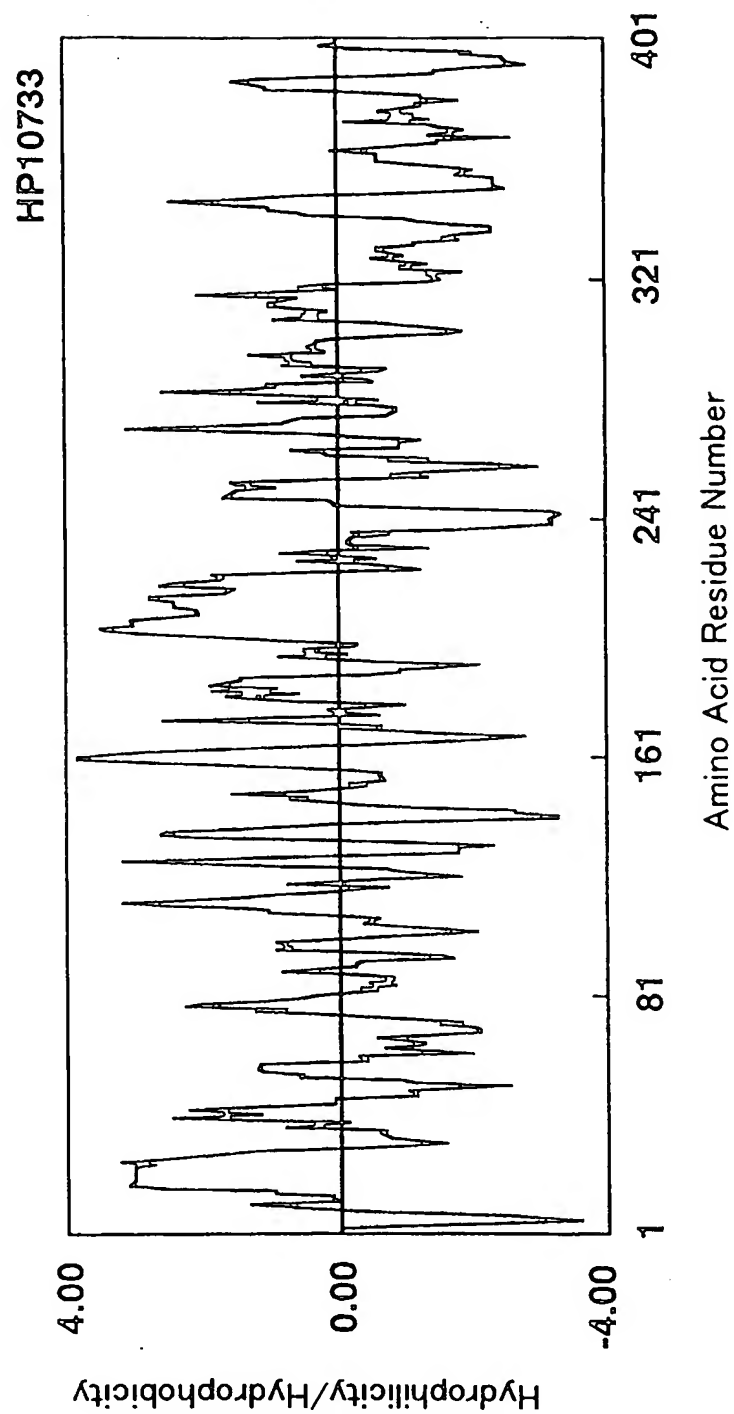


Fig.38

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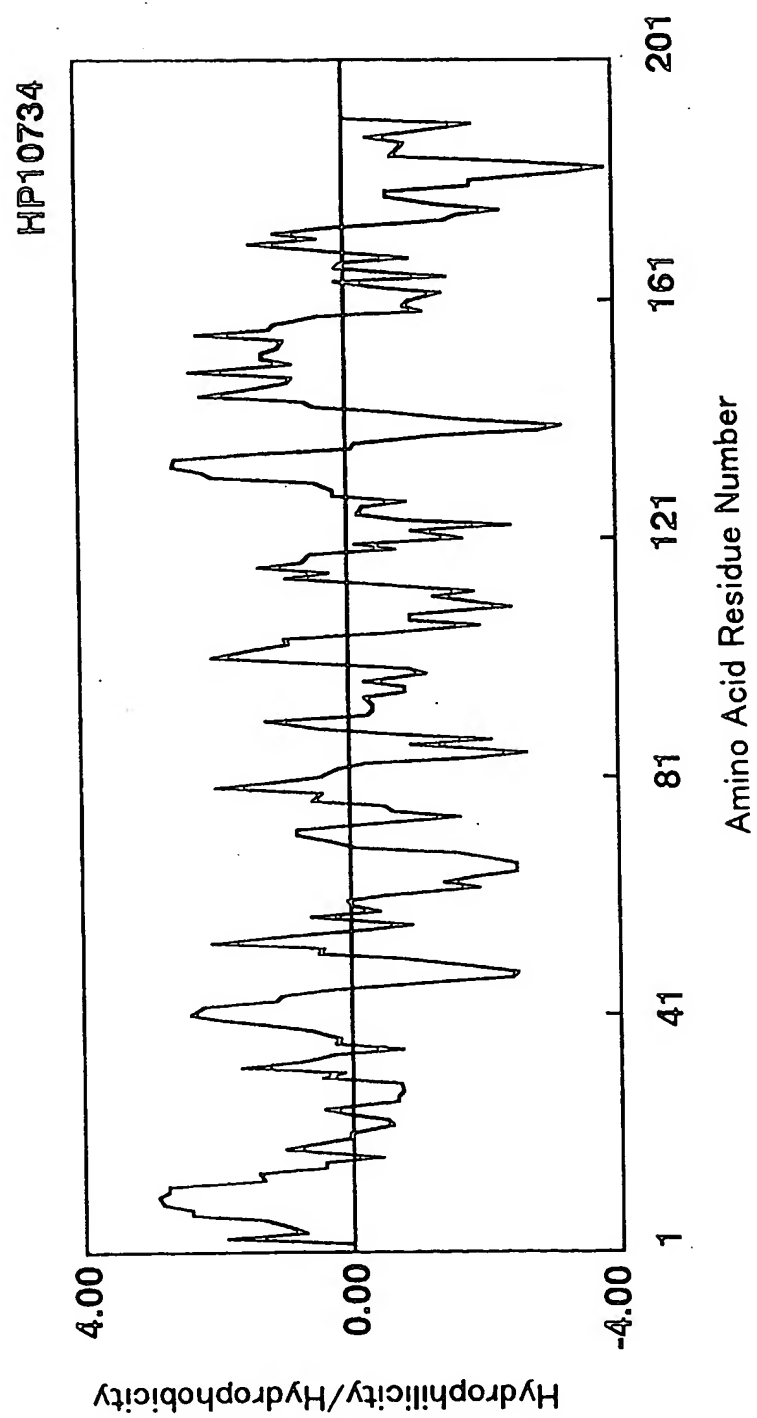


Fig.39

40/50

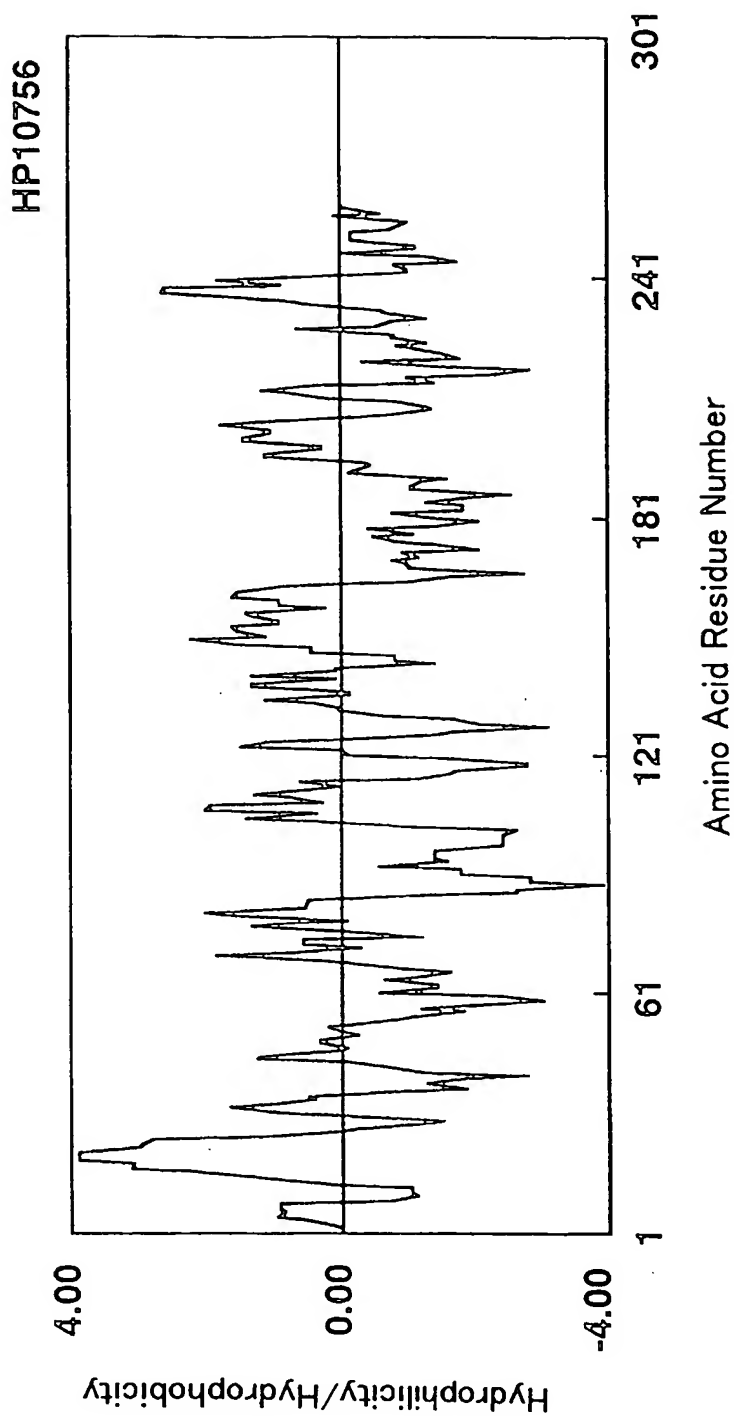


Fig.40

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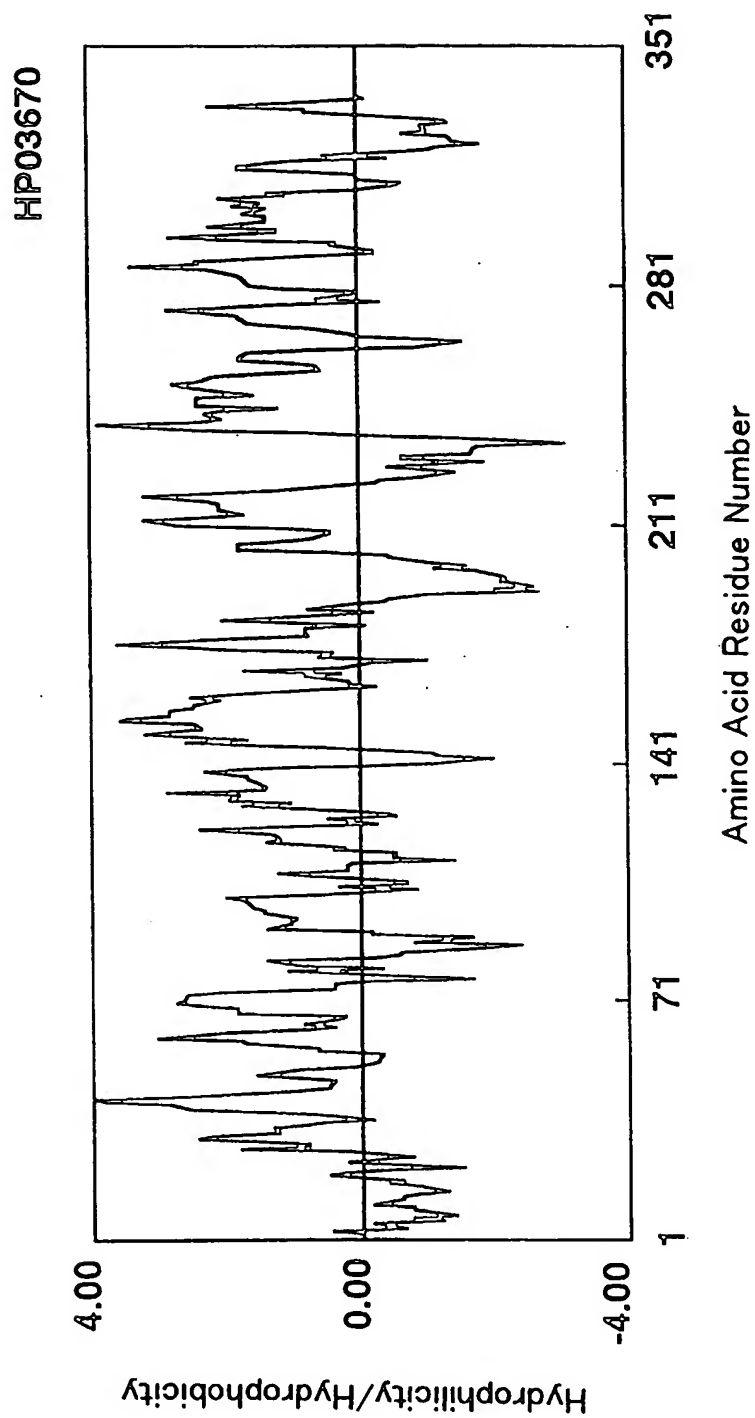


Fig.41



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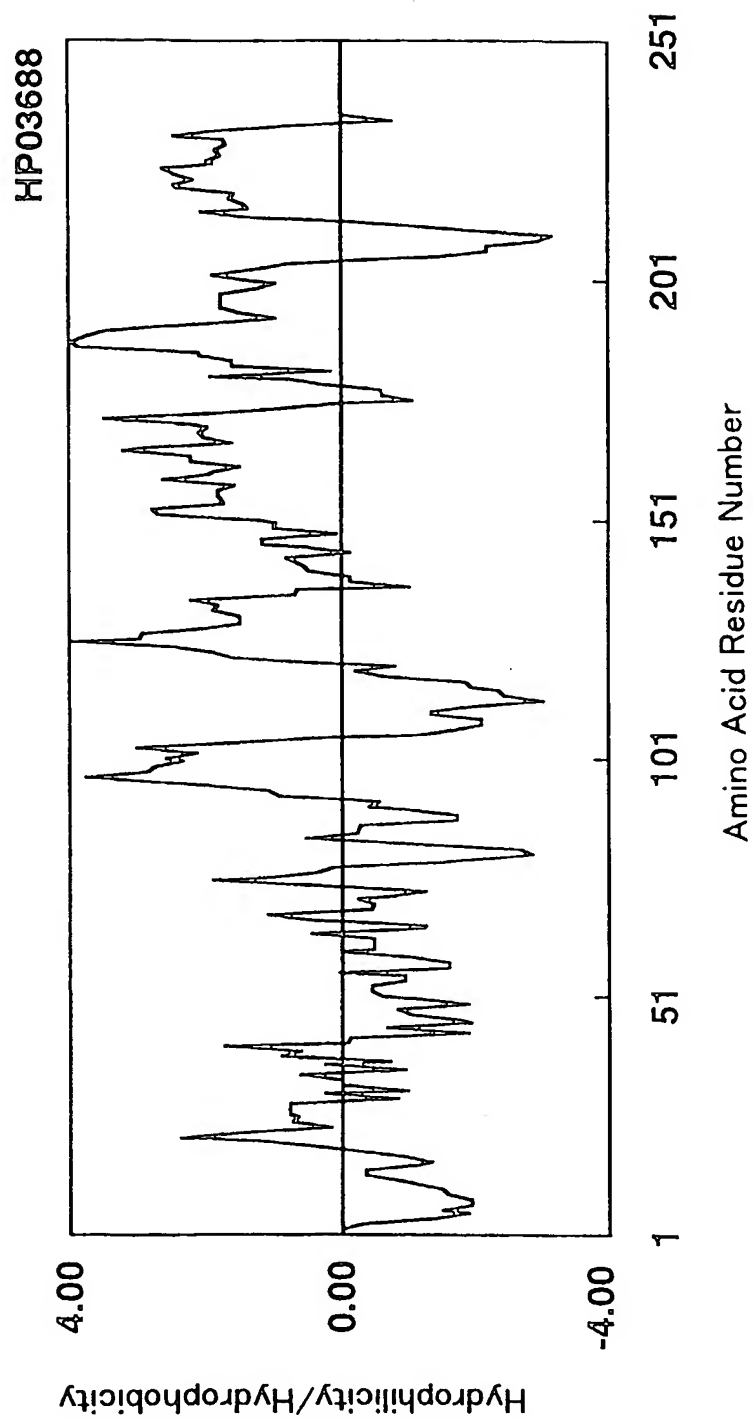


Fig.42

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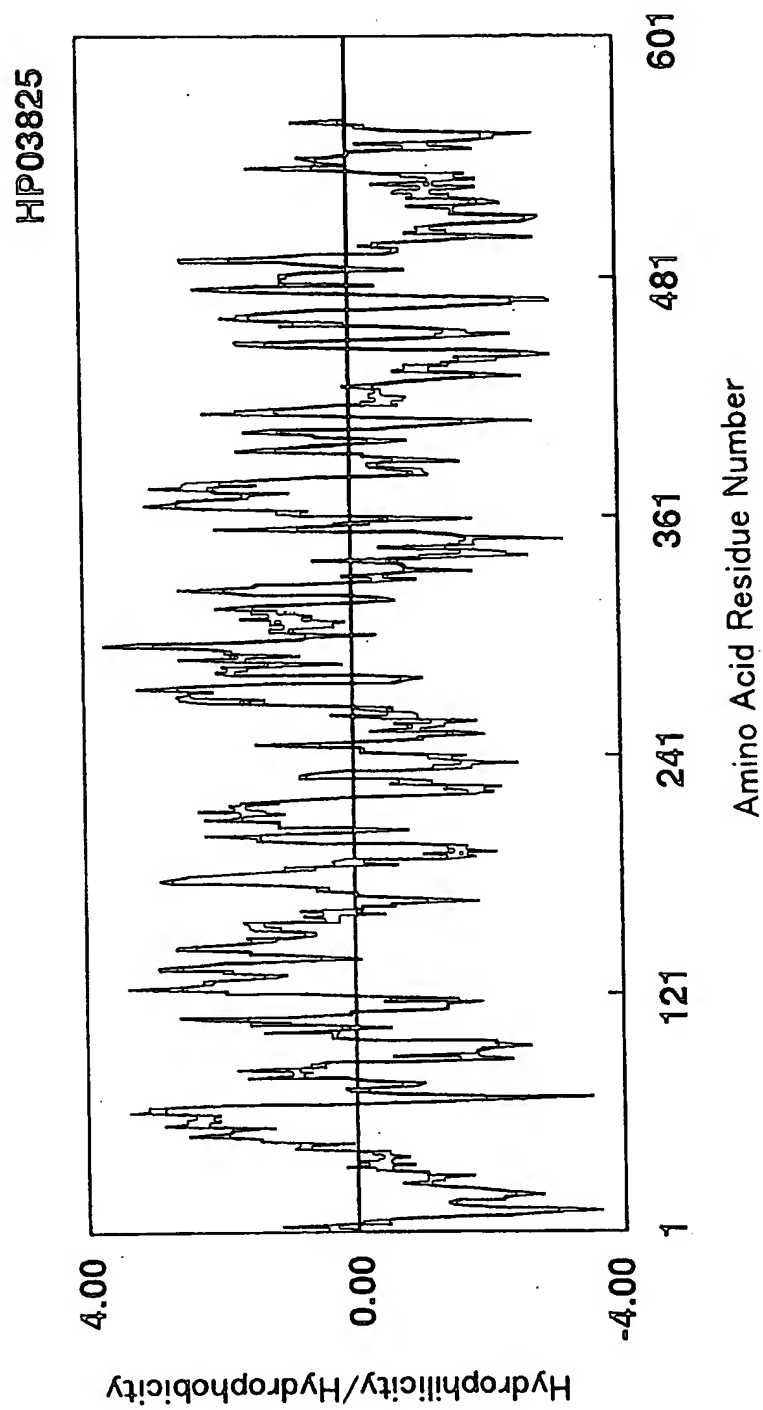


Fig.43

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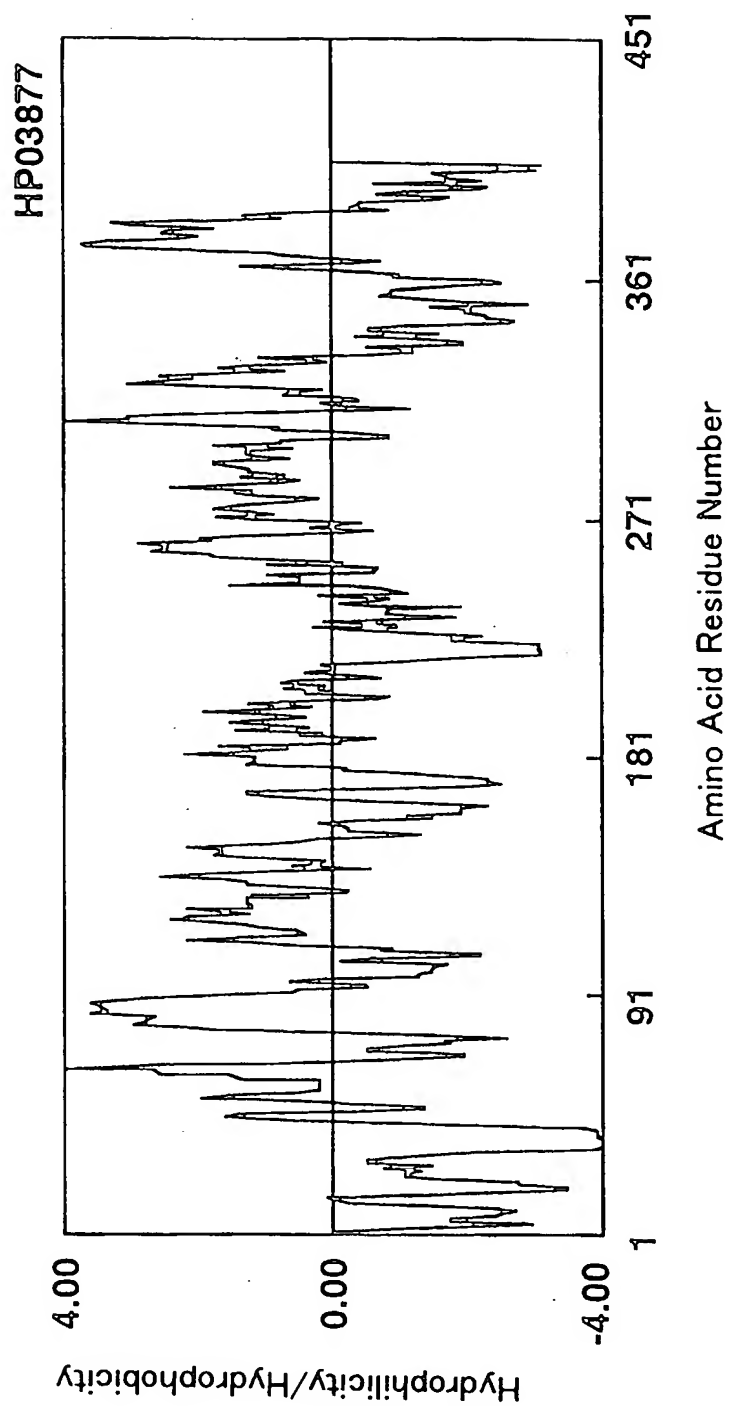


Fig.44

45/50

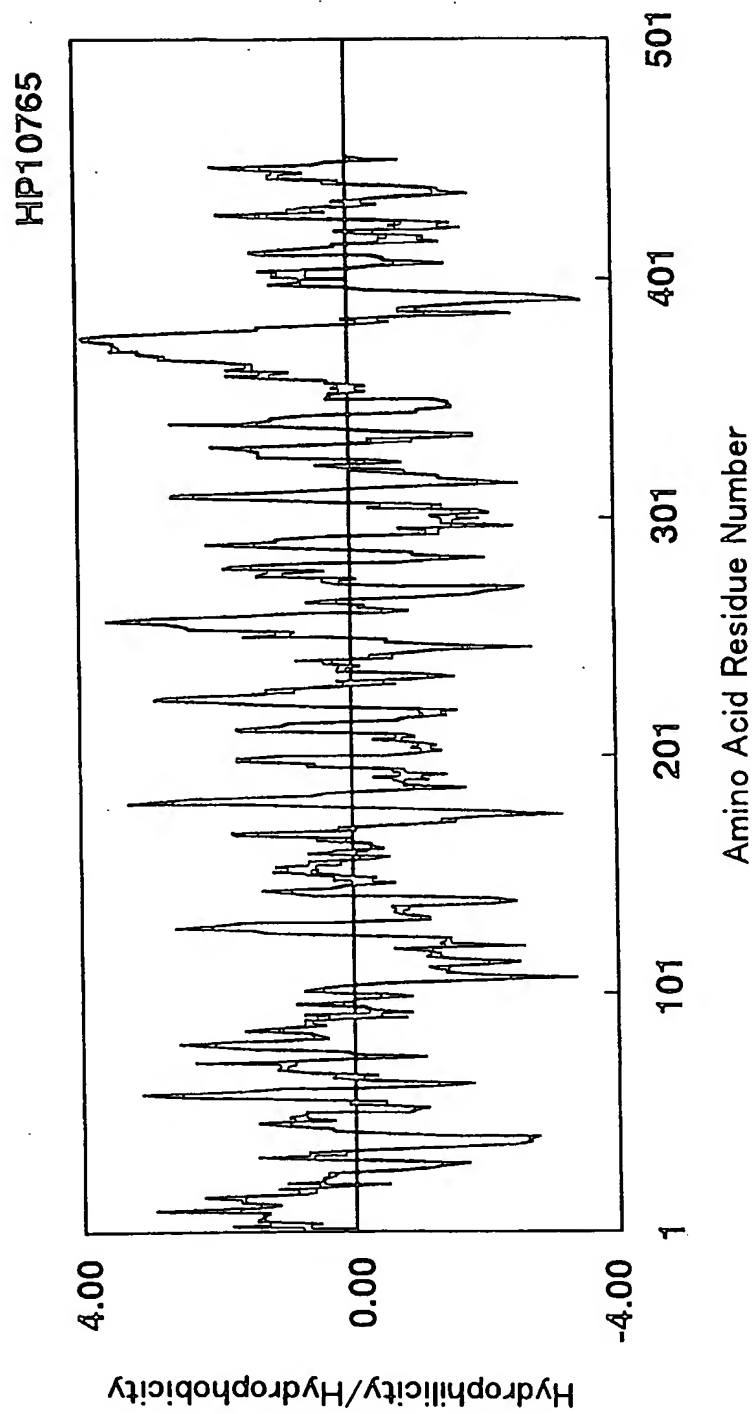


Fig.45

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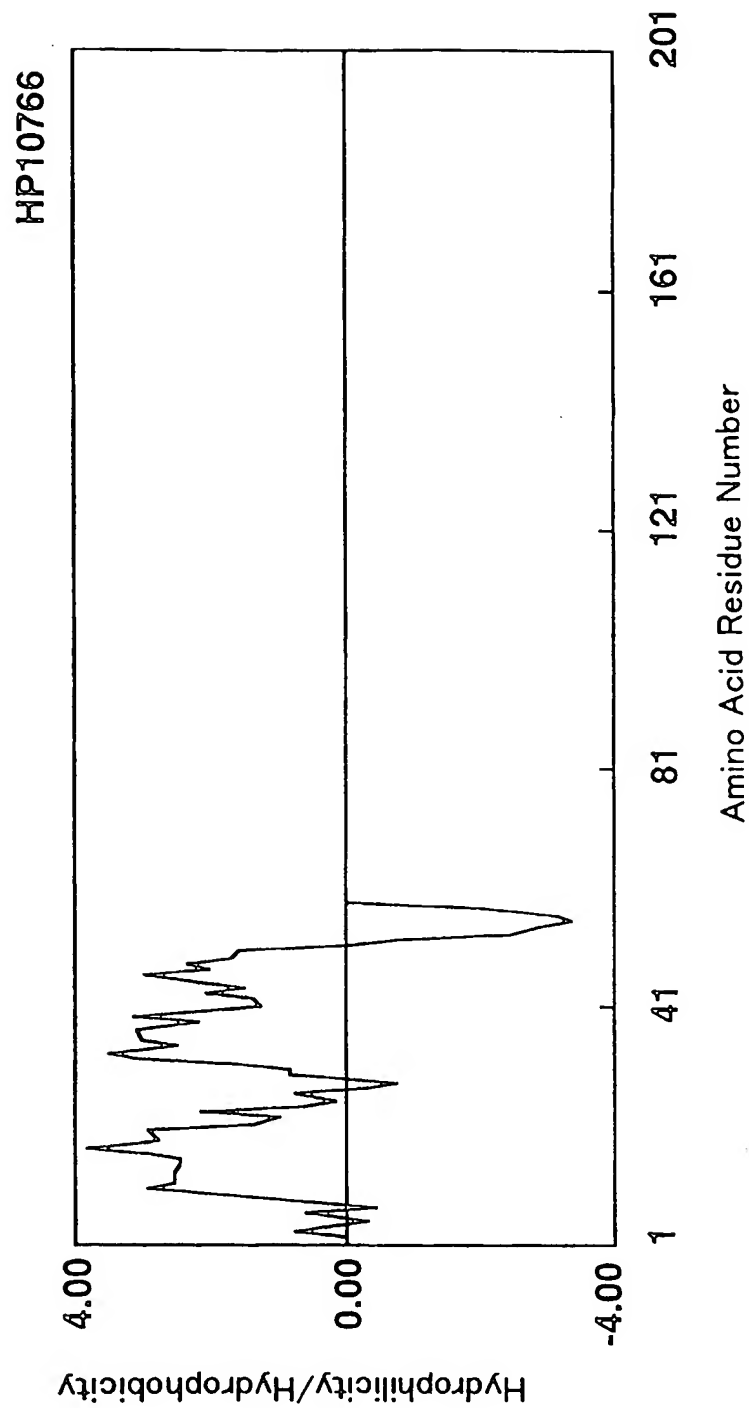


Fig.46

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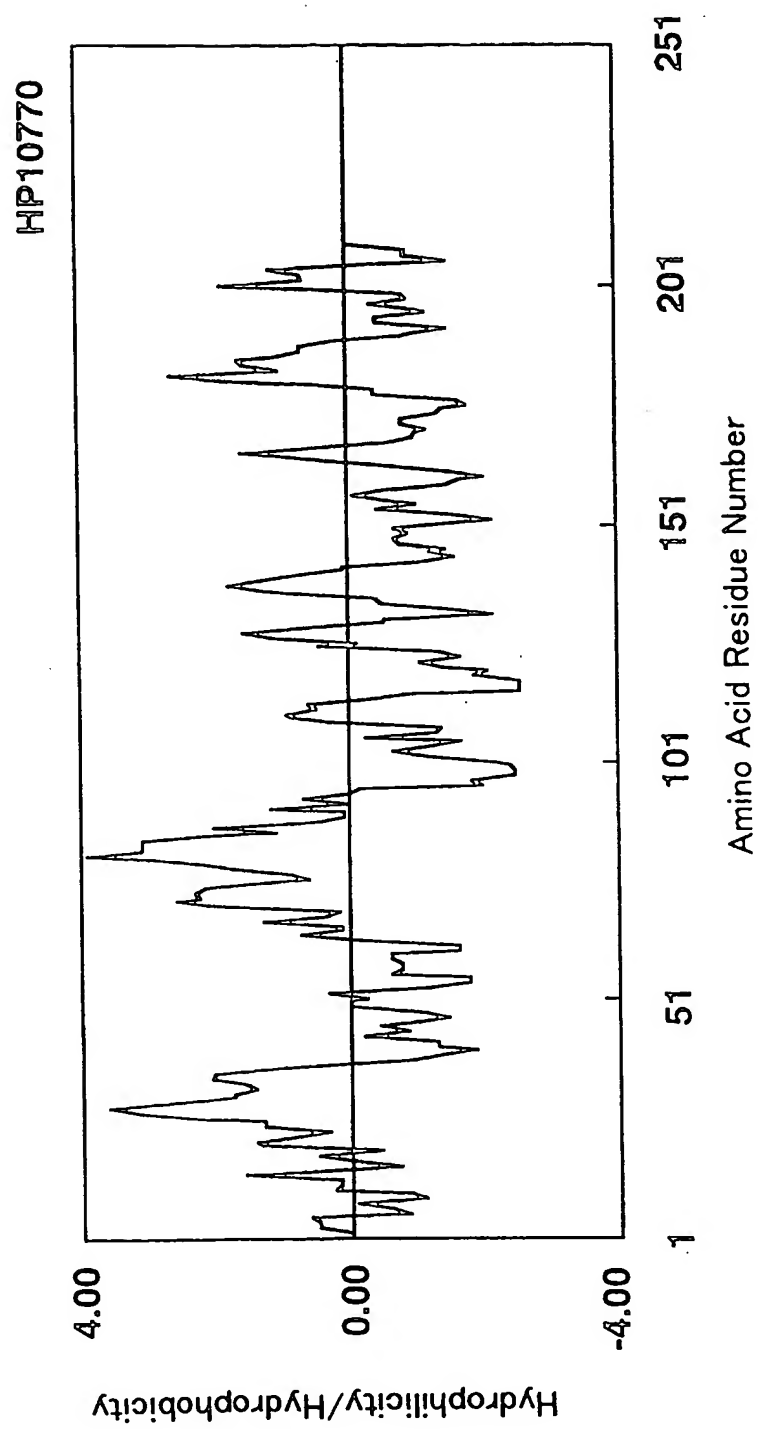


Fig.47

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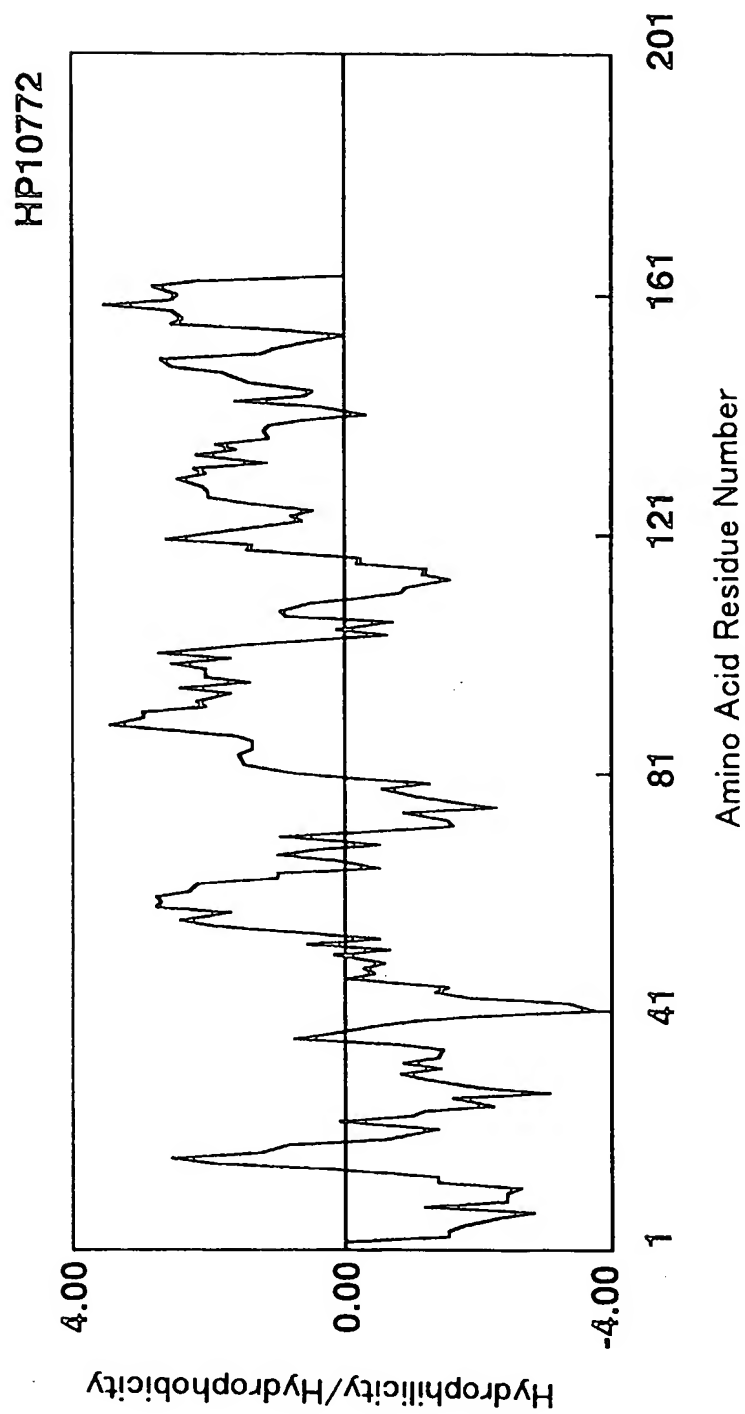


Fig.48

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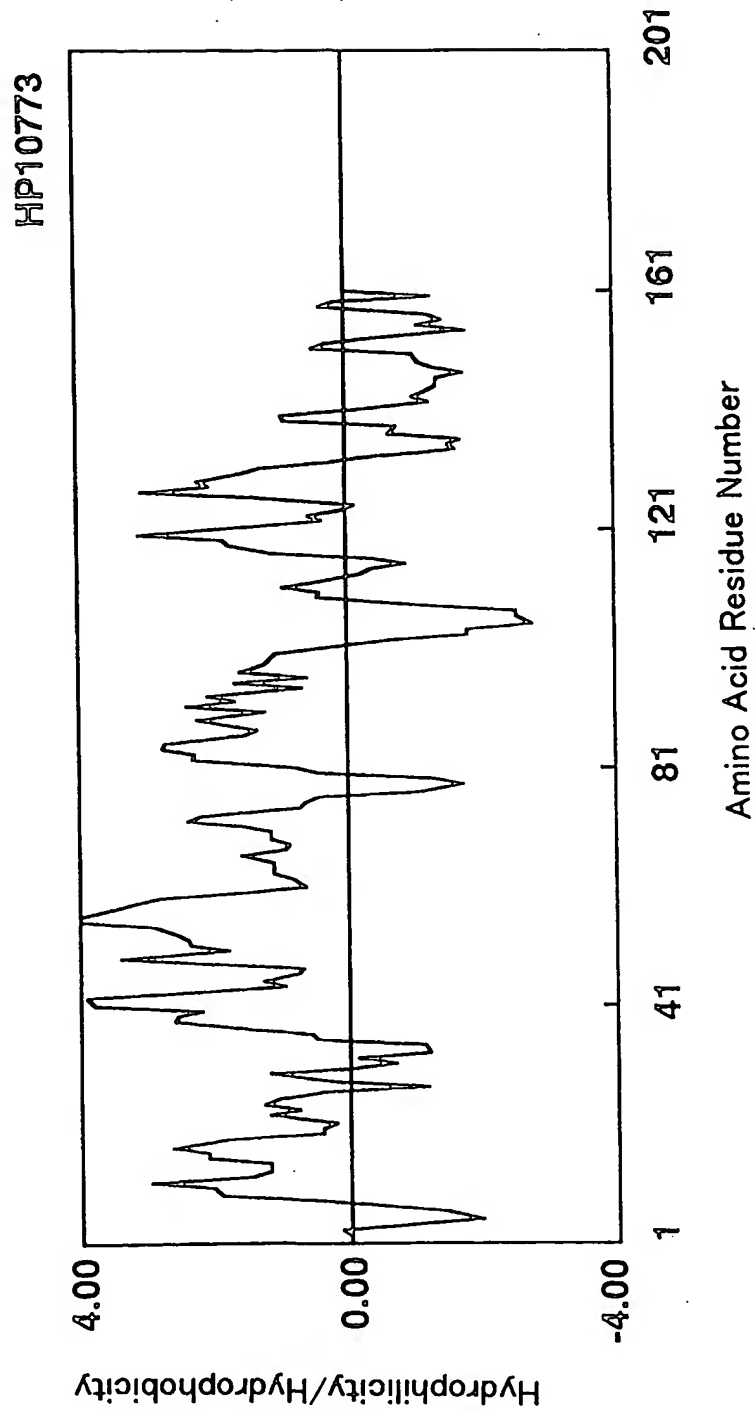


Fig.49



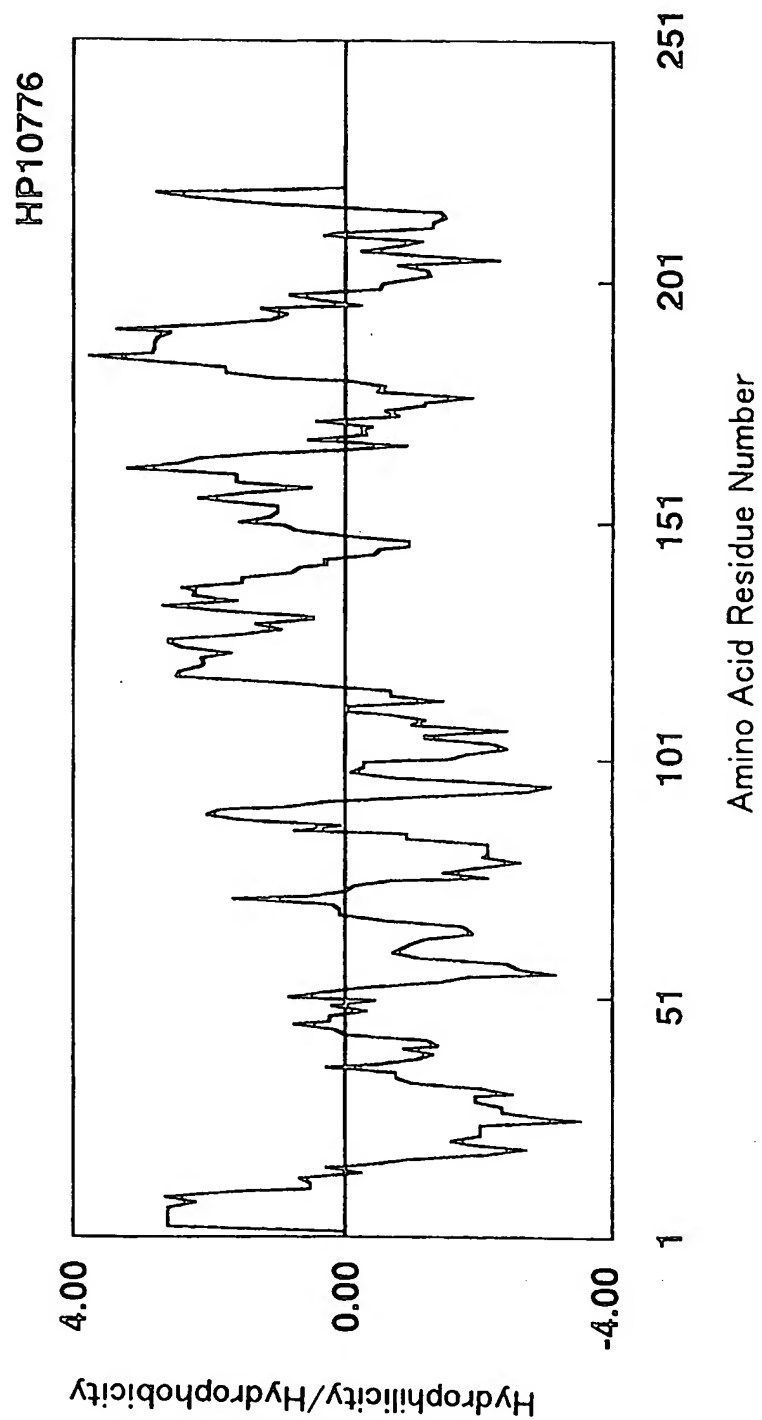


Fig.50

1 /307

SEQUENCE LISTING

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Protegene Inc.

<120> Human proteins having hydrophobic domains and DNAs encoding these  
proteins

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<151> 1999-08-17

<150> JP 11-252551

<151> 1999-09-07

<150> JP 11-281132

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2 /307

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&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1

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1 5 10 15

Lys Ala Asp Lys Ala Ser Ala Ser Ala Pro Ala Pro Ala Ser Ala Thr

20 25 30

Glu Ile Leu Leu Thr Pro Ala Arg Glu Glu Gln Pro Pro Gln His Arg

35 40 45

Ser Lys Arg Gly Ser Ser Val Gly Gly Val Cys Tyr Leu Ser Met Gly

50 55 60

Met Val Val Leu Leu Met Gly Leu Val Phe Ala Ser Val Tyr Ile Tyr

65 70 75 80

Arg Tyr Phe Phe Leu Ala Gln Leu Ala Arg Asp Asn Phe Phe Arg Cys

85 90 95

Gly Val Leu Tyr Glu Asp Ser Leu Ser Ser Gln Val Arg Thr Gln Met

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Glu Leu Glu Glu Asp Val Lys Ile Tyr Leu Asp Glu Asn Tyr Glu Arg

115 120 125

Ile Asn Val Pro Val Pro Gln Phe Gly Gly Gly Asp Pro Ala Asp Ile

130 135 140

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Ile His Asp Phe Gln Arg Gly Leu Thr Ala Tyr His Asp Ile Ser Leu

145 150 155 160

Asp Lys Cys Tyr Val Ile Glu Leu Asn Thr Thr Ile Val Leu Pro Pro

165 170 175

Arg Asn Phe Trp Glu Leu Leu Met Asn Val Lys Arg Gly Thr Tyr Leu

180 185 190

Pro Gln Thr Tyr Ile Ile Gln Glu Glu Met Val Val Thr Glu His Val

195 200 205

Ser Asp Lys Glu Ala Leu Gly Ser Phe Ile Tyr His Leu Cys Asn Gly

210 215 220

Lys Asp Thr Tyr Arg Leu Arg Arg Arg Ala Thr Arg Arg Arg Ile Asn

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Lys Arg Gly Ala Lys Asn Cys Asn Ala Ile Arg His Phe Glu Asn Thr

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Phe Val Val Glu Thr Leu Ile Cys Gly Val Val

260 265

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&lt;213&gt; Homo sapiens

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1 5 10 15

Leu Leu Thr Cys Ser Leu Trp Pro Ala Arg Ala Asp Asn Ala Ser Gln

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|   |     |     |     |
|---|-----|-----|-----|
| 20  | 25  | 30  |     |
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| 35  | 40  | 45  |     |
| Gly Ala Pro Leu Thr Phe Arg Ile Asp Arg Gly Arg Tyr Gly Leu Asp |     |     |     |
| 50  | 55  | 60  |     |
| Ser Pro Lys Ala Glu Val Arg Gly Gln Val Leu Ala Pro Leu Pro Leu |     |     |     |
| 65  | 70  | 75  | 80  |
| His Gly Val Ala Asp His Leu Gly Cys Asp Pro Gln Thr Arg Phe Phe |     |     |     |
| 85  | 90  | 95  |     |
| Val Pro Pro Asn Ile Lys Gln Trp Ile Ala Leu Leu Gln Arg Gly Asn |     |     |     |
| 100   | 105 | 110 |     |
| Cys Thr Phe Lys Glu Lys Ile Ser Arg Ala Ala Phe His Asn Ala Val |     |     |     |
| 115   | 120 | 125 |     |
| Ala Val Val Ile Tyr Asn Asn Lys Ser Lys Glu Glu Pro Val Thr Met |     |     |     |
| 130   | 135 | 140 |     |
| Thr His Pro Gly Thr Gly Asp Ile Ile Ala Val Met Ile Thr Glu Leu |     |     |     |
| 145   | 150 | 155 | 160 |
| Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser Val Gln |     |     |     |
| 165   | 170 | 175 |     |
| Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe Ser Arg |     |     |     |
| 180   | 185 | 190 |     |
| Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile Ile |     |     |     |
| 195   | 200 | 205 |     |
| Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg Tyr Thr |     |     |     |
| 210   | 215 | 220 |     |

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Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala Lys Lys

225 230 235 240

Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys Gly Asp Lys Glu

245 250 255

Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile Glu Ser Tyr Lys

260 265 270

Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His Val Phe His Lys

275 280 285

Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr Cys Pro Met Cys

290 295 300

Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro Asn Leu Pro Cys

305 310 315 320

Thr Asp Asn Val Ala Phe Asp Met Glu Arg Leu Thr Arg Thr Gln Ala

325 330 335

Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp Asn Ser Leu

340 345 350

Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu Pro Gln Asp

355 360 365

Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala Val Thr Lys

370 375 380

Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala Leu Thr Leu

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Glu Trp Phe

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&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala

1 5 10 15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr

20 25 30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly

35 40 45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr

50 55 60

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu

65 70 75 80

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly

85 90 95

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro

100 105 110

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser

115 120 125

Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala

130 135 140

Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg

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145                      150                      155                      160  
Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro  
                         165                      170                      175  
Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu  
                         180                      185                      190  
Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys  
                         195                      200                      205  
Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala  
                         210                      215                      220  
Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val  
225                      230                      235                      240  
Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu  
                         245                      250                      255  
Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu  
                         260                      265                      270  
Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr  
                         275                      280                      285  
Gly Leu Lys Thr Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr  
                         290                      295                      300  
Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly  
305                      310                      315                      320  
Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val  
                         325                      330                      335  
Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala  
                         340                      345                      350



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Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro

355

360

365

Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu

370

375

380

Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys

385

390

395

400

Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys

405

410

415

&lt;210&gt; 4

&lt;211&gt; 380

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

Met Leu Gln Thr Leu Tyr Asp Tyr Phe Trp Trp Glu Arg Leu Trp Leu

1

5

10

15

Pro Val Asn Leu Thr Trp Ala Asp Leu Glu Asp Arg Asp Gly Arg Val

20

25

30

Tyr Ala Lys Ala Ser Asp Leu Tyr Ile Thr Leu Pro Leu Ala Leu Leu

35

40

45

Phe Leu Ile Val Arg Tyr Phe Phe Glu Leu Tyr Val Ala Thr Pro Leu

50

55

60

Ala Ala Leu Leu Asn Ile Lys Glu Lys Thr Arg Leu Arg Ala Pro Pro

65

70

75

80

Asn Ala Thr Leu Glu His Phe Tyr Leu Thr Ser Gly Lys Gln Pro Lys

9 /307

|   |     |     |     |
|---|-----|-----|-----|
| 85  | 90  | 95  |     |
| Gln Val Glu Val Glu Leu Leu Ser Arg Gln Ser Gly Leu Ser Gly Arg |     |     |     |
| 100   | 105 | 110 |     |
| Gln Val Glu Arg Trp Phe Arg Arg Arg Arg Asn Gln Asp Arg Pro Ser |     |     |     |
| 115   | 120 | 125 |     |
| Leu Leu Lys Lys Phe Arg Glu Ala Ser Trp Arg Phe Thr Phe Tyr Leu |     |     |     |
| 130   | 135 | 140 |     |
| Ile Ala Phe Ile Ala Gly Met Ala Val Ile Val Asp Lys Pro Trp Phe |     |     |     |
| 145   | 150 | 155 | 160 |
| Tyr Asp Met Lys Lys Val Trp Glu Gly Tyr Pro Ile Gln Ser Thr Ile |     |     |     |
| 165   | 170 | 175 |     |
| Pro Ser Gln Tyr Trp Tyr Tyr Met Ile Glu Leu Ser Phe Tyr Trp Ser |     |     |     |
| 180   | 185 | 190 |     |
| Leu Leu Phe Ser Ile Ala Ser Asp Val Lys Arg Lys Asp Phe Lys Glu |     |     |     |
| 195   | 200 | 205 |     |
| Gln Ile Ile His His Val Ala Thr Ile Ile Leu Ile Ser Phe Ser Trp |     |     |     |
| 210   | 215 | 220 |     |
| Phe Ala Asn Tyr Ile Arg Ala Gly Thr Leu Ile Met Ala Leu His Asp |     |     |     |
| 225   | 230 | 235 | 240 |
| Ser Ser Asp Tyr Leu Leu Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly |     |     |     |
| 245   | 250 | 255 |     |
| Trp Lys Asn Thr Cys Asn Asn Ile Phe Ile Val Phe Ala Ile Val Phe |     |     |     |
| 260   | 265 | 270 |     |
| Ile Ile Thr Arg Leu Val Ile Leu Pro Phe Trp Ile Leu His Cys Thr |     |     |     |
| 275   | 280 | 285 |     |

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Leu Val Tyr Pro Leu Glu Leu Tyr Pro Ala Phe Phe Gly Tyr Tyr Phe

290 295 300

Phe Asn Ser Met Met Gly Val Leu Gln Leu Leu His Ile Phe Trp Ala

305 310 315 320

Tyr Leu Ile Leu Arg Met Ala His Lys Phe Ile Thr Gly Lys Leu Val

325 330 335

Glu Asp Glu Arg Ser Asp Arg Glu Glu Thr Glu Ser Ser Glu Gly Glu

340 345 350

Glu Ala Ala Ala Gly Gly Gly Ala Lys Ser Arg Pro Leu Ala Asn Gly

355 360 365

His Pro Ile Leu Asn Asn Asn His Arg Lys Asn Asp

370 375 380

<210> 5

<211> 585

<212> PRT

<213> Homo sapiens

<400> 5

Met Val Cys Arg Glu Gln Leu Ser Lys Asn Gln Val Lys Trp Val Phe

1 5 10 15

Ala Gly Ile Thr Cys Val Ser Val Val Val Ile Ala Ala Ile Val Leu

20 25 30

Ala Ile Thr Leu Arg Arg Pro Gly Cys Glu Leu Glu Ala Cys Ser Pro

35 40 45

Asp Ala Asp Met Leu Asp Tyr Leu Leu Ser Leu Gly Gln Ile Ser Arg

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|   |     |     |     |
|---|-----|-----|-----|
| 50  | 55  | 60  |     |
| Arg Asp Ala Leu Glu Val Thr Trp Tyr His Ala Ala Asn Ser Lys Lys |     |     |     |
| 65  | 70  | 75  | 80  |
| Ala Met Thr Ala Ala Leu Asn Ser Asn Ile Thr Val Leu Glu Ala Asp |     |     |     |
| 85  | 90  | 95  |     |
| Val Asn Val Glu Gly Leu Gly Thr Ala Asn Glu Thr Gly Val Pro Ile |     |     |     |
| 100   | 105 | 110 |     |
| Met Ala His Pro Pro Thr Ile Tyr Ser Asp Asn Thr Leu Glu Gln Trp |     |     |     |
| 115   | 120 | 125 |     |
| Leu Asp Ala Val Leu Gly Ser Ser Gln Lys Gly Ile Lys Leu Asp Phe |     |     |     |
| 130   | 135 | 140 |     |
| Lys Asn Ile Lys Ala Val Gly Pro Ser Leu Asp Leu Leu Arg Gln Leu |     |     |     |
| 145   | 150 | 155 | 160 |
| Thr Glu Glu Gly Lys Val Arg Arg Pro Ile Trp Ile Asn Ala Asp Ile |     |     |     |
| 165   | 170 | 175 |     |
| Leu Lys Gly Pro Asn Met Leu Ile Ser Thr Glu Val Asn Ala Thr Gln |     |     |     |
| 180   | 185 | 190 |     |
| Phe Leu Ala Leu Val Gln Glu Lys Tyr Pro Lys Ala Thr Leu Ser Pro |     |     |     |
| 195   | 200 | 205 |     |
| Gly Trp Thr Thr Phe Tyr Met Ser Thr Ser Pro Asn Arg Thr Tyr Thr |     |     |     |
| 210   | 215 | 220 |     |
| Gln Ala Met Val Glu Lys Met His Glu Leu Val Gly Gly Val Pro Gln |     |     |     |
| 225   | 230 | 235 | 240 |
| Arg Val Thr Phe Pro Val Arg Ser Ser Met Val Arg Ala Ala Trp Pro |     |     |     |
| 245   | 250 | 255 |     |

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His Phe Ser Trp Leu Leu Ser Gln Ser Glu Arg Tyr Ser Leu Thr Leu

260

265

270

Trp Gln Ala Ala Ser Asp Pro Met Ser Val Glu Asp Leu Leu Tyr Val

275

280

285

Arg Asp Asn Thr Ala Val His Gln Val Tyr Tyr Asp Ile Phe Glu Pro

290

295

300

Leu Leu Ser Gln Phe Lys Gln Leu Ala Leu Asn Ala Thr Arg Lys Pro

305

310

315

320

Met Tyr Tyr Thr Gly Gly Ser Leu Ile Pro Leu Leu Gln Leu Pro Gly

325

330

335

Asp Asp Gly Leu Asn Val Glu Trp Leu Val Pro Asp Val Gln Gly Ser

340

345

350

Gly Lys Thr Ala Thr Met Thr Leu Pro Asp Thr Glu Gly Met Ile Leu

355

360

365

Leu Asn Thr Gly Leu Glu Gly Thr Val Ala Glu Asn Pro Val Pro Ile

370

375

380

Val His Thr Pro Ser Gly Asn Ile Leu Thr Leu Glu Ser Cys Leu Gln

385

390

395

400

Gln Leu Ala Thr His Pro Gly His Trp Gly Ile His Leu Gln Ile Ala

405

410

415

Glu Pro Ala Ala Leu Arg Pro Ser Leu Ala Leu Leu Ala Arg Leu Ser

420

425

430

Ser Leu Gly Leu Leu His Trp Pro Val Trp Val Gly Ala Lys Ile Ser

435

440

445

His Gly Ser Phe Ser Val Pro Gly His Val Ala Gly Arg Glu Leu Leu

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450                      455                      460  
 Thr Ala Val Ala Glu Val Phe Pro His Val Thr Val Ala Pro Gly Trp  
 465                      470                      475                      480  
 Pro Glu Glu Val Leu Gly Ser Gly Tyr Arg Glu Gln Leu Leu Thr Asp  
                     485                      490                      495  
 Met Leu Glu Leu Cys Gln Gly Leu Trp Gln Pro Val Ser Phe Gln Met  
                     500                      505                      510  
 Gln Ala Met Leu Leu Gly His Ser Thr Ala Gly Ala Ile Gly Arg Leu  
                     515                      520                      525  
 Leu Ala Ser Ser Pro Arg Ala Thr Val Thr Val Glu His Asn Pro Ala  
                     530                      535                      540  
 Gly Gly Asp Tyr Ala Ser Val Arg Thr Ala Leu Leu Ala Ala Arg Ala  
 545                      550                      555                      560  
 Val Asp Arg Thr Arg Val Tyr Tyr Arg Leu Pro Gln Gly Tyr His Lys  
                     565                      570                      575  
 Asp Leu Leu Ala His Val Gly Arg Asn  
                     580                      585

&lt;210&gt; 6

&lt;211&gt; 331

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe

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Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys

20

25

30

Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu

35

40

45

Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg

50

55

60

Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn

65

70

75

80

Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val

85

90

95

Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His

100

105

110

Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp

115

120

125

Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg

130

135

140

Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Arg Glu Ala

145

150

155

160

Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys

165

170

175

Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu

180

185

190

Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu

195

200

205

Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu

15 / 307

|   |     |     |     |
|---|-----|-----|-----|
| 210   | 215 | 220 |     |
| Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg |     |     |     |
| 225   | 230 | 235 | 240 |
| Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu |     |     |     |
|   | 245 | 250 | 255 |
| Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser |     |     |     |
|   | 260 | 265 | 270 |
| Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys |     |     |     |
|   | 275 | 280 | 285 |
| Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe |     |     |     |
|   | 290 | 295 | 300 |
| Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser Tyr Ile Thr |     |     |     |
| 305   | 310 | 315 | 320 |
| Asp Ser Met Val Glu Asp Cys Glu Pro His Phe                     |     |     |     |
|   | 325 | 330 |     |

&lt;210&gt; 7

&lt;211&gt; 345

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 7

Met Ser Pro Glu Glu Trp Thr Tyr Leu Val Val Leu Leu Ile Ser Ile

1

5

10

15

Pro Ile Gly Phe Leu Phe Lys Lys Ala Gly Pro Gly Leu Lys Arg Trp

20

25

30



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Gly Ala Ala Ala Val Gly Leu Gly Leu Thr Leu Phe Thr Cys Gly Pro  
                   35                                  40                                  45  
 His Thr Leu His Ser Leu Val Thr Ile Leu Gly Thr Trp Ala Leu Ile  
                   50                                  55                                  60  
 Gln Ala Gln Pro Cys Ser Cys His Ala Leu Ala Leu Ala Trp Thr Phe  
                   65                                  70                                  75                                  80  
 Ser Tyr Leu Leu Phe Phe Arg Ala Leu Ser Leu Leu Gly Leu Pro Thr  
                                   85                                  90                                  95  
 Pro Thr Pro Phe Thr Asn Ala Val Gln Leu Leu Leu Thr Leu Lys Leu  
                                   100                                  105                                  110  
 Val Ser Leu Ala Ser Glu Val Gln Asp Leu His Leu Ala Gln Arg Lys  
                                   115                                  120                                  125  
 Glu Met Ala Ser Gly Phe Ser Lys Gly Pro Thr Leu Gly Leu Leu Pro  
                                   130                                  135                                  140  
 Asp Val Pro Ser Leu Met Glu Thr Leu Ser Tyr Ser Tyr Cys Tyr Val  
                                   145                                  150                                  155                                  160  
 Gly Ile Met Thr Gly Pro Phe Phe Arg Tyr Arg Thr Tyr Leu Asp Trp  
                                   165                                  170                                  175  
 Leu Glu Gln Pro Phe Pro Gly Ala Val Pro Ser Leu Arg Pro Leu Leu  
                                   180                                  185                                  190  
 Arg Arg Ala Trp Pro Ala Pro Leu Phe Gly Leu Leu Phe Leu Leu Ser  
                                   195                                  200                                  205  
 Ser His Leu Phe Pro Leu Glu Ala Val Arg Glu Asp Ala Phe Tyr Ala  
                                   210                                  215                                  220  
 Arg Pro Leu Pro Ala Arg Leu Phe Tyr Met Ile Pro Val Phe Phe Ala

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225                      230                      235                      240  
 Phe Arg Met Arg Phe Tyr Val Ala Trp Ile Ala Ala Glu Cys Gly Cys  
                          245                      250                      255  
 Ile Ala Ala Gly Phe Gly Ala Tyr Pro Val Ala Ala Lys Ala Arg Ala  
                          260                      265                      270  
 Gly Gly Gly Pro Thr Leu Gln Cys Pro Pro Pro Ser Ser Pro Glu Lys  
                          275                      280                      285  
 Ala Ala Ser Leu Glu Tyr Asp Tyr Glu Thr Ile Arg Asn Ile Asp Cys  
                          290                      295                      300  
 Tyr Ser Thr Asp Phe Cys Val Arg Val Arg Asp Gly Met Arg Tyr Trp  
 305                      310                      315                      320  
 Asn Met Thr Val Gln Trp Trp Leu Ala Gln Tyr Ile Tyr Lys Ser Ala  
                          325                      330                      335  
 Pro Ala Arg Ser Tyr Val Leu Arg Leu  
                          340                      345

&lt;210&gt; 8

&lt;211&gt; 89

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 8

Met Tyr Met Gln Asp Tyr Trp Arg Thr Trp Leu Lys Gly Leu Arg Gly  
     1                      5                      10                      15  
 Phe Phe Phe Val Gly Val Leu Phe Ser Ala Val Ser Ile Ala Ala Phe  
                          20                      25                      30

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Cys Thr Phe Leu Val Leu Ala Ile Thr Arg His Gln Ser Leu Thr Asp

35

40

45

Pro Thr Ser Tyr Tyr Leu Ser Ser Val Trp Ser Phe Ile Ser Phe Lys

50

55

60

Trp Ala Phe Leu Leu Ser Leu Tyr Ala His Arg Tyr Arg Ala Asp Phe

65

70

75

80

Ala Asp Ile Ser Ile Leu Ser Asp Phe

85

&lt;210&gt; 9

&lt;211&gt; 406

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 9

Met Arg Gly Ser Val Glu Cys Thr Trp Gly Trp Gly His Cys Ala Pro

1

5

10

15

Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly

20

25

30

Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu Val Ile Pro Asn

35

40

45

Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Ala Val Gly Thr

50

55

60

Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly Pro Leu Ala Val

65

70

75

80

Val Met Val Ala Thr Asn Thr Pro His Ser Thr Leu Ser Val Asn Trp

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|   |     |     |     |
|---|-----|-----|-----|
| 85  | 90  | 95  |     |
| Ser Leu Leu Leu Ser Pro Glu Pro Asp Gly Gly Leu Met Val Leu Pro |     |     |     |
| 100   | 105 | 110 |     |
| Lys Asp Ser Ile Gln Phe Ser Ser Ala Leu Val Phe Thr Arg Leu Leu |     |     |     |
| 115   | 120 | 125 |     |
| Glu Phe Asp Ser Thr Asn Val Ser Asp Thr Ala Ala Lys Pro Leu Gly |     |     |     |
| 130   | 135 | 140 |     |
| Arg Pro Tyr Pro Pro Tyr Ser Leu Ala Asp Phe Ser Trp Asn Asn Ile |     |     |     |
| 145   | 150 | 155 | 160 |
| Thr Asp Ser Leu Asp Pro Ala Thr Leu Ser Ala Thr Phe Gln Gly His |     |     |     |
| 165   | 170 | 175 |     |
| Pro Met Asn Asp Pro Thr Arg Thr Phe Ala Asn Gly Ser Leu Ala Phe |     |     |     |
| 180   | 185 | 190 |     |
| Arg Val Gln Ala Phe Ser Arg Ser Ser Arg Pro Ala Gln Pro Pro Arg |     |     |     |
| 195   | 200 | 205 |     |
| Leu Leu His Thr Ala Asp Thr Cys Gln Leu Glu Val Ala Leu Ile Gly |     |     |     |
| 210   | 215 | 220 |     |
| Ala Ser Pro Arg Gly Asn Arg Ser Leu Phe Gly Leu Glu Val Ala Thr |     |     |     |
| 225   | 230 | 235 | 240 |
| Leu Gly Gln Gly Pro Asp Cys Pro Ser Met Gln Glu Gln His Ser Ile |     |     |     |
| 245   | 250 | 255 |     |
| Asp Asp Glu Tyr Ala Pro Ala Val Phe Gln Leu Asp Gln Leu Leu Trp |     |     |     |
| 260   | 265 | 270 |     |
| Gly Ser Leu Pro Ser Gly Phe Ala Gln Trp Arg Pro Val Ala Tyr Ser |     |     |     |
| 275   | 280 | 285 |     |

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Gln Lys Pro Gly Gly Arg Glu Ser Ala Leu Pro Cys Gln Ala Ser Pro

290

295

300

Leu His Pro Ala Leu Ala Tyr Ser Leu Pro Gln Ser Pro Ile Val Arg

305

310

315

320

Ala Phe Phe Gly Ser Gln Asn Asn Phe Cys Ala Phe Asn Leu Thr Phe

325

330

335

Gly Ala Ser Thr Gly Pro Gly Tyr Trp Asp Gln His Tyr Leu Ser Trp

340

345

350

Ser Met Leu Leu Gly Val Gly Phe Pro Pro Val Asp Gly Leu Ser Pro

355

360

365

Leu Val Leu Gly Ile Met Ala Val Ala Leu Gly Ala Pro Gly Leu Met

370

375

380

Leu Leu Gly Gly Gly Leu Val Leu Leu Leu His His Lys Lys Tyr Ser

385

390

395

400

Glu Tyr Gln Ser Ile Asn

405

&lt;210&gt; 10

&lt;211&gt; 192

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 10

Met Thr Ala Val Gly Val Gln Ala Gln Arg Pro Leu Gly Gln Arg Gln

1

5

10

15

Pro Arg Arg Ser Phe Phe Glu Ser Phe Ile Arg Thr Leu Ile Ile Thr

21 /307

|   |     |     |     |
|---|-----|-----|-----|
| 20  | 25  | 30  |     |
| Cys Val Ala Leu Ala Val Val Leu Ser Ser Val Ser Ile Cys Asp Gly |     |     |     |
| 35  | 40  | 45  |     |
| His Trp Leu Leu Ala Glu Asp Arg Leu Phe Gly Leu Trp His Phe Cys |     |     |     |
| 50  | 55  | 60  |     |
| Thr Thr Thr Asn Gln Ser Val Pro Ile Cys Phe Arg Asp Leu Gly Gln |     |     |     |
| 65  | 70  | 75  | 80  |
| Ala His Val Pro Gly Leu Ala Val Gly Met Gly Leu Val Arg Ser Val |     |     |     |
| 85  | 90  | 95  |     |
| Gly Ala Leu Ala Val Val Ala Ala Ile Phe Gly Leu Glu Phe Leu Met |     |     |     |
| 100   | 105 | 110 |     |
| Val Ser Gln Leu Cys Glu Asp Lys His Ser Gln Cys Lys Trp Val Met |     |     |     |
| 115   | 120 | 125 |     |
| Gly Ser Ile Leu Leu Leu Val Ser Phe Val Leu Ser Ser Gly Gly Leu |     |     |     |
| 130   | 135 | 140 |     |
| Leu Gly Phe Val Ile Leu Leu Arg Asn Gln Val Thr Leu Ile Gly Phe |     |     |     |
| 145   | 150 | 155 | 160 |
| Thr Leu Met Phe Trp Cys Glu Phe Thr Ala Ser Phe Leu Leu Phe Leu |     |     |     |
| 165   | 170 | 175 |     |
| Asn Ala Ile Ser Gly Leu His Ile Asn Ser Ile Thr His Pro Trp Glu |     |     |     |
| 180   | 185 | 190 |     |

&lt;210&gt; 11

&lt;211&gt; 801

&lt;212&gt; DNA

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&lt;213&gt; Homo sapiens

&lt;400&gt; 11

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atggtgaaga ttagcttcca gcccgccgtg gctggcatca agggcgacaa ggctgacaag      60
gcgtcggcgt cggccctgc gccggcctcg gccaccgaga tcctgctgac gccggctagg      120
gaggagcagc cccacaaca tcgatccaag agggggagct cagtgggcgg cgtgtgctac      180
ctgtcgatgg gcatggctgt gctgctcatg ggcctcgtgt tcgcctctgt ctacatctac      240
agataacttct ttcttgaca gctggcccga gataacttct tccgctgtgg tgtgtgttat      300
gaggactccc tgtcctccca ggtccggact cagatggagc tggaagagga tgtgaaaatc      360
tacctcgacg agaactacga gcgcatcaac gtgcctgtgc ccagtttgg cggcggtgac      420
cctgcagaca tcatccatga cttccagcgg ggtctgactg cgtaccatga tatctccctg      480
gacaagtgt atgtcatoga actcaacacc accattgtgc tgccccctcg caacttctgg      540
gagtcctca tgaacgtgaa gagggggacc tacctgccgc agacgtacat catccaggag      600
gagatggtgg tcacggagca tgtcagtac aaggaggccc tggggtcctt catctaccac      660
ctgtgcaacg ggaaagacac ctaccggtc cggcgccggg caacgcggag gcggatcaac      720
aagcgtgggg ccaagaactg caatgccatc cgccacttcg agaacacctt cgtggtggag      780
acgtcatct gcggggtggt g                                     801

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&lt;210&gt; 12

&lt;211&gt; 1257

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 12

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atgagctgcg cggggcgggc gggccctgpc cggctcgccg cgctcgccct gctgacctgc      60
agcctgtggc cggcacgggc agacaacgcg agccaggagt actacacggc gtcatacaac      120
gtgacggtgc aggagcccgg ccgcggcgcc ccgctcacgt ttgcatacga ccgcgggcgc      180

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tacgggcttg actccccaa ggccgaggtc cgcgccagg tgctggcgcc gctgccctc 240  
 cacggagttg ctgatcatct gggctgtgat ccacaaaccc ggttctttgt cctcctaata 300  
 atcaaacagt ggattgcctt gctgcagagg ggaaactgca cgtttaaaga gaaaatatca 360  
 cgggcccgtt tccacaatgc agttgctgta gtcatttaca ataataaatc caaagaggag 420  
 ccagttacca tgactcatcc aggcaactgga gatattattg ctgtcatgat aacagaattg 480  
 aggggtaagg atattttgag ttatctggag aaaaacatct ctgtacaaat gacaatagct 540  
 gttggaactc gaatgccacc gaagaacttc agccgtggct ctctagtctt cgtgtcaata 600  
 tcctttattg ttttgatgat tattttctca gcatggctca tattctactt cattcagaag 660  
 atcaggtaca caaatgcacg cgacaggaac cagcgtcgtc tcggagatgc agccaagaaa 720  
 gccatcagta aattgacaac caggacagta aagaagggtg acaaggaaac tgaccagac 780  
 tttgatcatt gtgcagtctg catagagagc tataagcaga atgatgtcgt ccgaattctc 840  
 ccctgcaagc atgttttcca caaatctgc gtggatccct ggcttagtga acattgtacc 900  
 tgtctatgt gcaaaactaa tatattgaag gccctgggaa ttgtgccgaa tttgccatgt 960  
 actgataacg tagcattcga tatggaaagg ctaccagaa cccaagctgt taaccgaaga 1020  
 tcagccctcg gcgacctgc cgcgacaac tcccttgccc ttgagccact tcgaacttcg 1080  
 gggatctcac ctcttctca ggatggggag ctactccga gaacaggaga aatcaacatt 1140  
 gcagtaacaa aagaatggtt tattattgcc agttttggcc tctcagtgc cctcacactc 1200  
 tgctacatga tcatcagagc cacagctagc ttgaatgcta atgaggtaga atggttt 1257

&lt;210&gt; 13

&lt;211&gt; 1245

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 13

atgaggggog cgaacgcctg ggcgccactc tgcctgctgc tggctgccgc caccagctc 60



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|   |      |
|---|------|
| tcgcggcagc agtccccaga gagacctgtt ttcacatgtg gtggcattct tactggagag   | 120  |
| tctggattta ttggcagtga aggttttctt ggagtgtacc ctccaaatag caaatgtact   | 180  |
| tggaaaatca cagttcccgaggaaaagta gtctgttctca atttccgatt catagacctc    | 240  |
| gagagtgaca acctgtgccg ctatgacttt gtggatgtgt acaatggcca tgccaatggc   | 300  |
| cagcgcattg gccgcttctg tggcactttc cggcctggag cccttgtgtc cagtggcaac   | 360  |
| aagatgatgg tgcagatgat ttctgatgcc aacacagctg gcaatggctt catggccatg   | 420  |
| ttctccgctg ctgaacaaaa cgaaagaggg gatcagtatt gtggaggact ccttgacaga   | 480  |
| ccttccggct cttttaaaac cccaactgg ccagaccggg attacctgc aggagtcact     | 540  |
| tgtgtgtggc acattgtagc cccaaagaat cagcttatag aattaaagtt tgagaagttt   | 600  |
| gatgtggagc gagataacta ctgccgatat gattatgtgg ctgtgtttta tggcggggaa   | 660  |
| gtcaacgatg ctagaagaat tggaaagtat tgtggtgata gtccacctgc gccaatgtg    | 720  |
| tctgagagaa atgaacttct tattcagttt ttatcagact taagttaaac tgcagatggg   | 780  |
| tttattggtc actacatatt caggccaaaa aaactgccta caactacaga acagcctgtc   | 840  |
| accaccacat tccctgtaac cacgggttta aaaaccaccg tggccttgtg tcaacaaaag   | 900  |
| tgtagacgga cggggactct ggagggaat tattgttcaa gtgactttgt attagccggc    | 960  |
| actgttatca caaccatcac tcgcgatggg agtttgcacg ccacagtctc gatcatcaac   | 1020 |
| atctacaaag agggaaattt ggcgattcag caggcgggca agaacatgag tgccaggctg   | 1080 |
| actgtcgtct gcaagcagtg ccctctctctc agaagaggctc taaattacat tattatgggc | 1140 |
| caagtaggtg aagatgggag aggcaaaatc atgccaaaca gctttatcat gatgttcaag   | 1200 |
| accaagaatc agaagctcct ggatgcctta aaaaataagc aatgt                   | 1245 |

&lt;210&gt; 14

&lt;211&gt; 1140

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;400&gt; 14

|   |      |
|---|------|
| atgctccaga ccttgtatga ttacttctgg tgggaacgtc tgtggctgcc tgtgaacttg | 60   |
| acctgggccg atctagaaga ccgagatgga cgtgtctacg ccaaagcctc agatctctat | 120  |
| atcacgtgc ccctggcctt gctcttctc atcgttcgat acttctttga gctgtacgtg   | 180  |
| gctacaccac tggctgccct cttgaacata aaggagaaaa ctggctgcg ggcacctccc  | 240  |
| aacgccacct tggaacattt ctacctgacc agtggcaagc agcccaagca ggtggaagta | 300  |
| gagcttttgt cccggcagag cgggctctct ggccgccagg tagagcgttg gttccgtcgc | 360  |
| cgcgcgaacc aggaccggcc cagtctctc aagaagttcc gagaagccag ctggagattc  | 420  |
| acattttacc tgattgcctt cattgccggc atggccgtca ttgtggataa acctggttc  | 480  |
| tatgacatga agaaagtttg ggagggatat ccatacaga gcactatccc ttcccagtat  | 540  |
| tggtactaca tgattgaact ttccttctac tggtcctgc tcttcagcat tgcctctgat  | 600  |
| gtcaagcgaa aggatttcaa ggaacagatc atccaccatg tggccaccat cattctcatc | 660  |
| agcttttctt ggtttgcaa ttacatccga gctgggactc taatcatggc tctgcatgac  | 720  |
| tcttccgatt acctgctgga gtcagccaag atgtttaact acgcgggatg gaagaacacc | 780  |
| tgcaacaaca tcttcacgtt ctccgccatt gtttttatca tcacccgact ggtcatcctg | 840  |
| cccttctgga tctgcatg caccctgggtg taccactgg agctctatcc tgccttcttt   | 900  |
| ggctattact tcttcaattc catgatggga gttctacagc tgctgcatat cttctgggcc | 960  |
| tacctcattt tgcgcatggc ccacaagttc ataactggaa agctggtaga agatgaacgc | 1020 |
| agtgaccggg aagaaacaga gagctcagag ggggaggagg ctgcagctgg gggaggagca | 1080 |
| aagagccggc ccctagccaa tggccacccc atcctcaata acaaccatcg taagaatgac | 1140 |

&lt;210&gt; 15

&lt;211&gt; 1755

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;400&gt; 15

|  |      |
|--|------|
| atggtctgca gggagcagtt atcaaagaat caggtcaagt ggggtgtttgc cggcattacc | 60   |
| tgtgtgtctg tgggtggtcat tgccgcaata gtccttgcca tcacctgcg gcggccaggc  | 120  |
| tgtgagctgg aggctgcag cctgatgcc gacatgctgg actacctgct gagcctgggc    | 180  |
| cagatcagcc ggcgagatgc cttggaggtc acctggtacc acgcagccaa cagcaagaaa  | 240  |
| gccatgacag ctgccctgaa cagcaacatc acagtcctgg aggctgacgt caatgtagaa  | 300  |
| gggctcggca cagccaatga gacaggagtt cccatcatgg cacaccccc cactatctac   | 360  |
| agtgacaaca cactggagca gtggctggac gctgtgctgg gctcttccca aaagggcac   | 420  |
| aaactggact tcaagaacat caaggcagtg gccccctccc tggacctcct gcggcagctg  | 480  |
| acagaggaag gcaaagtccg gcggcccata tggatcaacg ctgacatctt aaagggcccc  | 540  |
| aacatgctca tctcaactga ggtcaatgcc acacagttcc tggccctggt ccaggagaag  | 600  |
| tatcccaagg ctacctatc tccaggtcgg accaccttct acatgtccac gtccccaaac   | 660  |
| aggacgtaca cccaagccat ggtggagaag atgcacgagc tgggtgggagg agtgccccag | 720  |
| agggtcacct tccctgtacg gtcttccatg gtgcgggctg cctggcccca cttcagctgg  | 780  |
| ctgctgagcc aatctgagag gtacagcctg acgctgtggc aggtgcctc ggaccccatg   | 840  |
| tcggtggaag atctgctcta cgtccgggat aacactgctg tccaccaagt ctactatgac  | 900  |
| atctttgagc ctctcctgtc acagttcaag cagctggcct tgaatgccac acggaaacca  | 960  |
| atgtactaca caggaggcag cctgatccct cttctccagc tgcctgggga tgacggtctg  | 1020 |
| aatgtggagt ggctggttcc tgacgtccag ggcagcggta aaacagcaac aatgaccctc  | 1080 |
| ccagacacag aaggcatgat cctgctgaac actggcctcg agggaaactgt ggtgaaaac  | 1140 |
| cccgtgcccc ttgttcatac tccaagtggc aacatcctga cgctggagtc ctgcctgcag  | 1200 |
| cagctggcca cacatcccg acactggggc atccatttgc aaatagcgga gcccgcagcc   | 1260 |
| ctccggccat ccctggcctt gctggcacgc ctctccagcc ttggcctctt gcattggcct  | 1320 |
| gtgtgggttg gggccaaaat ctcccacggg agtttttcgg tccccggcca tgttgctggc  | 1380 |
| agagagctgc ttacagctgt ggctgaggtc ttccccacg tgactgtggc accaggtcgg   | 1440 |

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cctgaggagg tgctgggcag tggctacagg gaacagctgc tcacagatat gctagagttg 1500  
 tgccaggggc tctggcaacc tgtgtccttc cagatgcagg ccatgctgct gggccacagc 1560  
 acagctggag ccataggcag gctgctggca tcttcccccc gggccaccgt cacagtggag 1620  
 cacaaccag ctgggggcga ctatgcctct gtgaggacag cattgctggc agctagggct 1680  
 gtggacagga cccgagtcta ctacaggcta cccagggt accacaagga cttgctggct 1740  
 catgttgta gaaac 1755

&lt;210&gt; 16

&lt;211&gt; 993

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

atgtggctgt gggaggacca gggcggcctc ctgggccctt tctcttcct gctgctagt 60  
 ctgctgctgg tgacgggag cccggtcaat gcctgcctcc tcaccggcag cctcttcgtt 120  
 ctactgcgg tcttcagctt tgagccggtg cctcttgca gggccctgca ggtgctcaag 180  
 ccccgggacc gcatttctgc catgcccac cgtggcgga gccacgacg gcccgagaac 240  
 acgctggcgg ccattcggca ggcagctaag aatggagcaa caggcgtgga gttggacatt 300  
 gagtttactt ctgacgggat tctgtctta atgcacgata acacagtaga taggacgact 360  
 gatgggactg ggcgatttg tgatttgaca ttgaacaaa ttaggaagct gaatcctgca 420  
 gcaaaccaca gactcaggaa tgatttcct gatgaaaaga tccctaccct aagggaagct 480  
 gttgcagagt gcctaaacca taacctcaca atcttcttg atgtcaaagg ccatgcacac 540  
 aaggctactg aggcctctaaa gaaaatgtat atggaatttc ctcaactgta taataatagt 600  
 gtggtctgtt ctttcttgcc agaagttatc tacaagatga gacaaacaga tcgggatgta 660  
 ataacagcat taactcacag accttgagc ctaagccata caggagatgg gaaaccacgc 720  
 tatgatactt tctggaacaa ttttatattt gttatgatgg acattttgct cgattggagc 780

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atgcataata tcttgtggta cctgtgtgga atttcagctt tctcatgca aaaggatttt 840  
 gtatccccgg cctacttgaa gaagtggta gctaaaggaa tccaggttgt tggttggact 900  
 gttataacct ttgatgaaaa gagttactac gaatcccatc ttggttccag ctatatcact 960  
 gacagcatgg tagaagactg cgaacctcac ttc 993

&lt;210&gt; 17

&lt;211&gt; 1035

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 17

atgtcgctg aagaatggac gtatctagt gttcttctta tctccatccc catcggttc 60  
 ctctttaaga aagccggtcc tgggctgaag agatggggag cagccgctgt gggcctgggg 120  
 ctcaccctgt tcacctgtgg cccccacact ttgcattctc tggtcacat cctcgggacc 180  
 tggggcctca ttcaggccca gccctgctcc tgccacgcc tggctctggc ctggactttc 240  
 tcctatctcc tgttcttcog agccctcage ctcttgggcc tgccactcc cagcccttc 300  
 accaatgccg tccagctgct gctgacgctg aagctggtga gcctggccag tgaagtccag 360  
 gacctgcac tggcccagag gaaggaaatg gcctcaggct tcagcaaggg gccaccctg 420  
 gggctgctgc ccgacgtgcc ctccctgatg gagacactca gctacagcta ctgctacgtg 480  
 ggaatcatga caggcccgtt ctccgctac cgcacctacc tggactggct ggagcagccc 540  
 ttccccgggg cagtgccag cctgcggccc ctgctgcgcc gcgctggcc ggccccgctc 600  
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 gccttctacg cccgccgct gcccgcccgc ctcttctaca tgatccccgt cttcttcgcc 720  
 ttccgcatgc gcttctacgt ggcttgatt gccgccgagt gcggtgcat tgccgcggc 780  
 tttggggcct acccgtggc cgccaaagcc cgggccggag gcggccccac cctccaatgc 840  
 ccacccccca gcagtcggga gaaggcggct tcttggagt atgactatga gaccatccgc 900

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aacatcgact gctacagcac agatttctgc gtgcgggtgc gcgatggcat gcggtactgg 960  
aacatgacgg tgcagtgtg gctggcgag tatatctaca agagcgacc tgcccgttcc 1020  
tatgtcctgc gcctt 1035

&lt;210&gt; 18

&lt;211&gt; 267

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 18

atgtacatgc aagattattg gaggacctgg ctcaaggggc tgcgcggctt cttcttcgtg 60  
ggcgctctct tctcgccgt ctccatgct gccttcgtca cttctctgt gctggccatc 120  
accggcatc agagcctcac agacccacc agctactacc tctccagcgt ctggagcttc 180  
atttccttca agtgggcctt cctgctcagc ctctatgcc accgctaccg ggctgacttt 240  
gctgacatca gcctcctcag cgatttc 267

&lt;210&gt; 19

&lt;211&gt; 1218

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 19

atgcgcggct ctgtggagt cacctggggt tgggggcact gtgccccag cccctgctc 60  
ctttggactc tactttgtt tgcagcccca tttggcctgc tgggggagaa gaccgcag 120  
gtgtctctgg aggtcatccc taactggtg gggccctgc agaacctgct tcatatacgg 180  
gcagtgggca ccaattccac actgcactat gtgtggagca gcctggggcc tctggcagt 240  
gtaatggtgg ccaccaacac ccccccacgc accctgagcg tcaactggag cctcctgcta 300

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tcccctgagc ccgatggggg cctgatgggtg ctccctaagg acagcattca gttttcttct 360  
 gcccttgttt ttaccagget gcttgagttt gacagcacca acgtgtccga tacggcagca 420  
 aagcctttgg gaagaccata tcctccatac tccttggccg atttctcttg gaacaacatc 480  
 actgattcat tggatcctgc caccctgagt gccacatttc aaggccaccc catgaacgac 540  
 cctaccagga cttttgcaa tggcagcctg gccttcaggg tccaggcctt ttccaggtec 600  
 agccgaccag cccaaccccc tcgcctcctg cacacagcag acacctgtca gctagaggtg 660  
 gccctgattg gagcctctcc ccggggaaac cgttccctgt ttgggctgga ggtagccaca 720  
 ttgggccagg gccctgactg cccctcaatg caggagcagc actccatcga cgatgaatat 780  
 gcaccggccg tcttccagtt ggaccagcta ctgtggggct ccctcccatc aggcctttgca 840  
 cagtggcgac cagtggctta ctcccagaag ccggggggcc gagaatcagc cctgccctgc 900  
 caagcttccc ctcttcatcc tgccttagca tactctcttc ccagtcacc cattgtccga 960  
 gccttctttg ggtcccagaa taacttctgt gccttcaatc tgacgttcgg ggcttccaca 1020  
 ggccctggct attgggacca aactacctc agctggctga tgctcctggg tgtgggcttc 1080  
 cctccagtgg acggcttgct ccactagtc ctgggcatca tggcagtggc cctgggtgcc 1140  
 ccagggtcga tgctgctagg gggcggttg gttctgctgc tgcaccacaa gaagtactca 1200  
 gagtaccagt ccataaat 1218

&lt;210&gt; 20

&lt;211&gt; 576

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 20

atgactgccg tcggcgtgca ggcccagagg cctttgggcc aaaggcagcc ccgccgtcc 60  
 ttctttgaat cttcatccg gacctcatc atcacgtgtg tggccctggc tgtggctctg 120  
 tcctcggtct ccatttgtga tgggcactgg ctctggctg aggaccgcct ctccggctc 180

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tggcacttct gcaccaccac caaccagagt gtgccgatct gcttcagaga cctgggccag 240  
 gcccatgtgc ccgggctggc cgtgggcatg ggcctggtac gcagcgtggg cgccttggcc 300  
 gtggtggccg ccatttttgg cctggagttc ctcatggtgt ccagttgtg cgaggacaaa 360  
 cactcacagt gcaagtgggt catgggttcc atcctcctcc tgggtgtctt cgctctctcc 420  
 tccggcgggc tcctgggttt tgtgatcctc ctccaggaacc aagtcacact catcggttc 480  
 accctaattgt ttggtgcga attcactgcc tccttcctcc tcttcctgaa cgccatcagc 540  
 ggccttcaca tcaacagcat caccatccc tgggaa 576

&lt;210&gt; 21

&lt;211&gt; 2042

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (91)... (894)

&lt;400&gt; 21

tccggtgcct gcagagctcg gagcggcgga ggcagagacc gaggtgcac cggcagaggc 60  
 tgcggggcgg acgcgcgggc cggcgcagcc atg gtg aag att agc ttc cag 111

Met Val Lys Ile Ser Phe Gln

1

5

ccc gcc gtg gct ggc atc aag ggc gac aag gct gac aag gcg tcg gcg 159  
 Pro Ala Val Ala Gly Ile Lys Gly Asp Lys Ala Asp Lys Ala Ser Ala

10

15

20

tcg gcc cct gcg ccg gcc tcg gcc acc gag atc ctg ctg acg ccg gct 207  
 Ser Ala Pro Ala Pro Ala Ser Ala Thr Glu Ile Leu Leu Thr Pro Ala



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|   |     |     |     |
|---|-----|-----|-----|
| 25  | 30  | 35  |     |
| agg gag gag cag ccc cca caa cat cga tcc aag agg ggg agc tca gtg |     |     | 255 |
| Arg Glu Glu Gln Pro Pro Gln His Arg Ser Lys Arg Gly Ser Ser Val |     |     |     |
| 40  | 45  | 50  | 55  |
| ggc ggc gtg tgc tac ctg tcg atg ggc atg gtc gtg ctg ctc atg ggc |     |     | 303 |
| Gly Gly Val Cys Tyr Leu Ser Met Gly Met Val Val Leu Leu Met Gly |     |     |     |
| 60  | 65  | 70  |     |
| ctc gtg ttc gcc tct gtc tac atc tac aga tac ttc ttt ctt gca cag |     |     | 351 |
| Leu Val Phe Ala Ser Val Tyr Ile Tyr Arg Tyr Phe Phe Leu Ala Gln |     |     |     |
| 75  | 80  | 85  |     |
| ctg gcc cga gat aac ttc ttc cgc tgt ggt gtg ctg tat gag gac tcc |     |     | 399 |
| Leu Ala Arg Asp Asn Phe Phe Arg Cys Gly Val Leu Tyr Glu Asp Ser |     |     |     |
| 90  | 95  | 100 |     |
| ctg tcc tcc cag gtc cgg act cag atg gag ctg gaa gag gat gtg aaa |     |     | 447 |
| Leu Ser Ser Gln Val Arg Thr Gln Met Glu Leu Glu Glu Asp Val Lys |     |     |     |
| 105   | 110 | 115 |     |
| atc tac ctc gac gag aac tac gag cgc atc aac gtg cct gtg ccc cag |     |     | 495 |
| Ile Tyr Leu Asp Glu Asn Tyr Glu Arg Ile Asn Val Pro Val Pro Gln |     |     |     |
| 120   | 125 | 130 | 135 |
| ttt ggc ggc ggt gac cct gca gac atc atc cat gac ttc cag cgg ggt |     |     | 543 |
| Phe Gly Gly Gly Asp Pro Ala Asp Ile Ile His Asp Phe Gln Arg Gly |     |     |     |
| 140   | 145 | 150 |     |
| ctg act gcg tac cat gat atc tcc ctg gac aag tgc tat gtc atc gaa |     |     | 591 |
| Leu Thr Ala Tyr His Asp Ile Ser Leu Asp Lys Cys Tyr Val Ile Glu |     |     |     |
| 155   | 160 | 165 |     |

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etc aac acc acc att gtg ctg ccc cct cgc aac ttc tgg gag ctc ctc 639  
 Leu Asn Thr Thr Ile Val Leu Pro Pro Arg Asn Phe Trp Glu Leu Leu  
 170 175 180  
 atg aac gtg aag agg ggg acc tac ctg ccg cag acg tac atc atc cag 687  
 Met Asn Val Lys Arg Gly Thr Tyr Leu Pro Gln Thr Tyr Ile Ile Gln  
 185 190 195  
 gag gag atg gtg gtc acg gag cat gtc agt gac aag gag gcc ctg ggg 735  
 Glu Glu Met Val Val Thr Glu His Val Ser Asp Lys Glu Ala Leu Gly  
 200 205 210 215  
 tcc ttc atc tac cac ctg tgc aac ggg aaa gac acc tac cgg ctc cgg 783  
 Ser Phe Ile Tyr His Leu Cys Asn Gly Lys Asp Thr Tyr Arg Leu Arg  
 220 225 230  
 cgc cgg gca acg cgg agg cgg atc aac aag cgt ggg gcc aag aac tgc 831  
 Arg Arg Ala Thr Arg Arg Arg Ile Asn Lys Arg Gly Ala Lys Asn Cys  
 235 240 245  
 aat gcc atc cgc cac ttc gag aac acc ttc gtg gtg gag acg ctc atc 879  
 Asn Ala Ile Arg His Phe Glu Asn Thr Phe Val Val Glu Thr Leu Ile  
 250 255 260  
 tgc ggg gtg gtg tgaggccctc ctccccaga accccctgcc gtgttctc 930  
 Cys Gly Val Val  
 265  
 tttttttttt tccggtgct ctctggccct cctccttccc cctgcttagc ttgtacttg 990  
 gacgcgtttc tatagaggtg acatgtctct ccattcctct ccaaccctgc ccacctccct 1050  
 gtaccagagc tgtgatctct cgggtgggggg cccatctctg ctgacctggg tgtggcggag 1110  
 ggagaggcga tgctgcaaag tgttttctgt gtcccactgt cttgaagctg ggccctgcaa 1170

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agcctgggcc cacagctgca ccggcagccc aaggggaagg accggttggg ggagccgggc 1230  
 atgtgaggcc ctgggcaagg ggatggggct gtggggcgcg gccggcatgg gcttcagaag 1290  
 tatctgcaca attagaaaag tcttcagaag ctttttcttg gaggtacac tttcttact 1350  
 gtccctattc ctagacctgg ggcttgagct gaggatggga cgatgtgcc agggagggac 1410  
 ccaccagagc acaagagaag gtggctacct gggggtgtcc cagggactct gtcagtgcct 1470  
 tcagcccacc agcaggagct tggagtttgg ggagtgggga tgagtccgtc aagcacaact 1530  
 gttctctgag tggaacaaa gaagcaagga gctaggacct ccagtcctgc ccccaggag 1590  
 cacaagcagg gtccctcag tcaaggcagt gggatgggcg gctgaggaac ggggcaggca 1650  
 aggtcactgc tcagtcacgt ccacggggga cgagccgtgg gttctgctga gtaggtggag 1710  
 ctcattgctt tctccaagct tggaactgtt ttgaaagata acacagagg aaaggagag 1770  
 ccacctggta cttgtccacc ctgcctctc tgttctgaaa ttccatcccc ctcagcttag 1830  
 gggaatgcac ctttttcct ttccttctca cttttgcatg tttttactga tcattcgata 1890  
 tgctaaccgt tctcagccct gagecttgga gaggagggt gtaacgcctt cagtcagtct 1950  
 ctggggatga aactcttaaa tgctttgtat attttctcaa ttagatctct tttcagaagt 2010  
 gtctatagaa caataaaaat cttttacttc tg 2042

&lt;210&gt; 22

&lt;211&gt; 1433

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (5)... (1264)

&lt;400&gt; 22

gacg atg agc tgc gcg ggg cgg gcg ggc cct gcc cgg ctc gcc gcg 46

Met Ser Cys Ala Gly Arg Ala Gly Pro Ala Arg Leu Ala Ala

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|   |     |     |     |
|---|-----|-----|-----|
| 1   | 5   | 10  |     |
| ctc gcc ctg ctg acc tgc agc ctg tgg ccg gca cgg gca gac aac gcg |     |     | 94  |
| Leu Ala Leu Leu Thr Cys Ser Leu Trp Pro Ala Arg Ala Asp Asn Ala |     |     |     |
| 15  | 20  | 25  | 30  |
| agc cag gag tac tac acg gcg ctc atc aac gtg acg gtg cag gag ccc |     |     | 142 |
| Ser Gln Glu Tyr Tyr Thr Ala Leu Ile Asn Val Thr Val Gln Glu Pro |     |     |     |
| 35  | 40  | 45  |     |
| ggc cgc ggc gcc ccg ctc acg ttt cgc atc gac cgc ggg cgc tac ggg |     |     | 190 |
| Gly Arg Gly Ala Pro Leu Thr Phe Arg Ile Asp Arg Gly Arg Tyr Gly |     |     |     |
| 50  | 55  | 60  |     |
| ctt gac tcc ccc aag gcc gag gtc cgc ggc cag gtg ctg gcg ccg ctg |     |     | 238 |
| Leu Asp Ser Pro Lys Ala Glu Val Arg Gly Gln Val Leu Ala Pro Leu |     |     |     |
| 65  | 70  | 75  |     |
| ccc ctc cac gga gtt gct gat cat ctg ggc tgt gat cca caa acc cgg |     |     | 286 |
| Pro Leu His Gly Val Ala Asp His Leu Gly Cys Asp Pro Gln Thr Arg |     |     |     |
| 80  | 85  | 90  |     |
| ttc ttt gtc cct cct aat atc aaa cag tgg att gcc ttg ctg cag agg |     |     | 334 |
| Phe Phe Val Pro Pro Asn Ile Lys Gln Trp Ile Ala Leu Leu Gln Arg |     |     |     |
| 95  | 100 | 105 | 110 |
| gga aac tgc acg ttt aaa gag aaa ata tca cgg gcc gct ttc cac aat |     |     | 382 |
| Gly Asn Cys Thr Phe Lys Glu Lys Ile Ser Arg Ala Ala Phe His Asn |     |     |     |
| 115   | 120 | 125 |     |
| gca gtt gct gta gtc atc tac aat aat aaa tcc aaa gag gag cca gtt |     |     | 430 |
| Ala Val Ala Val Val Ile Tyr Asn Asn Lys Ser Lys Glu Glu Pro Val |     |     |     |
| 130   | 135 | 140 |     |

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acc atg act cat cca ggc act gga gat att att gct gtc atg ata aca 478  
 Thr Met Thr His Pro Gly Thr Gly Asp Ile Ile Ala Val Met Ile Thr  
 145 150 155

gaa ttg agg ggt aag gat att ttg agt tat ctg gag aaa aac atc tct 526  
 Glu Leu Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser  
 160 165 170

gta caa atg aca ata gct gtt gga act cga atg cca ccg aag aac ttc 574  
 Val Gln Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe  
 175 180 185 190

agc cgt ggc tct cta gtc ttc gtg tca ata tcc ttt att gtt ttg atg 622  
 Ser Arg Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met  
 195 200 205

att att tct tca gca tgg ctc ata ttc tac ttc att cag aag atc agg 670  
 Ile Ile Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg  
 210 215 220

tac aca aat gca cgc gac agg aac cag cgt cgt ctc gga gat gca gcc 718  
 Tyr Thr Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala  
 225 230 235

aag aaa gcc atc agt aaa ttg aca acc agg aca gta aag aag ggt gac 766  
 Lys Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys Gly Asp  
 240 245 250

aag gaa act gac cca gac ttt gat cat tgt gca gtc tgc ata gag agc 814  
 Lys Glu Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile Glu Ser  
 255 260 265 270

tat aag cag aat gat gtc gtc cga att ctc ccc tgc aag cat gtt ttc 862

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Tyr Lys Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His Val Phe  
 275 280 285  
 cac aaa tcc tgc gtg gat ccc tgg ctt agt gaa cat tgt acc tgt cct 910  
 His Lys Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr Cys Pro  
 290 295 300  
 atg tgc aaa ctt aat ata ttg aag gcc ctg gga att gtg ccg aat ttg 958  
 Met Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro Asn Leu  
 305 310 315  
 cca tgt act gat aac gta gca ttc gat atg gaa agg ctc acc aga acc 1006  
 Pro Cys Thr Asp Asn Val Ala Phe Asp Met Glu Arg Leu Thr Arg Thr  
 320 325 330  
 caa gct gtt aac cga aga tca gcc ctc ggc gac ctc gcc ggc gac aac 1054  
 Gln Ala Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp Asn  
 335 340 345 350  
 tcc ctt ggc ctt gag cca ctt cga act tcg ggg atc tca cct ctt cct 1102  
 Ser Leu Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu Pro  
 355 360 365  
 cag gat ggg gag ctc act ccg aga aca gga gaa atc aac att gca gta 1150  
 Gln Asp Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala Val  
 370 375 380  
 aca aaa gaa tgg ttt att att gcc agt ttt ggc ctc ctc agt gcc ctc 1198  
 Thr Lys Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala Leu  
 385 390 395  
 aca ctc tgc tac atg atc atc aga gcc aca gct agc ttg aat gct aat 1246  
 Thr Leu Cys Tyr Met Ile Ile Arg Ala Thr Ala Ser Leu Asn Ala Asn

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400 405 410

gag gta gaa tgg ttt tgaagaagaa aaaacctgct ttctgactga ttttgcctt 1300

Glu Val Glu Trp Phe

415

gaaggaaaaa agaacctatt tttgtgcatc atttaccaat catgccacac aagcatttat 1360

ttttagtaca ttttattttt tcataaaatt gctaatacca aagctttgta ttaaaagaaa 1420

taaataataa aat 1433

&lt;210&gt; 23

&lt;211&gt; 1917

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (210)... (1457)

&lt;400&gt; 23

gtatcccccg gctacctggg ccgccccgcg gcggtgcgcg cgtgagaggg agcgcgcggg 60

cagccgagcg ccggtgtgag ccagcgctgc tgccagtgtg agccagcgct gctgccagtg 120

tgagcgggcg tgtgagcgcg gtgggtgcgg aggggcgtgt gtgccggcgc gcgcgccgtg 180

gggtgcaaac ccgagcgctc tacgctgcc atg agg ggc gcg aac gcc tgg gcg 233

Met Arg Gly Ala Asn Ala Trp Ala

1

5

cca ctc tgc ctg ctg ctg gct gcc gcc acc cag ctc tcg cgg cag cag 281

Pro Leu Cys Leu Leu Leu Ala Ala Ala Thr Gln Leu Ser Arg Gln Gln

10

15

20

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|   |     |
|---|-----|
| tcc cca gag aga cct gtt ttc aca tgt ggt ggc att ctt act gga gag | 329 |
| Ser Pro Glu Arg Pro Val Phe Thr Cys Gly Gly Ile Leu Thr Gly Glu |     |
| 25 30 35 40   |     |
| tct gga ttt att ggc agt gaa ggt ttt cct gga gtg tac cct cca aat | 377 |
| Ser Gly Phe Ile Gly Ser Glu Gly Phe Pro Gly Val Tyr Pro Pro Asn |     |
| 45 50 55  |     |
| agc aaa tgt act tgg aaa atc aca gtt ccc gaa gga aaa gta gtc gtt | 425 |
| Ser Lys Cys Thr Trp Lys Ile Thr Val Pro Glu Gly Lys Val Val Val |     |
| 60 65 70  |     |
| ctc aat ttc cga ttc ata gac ctc gag agt gac aac ctg tgc cgc tat | 473 |
| Leu Asn Phe Arg Phe Ile Asp Leu Glu Ser Asp Asn Leu Cys Arg Tyr |     |
| 75 80 85  |     |
| gac ttt gtg gat gtg tac aat ggc cat gcc aat ggc cag cgc att ggc | 521 |
| Asp Phe Val Asp Val Tyr Asn Gly His Ala Asn Gly Gln Arg Ile Gly |     |
| 90 95 100   |     |
| cgc ttc tgt ggc act ttc cgg cct gga gcc ctt gtg tcc agt ggc aac | 569 |
| Arg Phe Cys Gly Thr Phe Arg Pro Gly Ala Leu Val Ser Ser Gly Asn |     |
| 105 110 115 120   |     |
| aag atg atg gtg cag atg att tct gat gcc aac aca gct ggc aat ggc | 617 |
| Lys Met Met Val Gln Met Ile Ser Asp Ala Asn Thr Ala Gly Asn Gly |     |
| 125 130 135   |     |
| ttc atg gcc atg ttc tcc gct gct gaa cca aac gaa aga ggg gat cag | 665 |
| Phe Met Ala Met Phe Ser Ala Ala Glu Pro Asn Glu Arg Gly Asp Gln |     |
| 140 145 150   |     |
| tat tgt gga gga ctc ctt gac aga cct tcc ggc tct ttt aaa acc ccc | 713 |



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Tyr Cys Gly Gly Leu Leu Asp Arg Pro Ser Gly Ser Phe Lys Thr Pro  
 155 160 165  
 aac tgg cca gac cgg gat tac cct gca gga gtc act tgt gtg tgg cac 761  
 Asn Trp Pro Asp Arg Asp Tyr Pro Ala Gly Val Thr Cys Val Trp His  
 170 175 180  
 att gta gcc cca aag aat cag ctt ata gaa tta aag ttt gag aag ttt 809  
 Ile Val Ala Pro Lys Asn Gln Leu Ile Glu Leu Lys Phe Glu Lys Phe  
 185 190 195 200  
 gat gtg gag cga gat aac tac tgc cga tat gat tat gtg gct gtg ttt 857  
 Asp Val Glu Arg Asp Asn Tyr Cys Arg Tyr Asp Tyr Val Ala Val Phe  
 205 210 215  
 aat ggc ggg gaa gtc aac gat gct aga aga att gga aag tat tgt ggt 905  
 Asn Gly Gly Glu Val Asn Asp Ala Arg Arg Ile Gly Lys Tyr Cys Gly  
 220 225 230  
 gat agt cca cct gcg cca att gtg tct gag aga aat gaa ctt ctt att 953  
 Asp Ser Pro Pro Ala Pro Ile Val Ser Glu Arg Asn Glu Leu Leu Ile  
 235 240 245  
 cag ttt tta tca gac tta agt tta act gca gat ggg ttt att ggt cac 1001  
 Gln Phe Leu Ser Asp Leu Ser Leu Thr Ala Asp Gly Phe Ile Gly His  
 250 255 260  
 tac ata ttc agg cca aaa aaa ctg cct aca act aca gaa cag cct gtc 1049  
 Tyr Ile Phe Arg Pro Lys Lys Leu Pro Thr Thr Thr Glu Gln Pro Val  
 265 270 275 280  
 acc acc aca ttc cct gta acc acg ggt tta aaa acc acc gtg gcc ttg 1097  
 Thr Thr Thr Phe Pro Val Thr Thr Gly Leu Lys Thr Thr Val Ala Leu

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|   |     |     |      |
|---|-----|-----|------|
| 285   | 290 | 295 |      |
| tgt caa caa aag tgt aga cgg acg ggg act ctg gag ggc aat tat tgt |     |     | 1145 |
| Cys Gln Gln Lys Cys Arg Arg Thr Gly Thr Leu Glu Gly Asn Tyr Cys |     |     |      |
| 300   | 305 | 310 |      |
| tca agt gac ttt gta tta gcc ggc act gtt atc aca acc atc act cgc |     |     | 1193 |
| Ser Ser Asp Phe Val Leu Ala Gly Thr Val Ile Thr Thr Ile Thr Arg |     |     |      |
| 315   | 320 | 325 |      |
| gat ggg agt ttg cac gcc aca gtc tcg atc atc aac atc tac aaa gag |     |     | 1241 |
| Asp Gly Ser Leu His Ala Thr Val Ser Ile Ile Asn Ile Tyr Lys Glu |     |     |      |
| 330   | 335 | 340 |      |
| gga aat ttg gcg att cag cag gcg ggc aag aac atg agt gcc agg ctg |     |     | 1289 |
| Gly Asn Leu Ala Ile Gln Gln Ala Gly Lys Asn Met Ser Ala Arg Leu |     |     |      |
| 345   | 350 | 355 | 360  |
| act gtc gtc tgc aag cag tgc cct ctc ctc aga aga ggt cta aat tac |     |     | 1337 |
| Thr Val Val Cys Lys Gln Cys Pro Leu Leu Arg Arg Gly Leu Asn Tyr |     |     |      |
| 365   | 370 | 375 |      |
| att att atg ggc caa gta ggt gaa gat ggg cga ggc aaa atc atg cca |     |     | 1385 |
| Ile Ile Met Gly Gln Val Gly Glu Asp Gly Arg Gly Lys Ile Met Pro |     |     |      |
| 380   | 385 | 390 |      |
| aac agc ttt atc atg atg ttc aag acc aag aat cag aag ctc ctg gat |     |     | 1433 |
| Asn Ser Phe Ile Met Met Phe Lys Thr Lys Asn Gln Lys Leu Leu Asp |     |     |      |
| 395   | 400 | 405 |      |
| gcc tta aaa aat aag caa tgt taacagtga ctgtgtccat ttaage         |     |     | 1480 |
| Ala Leu Lys Asn Lys Gln Cys                                     |     |     |      |

410

415

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tgtattctgc cattgccttt gaaagatcta tggtctctca gtagaaaaaa aaatacttat 1540  
 aaaattacat attctgaaag aggattccga aagatgggac tggttgactc ttcacatgat 1600  
 ggaggtatga ggcctccgag atagctgagg gaagttcttt gcctgctgtc agaggagcag 1660  
 ctatctgatt ggaaacctgc cgacttagtg cggatgtagg aagctaaaag tgtcaagcgt 1720  
 tgacagcttg gaagcggtta ttatacatc tctgtaaaag gatatttttag aattgagttg 1780  
 tgtgaagatg tcaaaaaaag attttagaag tgcaatattt atagtgttat ttgtttcacc 1840  
 ttcaagcctt tgcctgagg tggtacaatc ttgtcttgcg ttttctaaat caatgcttaa 1900  
 taaaatattt ttaaagg 1917

&lt;210&gt; 24

&lt;211&gt; 2258

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (225)... (1367)

&lt;400&gt; 24

tttttcccg ctgggctcgg gctcagctcg actgggctcg gcgggcggcg gcggcggcgc 60  
 ccgcggctgg cggaggaggg agggcgaggg cgggcgcggg ccggcgggcg ggcggaagag 120  
 ggaggagagg cgcggggagc caggcctcgg ggctcggag caaccacccg agcagacgga 180  
 gtacacggag cagcggcccc ggccccgcca acgctgccgc cggg atg ctc cag 233

Met Leu Gln

1

acc ttg tat gat tac ttc tgg tgg gaa cgt ctg tgg ctg cct gtg aac 281  
 Thr Leu Tyr Asp Tyr Phe Trp Trp Glu Arg Leu Trp Leu Pro Val Asn

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|   |     |     |     |
|---|-----|-----|-----|
| 5   | 10  | 15  |     |
| ttg acc tgg gcc gat cta gaa gac cga gat gga cgt gtc tac gcc aaa |     |     | 329 |
| Leu Thr Trp Ala Asp Leu Glu Asp Arg Asp Gly Arg Val Tyr Ala Lys |     |     |     |
| 20  | 25  | 30  | 35  |
| gcc tca gat ctc tat atc acg ctg ccc ctg gcc ttg ctc ttc ctc atc |     |     | 377 |
| Ala Ser Asp Leu Tyr Ile Thr Leu Pro Leu Ala Leu Leu Phe Leu Ile |     |     |     |
| 40  | 45  | 50  |     |
| gtt cga tac ttc ttt gag ctg tac gtg gct aca cca ctg gct gcc ctc |     |     | 425 |
| Val Arg Tyr Phe Phe Glu Leu Tyr Val Ala Thr Pro Leu Ala Ala Leu |     |     |     |
| 55  | 60  | 65  |     |
| ttg aac ata aag gag aaa act cgg ctg cgg gca cct ccc aac gcc acc |     |     | 473 |
| Leu Asn Ile Lys Glu Lys Thr Arg Leu Arg Ala Pro Pro Asn Ala Thr |     |     |     |
| 70  | 75  | 80  |     |
| ttg gaa cat ttc tac ctg acc agt ggc aag cag ccc aag cag gtg gaa |     |     | 521 |
| Leu Glu His Phe Tyr Leu Thr Ser Gly Lys Gln Pro Lys Gln Val Glu |     |     |     |
| 85  | 90  | 95  |     |
| gta gag ctt ttg tcc cgg cag agc ggg ctc tct ggc cgc cag gta gag |     |     | 569 |
| Val Glu Leu Leu Ser Arg Gln Ser Gly Leu Ser Gly Arg Gln Val Glu |     |     |     |
| 100   | 105 | 110 | 115 |
| cgt tgg ttc cgt cgc cgc cgc aac cag gac cgg ccc agt ctc ctc aag |     |     | 617 |
| Arg Trp Phe Arg Arg Arg Arg Asn Gln Asp Arg Pro Ser Leu Leu Lys |     |     |     |
| 120   | 125 | 130 |     |
| aag ttc cga gaa gcc agc tgg aga ttc aca ttt tac ctg att gcc ttc |     |     | 665 |
| Lys Phe Arg Glu Ala Ser Trp Arg Phe Thr Phe Tyr Leu Ile Ala Phe |     |     |     |
| 135   | 140 | 145 |     |

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|   |      |
|---|------|
| att gcc ggc atg gcc gtc att gtg gat aaa ccc tgg ttc tat gac atg | 713  |
| Ile Ala Gly Met Ala Val Ile Val Asp Lys Pro Trp Phe Tyr Asp Met |      |
| 150 155 160   |      |
| aag aaa gtt tgg gag gga tat ccc ata cag agc act atc cct tcc cag | 761  |
| Lys Lys Val Trp Glu Gly Tyr Pro Ile Gln Ser Thr Ile Pro Ser Gln |      |
| 165 170 175   |      |
| tat tgg tac tac atg att gaa ctt tcc ttc tac tgg tcc ctg ctc ttc | 809  |
| Tyr Trp Tyr Tyr Met Ile Glu Leu Ser Phe Tyr Trp Ser Leu Leu Phe |      |
| 180 185 190 195   |      |
| agc att gcc tct gat gtc aag cga aag gat ttc aag gaa cag atc atc | 857  |
| Ser Ile Ala Ser Asp Val Lys Arg Lys Asp Phe Lys Glu Gln Ile Ile |      |
| 200 205 210   |      |
| cac cat gtg gcc acc atc att ctc atc agc ttt tcc tgg ttt gcc aat | 905  |
| His His Val Ala Thr Ile Ile Leu Ile Ser Phe Ser Trp Phe Ala Asn |      |
| 215 220 225   |      |
| tac atc cga gct ggg act cta atc atg gct ctg cat gac tct tcc gat | 953  |
| Tyr Ile Arg Ala Gly Thr Leu Ile Met Ala Leu His Asp Ser Ser Asp |      |
| 230 235 240   |      |
| tac ctg ctg gag tca gcc aag atg ttt aac tac gcg gga tgg aag aac | 1001 |
| Tyr Leu Leu Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly Trp Lys Asn |      |
| 245 250 255   |      |
| acc tgc aac aac atc ttc atc gtc ttc gcc att gtt ttt atc atc acc | 1049 |
| Thr Cys Asn Asn Ile Phe Ile Val Phe Ala Ile Val Phe Ile Ile Thr |      |
| 260 265 270 275   |      |
| cga ctg gtc atc ctg ccc ttc tgg atc ctg cat tgc acc ctg gtg tac | 1097 |

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Arg Leu Val Ile Leu Pro Phe Trp Ile Leu His Cys Thr Leu Val Tyr  
 280 285 290  
 cca ctg gag ctc tat cct gcc ttc ttt ggc tat tac ttc ttc aat tcc 1145  
 Pro Leu Glu Leu Tyr Pro Ala Phe Phe Gly Tyr Tyr Phe Phe Asn Ser  
 295 300 305  
 atg atg gga gtt cta cag ctg ctg cat atc ttc tgg gcc tac ctc att 1193  
 Met Met Gly Val Leu Gln Leu Leu His Ile Phe Trp Ala Tyr Leu Ile  
 310 315 320  
 ttg cgc atg gcc cac aag ttc ata act gga aag ctg gta gaa gat gaa 1241  
 Leu Arg Met Ala His Lys Phe Ile Thr Gly Lys Leu Val Glu Asp Glu  
 325 330 335  
 cgc agt gac cgg gaa gaa aca gag agc tca gag ggg gag gag gct gca 1289  
 Arg Ser Asp Arg Glu Glu Thr Glu Ser Ser Glu Gly Glu Glu Ala Ala  
 340 345 350 355  
 gct ggg gga gga gca aag agc cgg ccc cta gcc aat ggc cac ccc atc 1337  
 Ala Gly Gly Gly Ala Lys Ser Arg Pro Leu Ala Asn Gly His Pro Ile  
 360 365 370  
 ctc aat aac aac cat cgt aag aat gac tgaaccatta ttccagctgc ctccca 1390  
 Leu Asn Asn Asn His Arg Lys Asn Asp  
 375 380  
 gattaatgca taaagccaag gaactaccct gctccctgcg ctatagggtc actttaagct 1450  
 ctgggggaaaa aggagaaagt gagaggagag ttctctgcat cctccctcct tgcttggtcac 1510  
 ccagttgcct ttaaaccaaa ttctaaccag cctatcccca ggtaggggga cgttggttat 1570  
 attctgttag agggggacgg tcgtattttc ctccctaccc gccaaagtcac cctttctact 1630  
 gcttttgagg ccctccctca gctctctgtg ggtaggggtt acaattcaca ttccttattc 1690

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tgagaatttg gccccagctg tttgcctttg actccctgac ctccagagcc agggttgtgc 1750  
 cttattgtcc catctgtggg cctcattctg ccaaagctgg accaaggcta acctttctaa 1810  
 gctccctaac ttgggccaga aaccaaagct gagcttttaa cttctccct ctatgacaca 1870  
 aatgaattga gggtaggagg aggggtgcaca taacccttac cctacctctg ccaaaaagtg 1930  
 ggggctgtac tggggactgc tcggatgac tttcttagtg ctacttcttt cagctgtccc 1990  
 tgtagcgaca ggtctaagat ctgactgcct cctttctctg gcctcttccc ccttccctct 2050  
 tctcttcagc taggctagct gggttgagtg agaatggcaa ctaattctaa tttttattta 2110  
 ttaaataattt ggggttttgg ttttaaagcc agaattacgg ctagcaccta gcatttcagc 2170  
 agagggacca ttttagacca aaatgtactg ttaatgggtt tttttttaa attaaaagat 2230  
 taaataaaaa atattaaata aaacatgg 2258

&lt;210&gt; 25

&lt;211&gt; 1973

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (130)... (1887)

&lt;400&gt; 25

gagcagacca ggcccgttg agaattaggt gctgctggga gtcctgcct cccacaggat 60  
 tccagctgca gggagcctca gggactctgg gccgcacgga gttgggggca ttccccagag 120  
 agcgtcgcc atg gtc tgc agg gag cag tta tca aag aat cag gtc aag 168

Met Val Cys Arg Glu Gln Leu Ser Lys Asn Gln Val Lys

1

5

10

tgg gtg ttt gcc ggc att acc tgt gtg tct gtg gtg gtc att gcc gca 216

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Trp Val Phe Ala Gly Ile Thr Cys Val Ser Val Val Val Ile Ala Ala  
 15 20 25  
 ata gtc ctt gcc atc acc ctg cgg cgg cca ggc tgt gag ctg gag gcc 264  
 Ile Val Leu Ala Ile Thr Leu Arg Arg Pro Gly Cys Glu Leu Glu Ala  
 30 35 40 45  
 tgc agc cct gat gcc gac atg ctg gac tac ctg ctg agc ctg ggc cag 312  
 Cys Ser Pro Asp Ala Asp Met Leu Asp Tyr Leu Leu Ser Leu Gly Gln  
 50 55 60  
 atc agc cgg cga gat gcc ttg gag gtc acc tgg tac cac gca gcc aac 360  
 Ile Ser Arg Arg Asp Ala Leu Glu Val Thr Trp Tyr His Ala Ala Asn  
 65 70 75  
 agc aag aaa gcc atg aca gct gcc ctg aac agc aac atc aca gtc ctg 408  
 Ser Lys Lys Ala Met Thr Ala Ala Leu Asn Ser Asn Ile Thr Val Leu  
 80 85 90  
 gag gct gac gtc aat gta gaa ggg ctc ggc aca gcc aat gag aca gga 456  
 Glu Ala Asp Val Asn Val Glu Gly Leu Gly Thr Ala Asn Glu Thr Gly  
 95 100 105  
 gtt ccc atc atg gca cac ccc ccc act atc tac agt gac aac aca ctg 504  
 Val Pro Ile Met Ala His Pro Pro Thr Ile Tyr Ser Asp Asn Thr Leu  
 110 115 120 125  
 gag cag tgg ctg gac gct gtg ctg ggc tct tcc caa aag ggc atc aaa 552  
 Glu Gln Trp Leu Asp Ala Val Leu Gly Ser Ser Gln Lys Gly Ile Lys  
 130 135 140  
 ctg gac ttc aag aac atc aag gca gtg ggc ccc tcc ctg gac ctc ctg 600  
 Leu Asp Phe Lys Asn Ile Lys Ala Val Gly Pro Ser Leu Asp Leu Leu



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|   |     |     |     |
|---|-----|-----|-----|
| 145   | 150 | 155 |     |
| cgg cag ctg aca gag gaa ggc aaa gtc cgg cgg ccc ata tgg atc aac |     |     | 648 |
| Arg Gln Leu Thr Glu Glu Gly Lys Val Arg Arg Pro Ile Trp Ile Asn |     |     |     |
| 160   | 165 | 170 |     |
| gct gac atc tta aag ggc ccc aac atg ctc atc tca act gag gtc aat |     |     | 696 |
| Ala Asp Ile Leu Lys Gly Pro Asn Met Leu Ile Ser Thr Glu Val Asn |     |     |     |
| 175   | 180 | 185 |     |
| gcc aca cag ttc ctg gcc ctg gtc cag gag aag tat ccc aag gct acc |     |     | 744 |
| Ala Thr Gln Phe Leu Ala Leu Val Gln Glu Lys Tyr Pro Lys Ala Thr |     |     |     |
| 190   | 195 | 200 | 205 |
| cta tct cca ggc tgg acc acc ttc tac atg tcc acg tcc cca aac agg |     |     | 792 |
| Leu Ser Pro Gly Trp Thr Thr Phe Tyr Met Ser Thr Ser Pro Asn Arg |     |     |     |
| 210   | 215 | 220 |     |
| acg tac acc caa gcc atg gtg gag aag atg cac gag ctg gtg gga gga |     |     | 840 |
| Thr Tyr Thr Gln Ala Met Val Glu Lys Met His Glu Leu Val Gly Gly |     |     |     |
| 225   | 230 | 235 |     |
| gtg ccc cag agg gtc acc ttc cct gta cgg tct tcc atg gtg cgg gct |     |     | 888 |
| Val Pro Gln Arg Val Thr Phe Pro Val Arg Ser Ser Met Val Arg Ala |     |     |     |
| 240   | 245 | 250 |     |
| gcc tgg ccc cac ttc agc tgg ctg ctg agc caa tct gag agg tac agc |     |     | 936 |
| Ala Trp Pro His Phe Ser Trp Leu Leu Ser Gln Ser Glu Arg Tyr Ser |     |     |     |
| 255   | 260 | 265 |     |
| ctg acg ctg tgg cag gct gcc tcg gac ccc atg tcg gtg gaa gat ctg |     |     | 984 |
| Leu Thr Leu Trp Gln Ala Ala Ser Asp Pro Met Ser Val Glu Asp Leu |     |     |     |
| 270   | 275 | 280 | 285 |

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|   |      |
|---|------|
| ctc tac gtc cgg gat aac act gct gtc cac caa gtc tac tat gac atc | 1032 |
| Leu Tyr Val Arg Asp Asn Thr Ala Val His Gln Val Tyr Tyr Asp Ile |      |
| 290 295 300   |      |
| ttt gag cct ctc ctg tca cag ttc aag cag ctg gcc ttg aat gcc aca | 1080 |
| Phe Glu Pro Leu Leu Ser Gln Phe Lys Gln Leu Ala Leu Asn Ala Thr |      |
| 305 310 315   |      |
| cgg aaa cca atg tac tac aca gga ggc agc ctg atc cct ctt ctc cag | 1128 |
| Arg Lys Pro Met Tyr Tyr Thr Gly Gly Ser Leu Ile Pro Leu Leu Gln |      |
| 320 325 330   |      |
| ctg cct ggg gat gac ggt ctg aat gtg gag tgg ctg gtt cct gac gtc | 1176 |
| Leu Pro Gly Asp Asp Gly Leu Asn Val Glu Trp Leu Val Pro Asp Val |      |
| 335 340 345   |      |
| cag ggc agc ggt aaa aca gca aca atg acc ctc cca gac aca gaa ggc | 1224 |
| Gln Gly Ser Gly Lys Thr Ala Thr Met Thr Leu Pro Asp Thr Glu Gly |      |
| 350 355 360 365   |      |
| atg atc ctg ctg aac act ggc ctc gag gga act gtg gct gaa aac ccc | 1272 |
| Met Ile Leu Leu Asn Thr Gly Leu Glu Gly Thr Val Ala Glu Asn Pro |      |
| 370 375 380   |      |
| gtg ccc att gtt cat act cca agt ggc aac atc ctg acg ctg gag tcc | 1320 |
| Val Pro Ile Val His Thr Pro Ser Gly Asn Ile Leu Thr Leu Glu Ser |      |
| 385 390 395   |      |
| tgc ctg cag cag ctg gcc aca cat ccc gga cac tgg ggc atc cat ttg | 1368 |
| Cys Leu Gln Gln Leu Ala Thr His Pro Gly His Trp Gly Ile His Leu |      |
| 400 405 410   |      |
| caa ata gcg gag ccc gca gcc ctc cgg cca tcc ctg gcc ttg ctg gca | 1416 |

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Gln Ile Ala Glu Pro Ala Ala Leu Arg Pro Ser Leu Ala Leu Leu Ala  
 415 420 425  
 cgc ctc tcc agc ctt ggc ctc ttg cat tgg cct gtg tgg gtt ggg gcc 1464  
 Arg Leu Ser Ser Leu Gly Leu Leu His Trp Pro Val Trp Val Gly Ala  
 430 435 440 445  
 aaa atc tcc cac ggg agt ttt tcg gtc ccc ggc cat gtg gct ggc aga 1512  
 Lys Ile Ser His Gly Ser Phe Ser Val Pro Gly His Val Ala Gly Arg  
 450 455 460  
 gag ctg ctt aca gct gtg gct gag gtc ttc ccc cac gtg act gtg gca 1560  
 Glu Leu Leu Thr Ala Val Ala Glu Val Phe Pro His Val Thr Val Ala  
 465 470 475  
 cca ggc tgg cct gag gag gtg ctg ggc agt ggc tac agg gaa cag ctg 1608  
 Pro Gly Trp Pro Glu Glu Val Leu Gly Ser Gly Tyr Arg Glu Gln Leu  
 480 485 490  
 ctc aca gat atg cta gag ttg tgc cag ggg ctc tgg caa cct gtg tcc 1656  
 Leu Thr Asp Met Leu Glu Leu Cys Gln Gly Leu Trp Gln Pro Val Ser  
 495 500 505  
 ttc cag atg cag gcc atg ctg ctg ggc cac agc aca gct gga gcc ata 1704  
 Phe Gln Met Gln Ala Met Leu Leu Gly His Ser Thr Ala Gly Ala Ile  
 510 515 520 525  
 ggc agg ctg ctg gca tcc tcc ccc cgg gcc acc gtc aca gtg gag cac 1752  
 Gly Arg Leu Leu Ala Ser Ser Pro Arg Ala Thr Val Thr Val Glu His  
 530 535 540  
 aac cca gct ggg ggc gac tat gcc tct gtg agg aca gca ttg ctg gca 1800  
 Asn Pro Ala Gly Gly Asp Tyr Ala Ser Val Arg Thr Ala Leu Leu Ala

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|  |     |     |      |
|--|-----|-----|------|
| 545  | 550 | 555 |      |
| gct agg gct gtg gac agg acc cga gtc tac tac agg cta ccc cag ggc    |     |     | 1848 |
| Ala Arg Ala Val Asp Arg Thr Arg Val Tyr Tyr Arg Leu Pro Gln Gly    |     |     |      |
| 560  | 565 | 570 |      |
| tac cac aag gac ttg ctg gct cat gtt ggt aga aac tgagcaccca ggggtg  |     |     | 1900 |
| Tyr His Lys Asp Leu Leu Ala His Val Gly Arg Asn                    |     |     |      |
| 575  | 580 | 585 |      |
| gtgggccagc ggacctcagg gcggaggctt cccacgggga ggcaggaaga aataaaggctc |     |     | 1960 |
| tttggtttc tcc  |     |     | 1973 |

&lt;210&gt; 26

&lt;211&gt; 1606

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (135)... (1130)

&lt;400&gt; 26

|  |     |
|--|-----|
| attgtgcggc gctggtcccc tcagagggtt cctgctgctg ccggtgcctt ggacctccc | 60  |
| cctcgtttct cgtttactg ccccaggagc ccggcgggtc cgggactccc gtccgtgccg | 120 |
| gtgcgggcgc cggc atg tgg ctg tgg gag gac cag ggc ggc ctc ctg ggc  | 170 |
| Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly                  |     |

1

5

10

|   |     |
|---|-----|
| cct ttc tcc ttc ctg ctg cta gtg ctg ctg ctg gtg acg cgg agc ccg | 218 |
| Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro |     |

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|   |     |     |     |
|---|-----|-----|-----|
| 15  | 20  | 25  |     |
| gtc aat gcc tgc ctc ctc acc ggc agc ctc ttc gtt cta ctg cgc gtc |     |     | 266 |
| Val Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val |     |     |     |
| 30  | 35  | 40  |     |
| ttc agc ttt gag ccg gtg ccc tct tgc agg gcc ctg cag gtg ctc aag |     |     | 314 |
| Phe Ser Phe Glu Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys |     |     |     |
| 45  | 50  | 55  | 60  |
| ccc cgg gac cgc att tct gcc atc gcc cac cgt ggc ggc agc cac gac |     |     | 362 |
| Pro Arg Asp Arg Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp |     |     |     |
| 65  | 70  | 75  |     |
| gcg ccc gag aac acg ctg gcg gcc att cgg cag gca gct aag aat gga |     |     | 410 |
| Ala Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly |     |     |     |
| 80  | 85  | 90  |     |
| gca aca ggc gtg gag ttg gac att gag ttt act tct gac ggg att cct |     |     | 458 |
| Ala Thr Gly Val Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro |     |     |     |
| 95  | 100 | 105 |     |
| gtc tta atg cac gat aac aca gta gat agg acg act gat ggg act ggg |     |     | 506 |
| Val Leu Met His Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly |     |     |     |
| 110   | 115 | 120 |     |
| cga ttg tgt gat ttg aca ttt gaa caa att agg aag ctg aat cct gca |     |     | 554 |
| Arg Leu Cys Asp Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala |     |     |     |
| 125   | 130 | 135 | 140 |
| gca aac cac aga ctc agg aat gat ttc cct gat gaa aag atc cct acc |     |     | 602 |
| Ala Asn His Arg Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr |     |     |     |
| 145   | 150 | 155 |     |

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|   |      |
|---|------|
| cta agg gaa gct gtt gca gag tgc cta aac cat aac ctc aca atc ttc | 650  |
| Leu Arg Glu Ala Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe |      |
| 160 165 170   |      |
| ttt gat gtc aaa ggc cat gca cac aag gct act gag gct cta aag aaa | 698  |
| Phe Asp Val Lys Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys |      |
| 175 180 185   |      |
| atg tat atg gaa ttt cct caa ctg tat aat aat agt gtg gtc tgt tct | 746  |
| Met Tyr Met Glu Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser |      |
| 190 195 200   |      |
| ttc ttg cca gaa gtt atc tac aag atg aga caa aca gat cgg gat gta | 794  |
| Phe Leu Pro Glu Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val |      |
| 205 210 215 220   |      |
| ata aca gca tta act cac aga cct tgg agc cta agc cat aca gga gat | 842  |
| Ile Thr Ala Leu Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp |      |
| 225 230 235   |      |
| ggg aaa cca cgc tat gat act ttc tgg aaa cat ttt ata ttt gtt atg | 890  |
| Gly Lys Pro Arg Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met |      |
| 240 245 250   |      |
| atg gac att ttg ctc gat tgg agc atg cat aat atc ttg tgg tac ctg | 938  |
| Met Asp Ile Leu Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu |      |
| 255 260 265   |      |
| tgt gga att tca gct ttc ctc atg caa aag gat ttt gta tcc ccg gcc | 986  |
| Cys Gly Ile Ser Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala |      |
| 270 275 280   |      |
| tac ttg aag aag tgg tca gct aaa gga atc cag gtt gtt ggt tgg act | 1034 |

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Tyr Leu Lys Lys Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr  
 285                                      290                                      295                                      300  
 gtt aat acc ttt gat gaa aag agt tac tac gaa tcc cat ctt ggt tcc      1082  
 Val Asn Thr Phe Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser  
    305                                      310                                      315  
 agc tat atc act gac agc atg gta gaa gac tgc gaa cct cac ttc      1127  
 Ser Tyr Ile Thr Asp Ser Met Val Glu Asp Cys Glu Pro His Phe  
    320                                      325                                      330  
 tag actttcacgg tgggacgaaa cgggttcaga aactgccagg ggcctcatac      1180  
 agggatatca aaataccctt tgtgctagcc caggccctgg ggaatcaggt gactcacaca      1240  
 aatgcaatag ttggtcactg catttttacc tgaaccaaag ctaaaccggt tgttgccacc      1300  
 atgcaccatg gcatgccaga gttcaacact gttgctcttg aaaatctggg tctgaaaaaa      1360  
 cgcacaagag cccctgccct gccctagctg aggcacacag ggagaccag tgaggataag      1420  
 cacagattga attgtacaat ttgcagatgc agatgtaaat gcatgggaca tgcataataa      1480  
 ctcagagttg acatitttaa acttgccaca cttatttcaa atatttgtac tcagctatgt      1540  
 taacatgtac ttagacatc aaacttgtgg ccatactaata aaaattatta aaaggagcac      1600  
 taaagg      1606

&lt;210&gt; 27

&lt;211&gt; 2380

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (247)... (1284)

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&lt;400&gt; 27

agtgtggacc tggactcgaa tcccgttgcc gactcgcgt ctcggcttct gtcgccgggc 60  
 ttcttcctg cccgccggg gccctgaccg tggtctcttc cccggcctga tctgcgcagc 120  
 ccggcgggcg ccagaagga gcaggcggcg cggggcgcg ctggcgggg gaggcgtggc 180  
 cggagctgcg gcggcaagcg ggctgggact gctcgccgc ctcctgcccg gcgagcagct 240  
 cagacc atg tcg cct gaa gaa tgg acg tat cta gtg gtt ctt ctt atc 288

Met Ser Pro Glu Glu Trp Thr Tyr Leu Val Val Leu Leu Ile

1

5

10

tcc atc ccc atc ggc ttc ctc ttt aag aaa gcc ggt cct ggg ctg aag 336

Ser Ile Pro Ile Gly Phe Leu Phe Lys Lys Ala Gly Pro Gly Leu Lys

15

20

25

30

aga tgg gga gca gcc gct gtg ggc ctg ggg ctc acc ctg ttc acc tgt 384

Arg Trp Gly Ala Ala Ala Val Gly Leu Gly Leu Thr Leu Phe Thr Cys

35

40

45

ggc ccc cac act ttg cat tct ctg gtc acc atc ctc ggg acc tgg gcc 432

Gly Pro His Thr Leu His Ser Leu Val Thr Ile Leu Gly Thr Trp Ala

50

55

60

ctc att cag gcc cag ccc tgc tcc tgc cac gcc ctg gct ctg gcc tgg 480

Leu Ile Gln Ala Gln Pro Cys Ser Cys His Ala Leu Ala Leu Ala Trp

65

70

75

act ttc tcc tat ctc ctg ttc ttc cga gcc ctc agc ctc ctg ggc ctg 528

Thr Phe Ser Tyr Leu Leu Phe Phe Arg Ala Leu Ser Leu Leu Gly Leu

80

85

90

ccc act ccc acg ccc ttc acc aat gcc gtc cag ctg ctg ctg acg ctg 576

Pro Thr Pro Thr Pro Phe Thr Asn Ala Val Gln Leu Leu Leu Thr Leu



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|   |     |     |     |     |
|---|-----|-----|-----|-----|
| 95  | 100 | 105 | 110 |     |
| aag ctg gtg agc ctg gcc agt gaa gtc cag gac ctg cat ctg gcc cag |     |     |     | 624 |
| Lys Leu Val Ser Leu Ala Ser Glu Val Gln Asp Leu His Leu Ala Gln |     |     |     |     |
|   | 115 | 120 | 125 |     |
| agg aag gaa atg gcc tca ggc ttc agc aag ggg ccc acc ctg ggg ctg |     |     |     | 672 |
| Arg Lys Glu Met Ala Ser Gly Phe Ser Lys Gly Pro Thr Leu Gly Leu |     |     |     |     |
|   | 130 | 135 | 140 |     |
| ctg ccc gac gtg ccc tcc ctg atg gag aca ctc agc tac agc tac tgc |     |     |     | 720 |
| Leu Pro Asp Val Pro Ser Leu Met Glu Thr Leu Ser Tyr Ser Tyr Cys |     |     |     |     |
|   | 145 | 150 | 155 |     |
| tac gtg gga atc atg aca ggc ccg ttc ttc cgc tac cgc acc tac ctg |     |     |     | 768 |
| Tyr Val Gly Ile Met Thr Gly Pro Phe Phe Arg Tyr Arg Thr Tyr Leu |     |     |     |     |
|   | 160 | 165 | 170 |     |
| gac tgg ctg gag cag ccc ttc ccc ggg gca gtg ccc agc ctg cgg ccc |     |     |     | 816 |
| Asp Trp Leu Glu Gln Pro Phe Pro Gly Ala Val Pro Ser Leu Arg Pro |     |     |     |     |
|   | 175 | 180 | 185 | 190 |
| ctg ctg cgc cgc gcc tgg ccg gcc ccg ctc ttc ggc ctg ctg ttc ctg |     |     |     | 864 |
| Leu Leu Arg Arg Ala Trp Pro Ala Pro Leu Phe Gly Leu Leu Phe Leu |     |     |     |     |
|   | 195 | 200 | 205 |     |
| ctc tcc tct cac ctc ttc ccg ctg gag gcc gtg cgc gag gac gcc ttc |     |     |     | 912 |
| Leu Ser Ser His Leu Phe Pro Leu Glu Ala Val Arg Glu Asp Ala Phe |     |     |     |     |
|   | 210 | 215 | 220 |     |
| tac gcc cgc ccg ctg ccc gcc cgc ctc ttc tac atg atc ccc gtc ttc |     |     |     | 960 |
| Tyr Ala Arg Pro Leu Pro Ala Arg Leu Phe Tyr Met Ile Pro Val Phe |     |     |     |     |
|   | 225 | 230 | 235 |     |

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|  |      |
|--|------|
| ttc gcc ttc cgc atg cgc ttc tac gtg gcc tgg att gcc gcc gag tgc    | 1008 |
| Phe Ala Phe Arg Met Arg Phe Tyr Val Ala Trp Ile Ala Ala Glu Cys    |      |
| 240 245 250  |      |
| ggc tgc att gcc gcc ggc ttt ggg gcc tac ccc gtg gcc gcc aaa gcc    | 1056 |
| Gly Cys Ile Ala Ala Gly Phe Gly Ala Tyr Pro Val Ala Ala Lys Ala    |      |
| 255 260 265 270  |      |
| cgg gcc gga ggc ggc ccc acc ctc caa tgc cca ccc ccc agc agt ccg    | 1104 |
| Arg Ala Gly Gly Gly Pro Thr Leu Gln Cys Pro Pro Pro Ser Ser Pro    |      |
| 275 280 285  |      |
| gag aag gcg gct tcc ttg gag tat gac tat gag acc atc cgc aac atc    | 1152 |
| Glu Lys Ala Ala Ser Leu Glu Tyr Asp Tyr Glu Thr Ile Arg Asn Ile    |      |
| 290 295 300  |      |
| gac tgc tac agc aca gat ttc tgc gtg cgg gtg cgc gat ggc atg cgg    | 1200 |
| Asp Cys Tyr Ser Thr Asp Phe Cys Val Arg Val Arg Asp Gly Met Arg    |      |
| 305 310 315  |      |
| tac tgg aac atg acg gtg cag tgg tgg ctg gcg cag tat atc tac aag    | 1248 |
| Tyr Trp Asn Met Thr Val Gln Trp Trp Leu Ala Gln Tyr Ile Tyr Lys    |      |
| 320 325 330  |      |
| agc gca cct gcc cgt tcc tat gtc ctg cgc ctt tagaagcaga aactcagcc   | 1300 |
| Ser Ala Pro Ala Arg Ser Tyr Val Leu Arg Leu                        |      |
| 335 340 345  |      |
| gggtgcggcg gctcacgcct ggaatcccag cactttggga ggcccaagca ggtggatcat  | 1360 |
| gaggagcgcc tggaccatgc tgctgagcgc ctactggcac ggcctccacc cgggctacta  | 1420 |
| cctgagcttc ctgaccatcc cgctgtgcct ggctgccgag ggccggctgg agtcagccct  | 1480 |
| gcggggggcg ctgagcccag ggggcccagaa ggcctgggac tgggtgcact ggttcctgaa | 1540 |

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gatgcgcgcc tatgactaca tgtgcatggg cttcgtgctg ctctccttgg cgcacaccct 1600  
tcgggtactgg gcctccatct acttctgtat ccacttcctg gccctggcag ccctggggct 1660  
ggggctggct ttaggtgggg gcagccccag ccggcggaag gcagcatccc agcccaccag 1720  
ccttgccccg gagaagctcc gggaggagta agctgtcacg acgtccctc tgccagctgg 1780  
tcccgggaat tctgtgaacc aggtgctgt ctcctcccca gaaagagtcc ttaccttga 1840  
gagggtcctg gagagaattt cctcttcccc agctaaatac cctgcctgca actgaagcag 1900  
acccgggggt gtctccctg ccctctgccc agaggccacc tccactccta caaaatcaaa 1960  
gtattgtcca gacaagagtc actggcccct gctccagctt ctgggtatcc agagagcact 2020  
gcacttcccc aaaacggaag gggcccctgg gcagtgggtt ttgggcaaata tccctttctt 2080  
tgcattccaca atgtggggtc ggagcttggg ggcaggtcct gggagtggga agcctcttcc 2140  
ttgtgtcttt cgctccactt ttagctcatc gcaccaatat tgcagacttg gaaggaagca 2200  
taagcttccc atttcacaaa ggggaaactg aggtgcgggt gcgcgggcct ggggacggcc 2260  
gtcccatggc ttccatctga gccacctgg gacccagca ctctggcgc cctcttctca 2320  
tcgcttggcc tatgacaggt caccgtgtgt aaatctttcc caataaagtg ttgcacaaag 2380

&lt;210&gt; 28

&lt;211&gt; 2017

&lt;212&gt; DNA

&lt;213&gt; Homo. sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (360)... (629)

&lt;400&gt; 28

tccacacatt aagaaacgct ggtggagttt taaatgcctc tccggggaag gaggaagcc 60  
tgagaatgaa tctgacctca gacccaaatc cattcaacgg agttctggta atttgaaga 120

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aggaagagca acctggaaac tgacaggaaa ggatgacaag ttgggagtca caggtatatg 180  
 atgggcctcc ccatgtggat ccttagtgct gtggcagagc ccttggtatt gtgctgggat 240  
 tttccctcca gctcccggcc ggaagctggg ctcacgtggg agctcagtgc cctcctgcta 300  
 cagatctgtc tcttccttac aatgggggtgc tggcactgtg ggtcctggtg acgcacgtg 359  
 atg tac atg caa gat tat tgg agg acc tgg ctc aag ggg ctg cgc ggc 407  
 Met Tyr Met Gln Asp Tyr Trp Arg Thr Trp Leu Lys Gly Leu Arg Gly  
 1 5 10 15  
 ttc ttc ttc gtg ggc gtc ctc ttc tgc gcc gtc tcc atc gct gcc ttc 455  
 Phe Phe Phe Val Gly Val Leu Phe Ser Ala Val Ser Ile Ala Ala Phe  
 20 25 30  
 tgc acc ttc ctc gtg ctg gcc atc acc cgg cat cag agc ctc aca gac 503  
 Cys Thr Phe Leu Val Leu Ala Ile Thr Arg His Gln Ser Leu Thr Asp  
 35 40 45  
 ccc acc agc tac tac ctc tcc agc gtc tgg agc ttc att tcc ttc aag 551  
 Pro Thr Ser Tyr Tyr Leu Ser Ser Val Trp Ser Phe Ile Ser Phe Lys  
 50 55 60  
 tgg gcc ttc ctg ctc agc ctc tat gcc cac cgc tac cgg gct gac ttt 599  
 Trp Ala Phe Leu Leu Ser Leu Tyr Ala His Arg Tyr Arg Ala Asp Phe  
 65 70 75 80  
 gct gac atc agc atc ctc agc gat ttc tgaccaggg ggtg 640  
 Ala Asp Ile Ser Ile Leu Ser Asp Phe  
 85  
 aggtctctgc accctggggg ggccttagga cctggactca gcctctgaga tgttgggaga 700  
 ggctactccc accccctggt gaccccagaa ctgtggcaga aaatacacag caggacgagt 760  
 gtgggtctccc aggaagctgt cctgcccgtc ccctttcgag gaaacctgag tgtggtagag 820

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aggggatect gccatgttgt tctcatcag cctggccaga gggcagcttt agaccttttc 880  
 aaatgaatct gttttctttt ctttctttt ttttctttt ttttttttt ttgagatgga 940  
 gtcttactct gtcaccagg ctggagtga gtagtgcgat ctcagctcac tgcaacctcc 1000  
 gcctcccagg ttcaagcaat tctctgcct tggcctctca agtagctggg attacaggca 1060  
 tctgccacca tgcccggcaa attttttgtt ttttagtaga gacagggttt tgccatgttg 1120  
 gccaggettg tctgaactc ctgatctcag gtgattcacc cgcctcagcc ttccaaagtg 1180  
 ctgggattat aggtgtgagc caccgcgcc ggcctggatc tgttttctta gcacgcagtg 1240  
 aggaatcttt gtacttaagg ccagggaac aaagtcaaga ggtcaagggtg tagggccatg 1300  
 aggcctggac ctatgctga ggcaagggtt tccatccccg ctgccctagg cactctcttc 1360  
 ccaaggccag gttgggcacc tggggaggtc agttcagaaa tatctagcag agacctctta 1420  
 aacccccatc ccagcacccc atcctgttgt tcccagagct ggtctcccat gagtgtgcta 1480  
 gagccagata gccgtggccc cccaccatc tcaactcac acacaggcat ccatacacc 1540  
 cagaagactt cccaaatgag gccagactca gggtcacggg gaatgtgctt ctgcccctgt 1600  
 aagggtttg gggaaggggg caacatagta gaggctggaa agagccccca aacctgtgcc 1660  
 catgcccctc cagccctgcg tttccattct gccttctcag agtgcccttg ctgcaccag 1720  
 accaccggcc aggagagacc ttctctccca ctccagcccc tctcaactgcc cttcaactag 1780  
 agctttcacc tttttacatt tcccttctga aggacacaaa tctgcttttc tgcccataca 1840  
 ctggcccaag ggctcaccta acttgggagg gaaggggctg ttggtacaag gatgattttc 1900  
 tgttagactg ccattttgca cggctctccc ctcccatct gatgtgtcct gcccctcagc 1960  
 tctttgcctt atctgtgtca ctgtcacttt agcaaaaata cagcgccat ttgtatc 2017

&lt;210&gt; 29

&lt;211&gt; 1606

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (30)... (1250)

&lt;400&gt; 29

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acctcttcgc tcggctgaat tgcggccgt atg cgc ggc tct gtg gag tgc acc      53
                                Met Arg Gly Ser Val Glu Cys Thr
                                1           5

tgg ggt tgg ggg cac tgt gcc ccc agc ccc ctg ctc ctt tgg act cta      101
Trp Gly Trp Gly His Cys Ala Pro Ser Pro Leu Leu Leu Trp Thr Leu
    10           15           20

ctt ctg ttt gca gcc cca ttt ggc ctg ctg ggg gag aag acc cgc cag      149
Leu Leu Phe Ala Ala Pro Phe Gly Leu Leu Gly Glu Lys Thr Arg Gln
    25           30           35           40

gtg tct ctg gag gtc atc cct aac tgg ctg ggc ccc ctg cag aac ctg      197
Val Ser Leu Glu Val Ile Pro Asn Trp Leu Gly Pro Leu Gln Asn Leu
           45           50           55

ctt cat ata cgg gca gtg ggc acc aat tcc aca ctg cac tat gtg tgg      245
Leu His Ile Arg Ala Val Gly Thr Asn Ser Thr Leu His Tyr Val Trp
           60           65           70

agc agc ctg ggg cct ctg gca gtg gta atg gtg gcc acc aac acc ccc      293
Ser Ser Leu Gly Pro Leu Ala Val Val Met Val Ala Thr Asn Thr Pro
           75           80           85

cac agc acc ctg agc gtc aac tgg agc ctc ctg cta tcc cct gag ccc      341
His Ser Thr Leu Ser Val Asn Trp Ser Leu Leu Leu Ser Pro Glu Pro
           90           95          100

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|  |     |
|--|-----|
| gat ggg ggc ctg atg gtg ctc cct aag gac agc att cag ttt tct tct                | 389 |
| Asp Gly Gly Leu Met Val Leu Pro Lys Asp Ser Ile Gln Phe Ser Ser                |     |
| 105                      110                      115                      120 |     |
| gcc ctt gtt ttt acc agg ctg ctt gag ttt gac agc acc aac gtg tcc                | 437 |
| Ala Leu Val Phe Thr Arg Leu Leu Glu Phe Asp Ser Thr Asn Val Ser                |     |
| 125                      130                      135                          |     |
| gat acg gca gca aag cct ttg gga aga cca tat cct cca tac tcc ttg                | 485 |
| Asp Thr Ala Ala Lys Pro Leu Gly Arg Pro Tyr Pro Pro Tyr Ser Leu                |     |
| 140                      145                      150                          |     |
| gcc gat ttc tct tgg aac aac atc act gat tca ttg gat cct gcc acc                | 533 |
| Ala Asp Phe Ser Trp Asn Asn Ile Thr Asp Ser Leu Asp Pro Ala Thr                |     |
| 155                      160                      165                          |     |
| ctg agt gcc aca ttt caa ggc cac ccc atg aac gac cct acc agg act                | 581 |
| Leu Ser Ala Thr Phe Gln Gly His Pro Met Asn Asp Pro Thr Arg Thr                |     |
| 170                      175                      180                          |     |
| ttt gcc aat ggc agc ctg gcc ttc agg gtc cag gcc ttt tcc agg tcc                | 629 |
| Phe Ala Asn Gly Ser Leu Ala Phe Arg Val Gln Ala Phe Ser Arg Ser                |     |
| 185                      190                      195                      200 |     |
| agc cga cca gcc caa ccc cct cgc ctc ctg cac aca gca gac acc tgt                | 677 |
| Ser Arg Pro Ala Gln Pro Pro Arg Leu Leu His Thr Ala Asp Thr Cys                |     |
| 205                      210                      215                          |     |
| cag cta gag gtg gcc ctg att gga gcc tct ccc cgg gga aac cgt tcc                | 725 |
| Gln Leu Glu Val Ala Leu Ile Gly Ala Ser Pro Arg Gly Asn Arg Ser                |     |
| 220                      225                      230                          |     |
| ctg ttt ggg ctg gag gta gcc aca ttg ggc cag ggc cct gac tgc ccc                | 773 |

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Leu Phe Gly Leu Glu Val Ala Thr Leu Gly Gln Gly Pro Asp Cys Pro  
 235 240 245  
 tca atg cag gag cag cac tcc atc gac gat gaa tat gca ccg gcc gtc 821  
 Ser Met Gln Glu Gln His Ser Ile Asp Asp Glu Tyr Ala Pro Ala Val  
 250 255 260  
 ttc cag ttg gac cag cta ctg tgg ggc tcc ctc cca tca ggc ttt gca 869  
 Phe Gln Leu Asp Gln Leu Leu Trp Gly Ser Leu Pro Ser Gly Phe Ala  
 265 270 275 280  
 cag tgg cga cca gtg gct tac tcc cag aag ccg ggg ggc cga gaa tca 917  
 Gln Trp Arg Pro Val Ala Tyr Ser Gln Lys Pro Gly Gly Arg Glu Ser  
 285 290 295  
 gcc ctg ccc tgc caa gct tcc cct ctt cat cct gcc tta gca tac tct 965  
 Ala Leu Pro Cys Gln Ala Ser Pro Leu His Pro Ala Leu Ala Tyr Ser  
 300 305 310  
 ctt ccc cag tca ccc att gtc cga gcc ttc ttt ggg tcc cag aat aac 1013  
 Leu Pro Gln Ser Pro Ile Val Arg Ala Phe Phe Gly Ser Gln Asn Asn  
 315 320 325  
 ttc tgt gcc ttc aat ctg acg ttc ggg gct tcc aca ggc cct ggc tat 1061  
 Phe Cys Ala Phe Asn Leu Thr Phe Gly Ala Ser Thr Gly Pro Gly Tyr  
 330 335 340  
 tgg gac caa cac tac ctc agc tgg tcg atg ctc ctg ggt gtg ggc ttc 1109  
 Trp Asp Gln His Tyr Leu Ser Trp Ser Met Leu Leu Gly Val Gly Phe  
 345 350 355 360  
 cct cca gtg gac ggc ttg tcc cca cta gtc ctg ggc atc atg gca gtg 1157  
 Pro Pro Val Asp Gly Leu Ser Pro Leu Val Leu Gly Ile Met Ala Val



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|   |     |     |      |
|---|-----|-----|------|
| 365   | 370 | 375 |      |
| gcc ctg ggt gcc cca ggg ctc atg ctg cta ggg ggc ggc ttg gtt ctg   |     |     | 1205 |
| Ala Leu Gly Ala Pro Gly Leu Met Leu Leu Gly Gly Gly Leu Val Leu   |     |     |      |
| 380   | 385 | 390 |      |
| ctg ctg cac cac aag aag tac tca gag tac cag tcc ata aat taa       |     |     | 1250 |
| Leu Leu His His Lys Lys Tyr Ser Glu Tyr Gln Ser Ile Asn           |     |     |      |
| 395   | 400 | 405 |      |
| ggcccgtct ctggagggaa ggacattact gaacctgtct tgctgtgcct cgaaactctg  |     |     | 1310 |
| gaggttgag catcaagttc cagccggccc cttactccc ccatcttgct tttctgtgga   |     |     | 1370 |
| acctcagagg ccagcctcga cttcctggag acccccaggt ggggttctt tcatactttg  |     |     | 1430 |
| ttgggggact ttggaggcgg gcaggggaca gggctattga taaggcccc ttggtgttgc  |     |     | 1490 |
| cttcttgcat ctccacacat ttcccttgga tgggacttgc aggcctaaat gagaggcatt |     |     | 1550 |
| ctgactgggt ggctgccctg gaaggcaaga aaatagattt attttttttc acaggg     |     |     | 1606 |

&lt;210&gt; 30

&lt;211&gt; 1695

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (53)... (631)

&lt;400&gt; 30

|   |    |
|---|----|
| acagccgagc agctggagcg atcgaggctg cagcgcggcc gccgggcgca gc atg | 55 |
|---|----|

Met

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|   |     |
|---|-----|
| act gcc gtc ggc gtg cag gcc cag agg cct ttg ggc caa agg cag ccc | 103 |
| Thr Ala Val Gly Val Gln Ala Gln Arg Pro Leu Gly Gln Arg Gln Pro |     |
| 5 10 15   |     |
| cgc cgg tcc ttc ttt gaa tcc ttc atc cgg acc ctc atc atc acg tgt | 151 |
| Arg Arg Ser Phe Phe Glu Ser Phe Ile Arg Thr Leu Ile Ile Thr Cys |     |
| 20 25 30  |     |
| gtg gcc ctg gct gtg gtc ctg tcc tgc gtc tcc att tgt gat ggg cac | 199 |
| Val Ala Leu Ala Val Val Leu Ser Ser Val Ser Ile Cys Asp Gly His |     |
| 35 40 45  |     |
| tgg ctc ctg gct gag gac cgc ctc ttc ggg ctc tgg cac ttc tgc acc | 247 |
| Trp Leu Leu Ala Glu Asp Arg Leu Phe Gly Leu Trp His Phe Cys Thr |     |
| 50 55 60 65   |     |
| acc acc aac cag agt gtg ccg atc tgc ttc aga gac ctg ggc cag gcc | 295 |
| Thr Thr Asn Gln Ser Val Pro Ile Cys Phe Arg Asp Leu Gly Gln Ala |     |
| 70 75 80  |     |
| cat gtg ccc ggg ctg gcc gtg ggc atg ggc ctg gta cgc agc gtg ggc | 343 |
| His Val Pro Gly Leu Ala Val Gly Met Gly Leu Val Arg Ser Val Gly |     |
| 85 90 95  |     |
| gcc ttg gcc gtg gtg gcc gcc att ttt ggc ctg gag ttc ctc atg gtg | 391 |
| Ala Leu Ala Val Val Ala Ala Ile Phe Gly Leu Glu Phe Leu Met Val |     |
| 100 105 110   |     |
| tcc cag ttg tgc gag gac aaa cac tca cag tgc aag tgg gtc atg ggt | 439 |
| Ser Gln Leu Cys Glu Asp Lys His Ser Gln Cys Lys Trp Val Met Gly |     |
| 115 120 125   |     |
| tcc atc ctc ctc ctg gtg tct ttc gtc ctc tcc tcc ggc ggg ctc ctg | 487 |

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Ser Ile Leu Leu Leu Val Ser Phe Val Leu Ser Ser Gly Gly Leu Leu  
 130 135 140 145  
 ggt ttt gtg atc ctc ctc agg aac caa gtc aca ctc atc ggc ttc acc 535  
 Gly Phe Val Ile Leu Leu Arg Asn Gln Val Thr Leu Ile Gly Phe Thr  
 150 155 160  
 cta atg ttt tgg tgc gaa ttc act gcc tcc ttc ctc ctc ttc ctg aac 583  
 Leu Met Phe Trp Cys Glu Phe Thr Ala Ser Phe Leu Leu Phe Leu Asn  
 165 170 175  
 gcc atc agc ggc ctt cac atc aac agc atc acc cat ccc tgg gaa tg 630  
 Ala Ile Ser Gly Leu His Ile Asn Ser Ile Thr His Pro Trp Glu  
 180 185 190  
 accgttgaaa ttttaggcc cctccaggga catcagattc cacaagaaaa tatggtcaaa 690  
 atgggacttt tccagcatgt ggcctctggt ggggctgggt tggacaagg ccttgaaacg 750  
 gctgcctgtt tgccgataac ttgtgggtgg tcagccagaa atggcccggg ggcctctgca 810  
 cctggtctgc agggccagag gccaggaggg tgccctcagt ccaccaactg cacaggctta 870  
 gccagatgtt gattttagag gaagaaaaaa acattttaaa actccttctt gaattttctt 930  
 ccttgactg gaatacagtt ggaagcacag gggtaactgg tacctgagct agctgcacag 990  
 ccaaggatag ttcattgctg ttccattgac acgtgctggg ataggggctg cagaatccct 1050  
 ggggctccca ggggtgttaa gaatggatca ttcttcagc taagggtcca atcagtgcct 1110  
 attcttcac cagctcaaag ggccttcgta tgtatgtccc tggcttcagc tttggtcatg 1170  
 ccaaaggagc agagttcagg attccctcag aatgccctgc acacagtagg tttccaaacc 1230  
 atttgactcg gtttgctcc ctgccgttg tttaaaccct acaaaccctg gataacccca 1290  
 tcttctagca gctggctgtc ccctctggga gctctgccta tcagaaccct accttaaggt 1350  
 gggtttcctt ccgagaagag ttcttgagca agctctccca ggagggccca cctgactgct 1410  
 aatacacagc cctccccaag gcccggtgtg gcatgtgtct gtcttttgtg agggttagac 1470

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agcctcaggg caccattttt aatcccagaa cacatttcaa agagcacgta tctagacctg 1530  
 ctggactctg caggggggtga gggggaacag cgagagcttg ggtaatgatt aacacccatg 1590  
 ctggggatgc atggaggtga agggggccag gaaccagtgg agatttccat ccttgccagc 1650  
 acgtctgtac ttctgttcat taaagtgtc cctttctagt ccttt 1695

&lt;210&gt; 31

&lt;211&gt; 377

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 31

Met Asp Ser Ala Leu Ser Asp Pro His Asn Gly Ser Ala Glu Ala Gly

|   |   |    |    |
|---|---|----|----|
| 1 | 5 | 10 | 15 |
|---|---|----|----|

Gly Pro Thr Asn Ser Thr Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile

|    |    |    |
|----|----|----|
| 20 | 25 | 30 |
|----|----|----|

Ala Leu Ala Tyr Gly Ser Leu Leu Leu Met Ala Leu Leu Pro Ile Phe

|    |    |    |
|----|----|----|
| 35 | 40 | 45 |
|----|----|----|

Phe Gly Ala Leu Arg Ser Val Arg Cys Ala Arg Gly Lys Asn Ala Ser

|    |    |    |
|----|----|----|
| 50 | 55 | 60 |
|----|----|----|

Asp Met Pro Glu Thr Ile Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile

|    |    |    |    |
|----|----|----|----|
| 65 | 70 | 75 | 80 |
|----|----|----|----|

Ile Ala Ser Cys Thr Leu Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe

|    |    |    |
|----|----|----|
| 85 | 90 | 95 |
|----|----|----|

Ser Gln Glu Tyr Ile Asn Leu Leu Leu Ser Met Tyr Phe Phe Val Leu

|     |     |     |
|-----|-----|-----|
| 100 | 105 | 110 |
|-----|-----|-----|

Gly Ile Leu Ala Leu Ser His Thr Ile Ser Pro Phe Met Asn Lys Phe

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|   |     |     |     |
|---|-----|-----|-----|
| 115   | 120 | 125 |     |
| Phe Pro Ala Ser Phe Pro Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln |     |     |     |
| 130   | 135 | 140 |     |
| Gly Ser Gly Glu Asn Lys Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr |     |     |     |
| 145   | 150 | 155 | 160 |
| Lys Asp Leu Val Cys Leu Gly Leu Ser Ser Ile Val Gly Val Trp Tyr |     |     |     |
| 165   | 170 | 175 |     |
| Leu Leu Arg Lys His Trp Ile Ala Asn Asn Leu Phe Gly Leu Ala Phe |     |     |     |
| 180   | 185 | 190 |     |
| Ser Leu Asn Gly Val Glu Leu Leu His Leu Asn Asn Val Ser Thr Gly |     |     |     |
| 195   | 200 | 205 |     |
| Cys Ile Leu Leu Gly Gly Leu Phe Ile Tyr Asp Val Phe Trp Val Phe |     |     |     |
| 210   | 215 | 220 |     |
| Gly Thr Asn Val Met Val Thr Val Ala Lys Ser Phe Glu Ala Pro Ile |     |     |     |
| 225   | 230 | 235 | 240 |
| Lys Leu Val Phe Pro Gln Asp Leu Leu Glu Lys Gly Leu Glu Ala Asn |     |     |     |
| 245   | 250 | 255 |     |
| Asn Phe Ala Met Leu Gly Leu Gly Asp Val Val Ile Pro Gly Ile Phe |     |     |     |
| 260   | 265 | 270 |     |
| Ile Ala Leu Leu Leu Arg Phe Asp Ile Ser Leu Lys Lys Asn Thr His |     |     |     |
| 275   | 280 | 285 |     |
| Thr Tyr Phe Tyr Thr Ser Phe Ala Ala Tyr Ile Phe Gly Leu Gly Leu |     |     |     |
| 290   | 295 | 300 |     |
| Thr Ile Phe Ile Met His Ile Phe Lys His Ala Gln Pro Ala Leu Leu |     |     |     |
| 305   | 310 | 315 | 320 |

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Tyr Leu Val Pro Ala Cys Ile Gly Phe Pro Val Leu Val Ala Leu Ala

325

330

335

Lys Gly Glu Val Thr Glu Met Phe Ser Tyr Glu Glu Ser Asn Pro Lys

340

345

350

Asp Pro Ala Ala Val Thr Glu Ser Lys Glu Gly Thr Glu Ala Ser Ala

355

360

365

Ser Lys Gly Leu Glu Lys Lys Glu Lys

370

375

&lt;210&gt; 32

&lt;211&gt; 81

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 32

Met Thr Ala His Ser Phe Ala Leu Pro Val Ile Ile Phe Thr Thr Phe

1

5

10

15

Trp Gly Leu Val Gly Ile Ala Gly Pro Trp Phe Val Pro Lys Gly Pro

20

25

30

Asn Arg Gly Val Ile Ile Thr Met Leu Val Ala Thr Ala Val Cys Cys

35

40

45

Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln Leu Asn Pro Leu Phe

50

55

60

Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr Val Arg Phe Leu Trp

65

70

75

80

Glu

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&lt;210&gt; 33

&lt;211&gt; 487

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 33

Met Gly Asp Thr Gly Leu Arg Lys Arg Arg Glu Asp Glu Lys Ser Ile  
1 5 10 15  
Gln Ser Gln Glu Pro Lys Thr Thr Ser Leu Gln Lys Glu Leu Gly Leu  
20 25 30  
Ile Ser Gly Ile Ser Ile Ile Val Gly Thr Ile Ile Gly Ser Gly Ile  
35 40 45  
Phe Val Ser Pro Lys Ser Val Leu Ser Asn Thr Glu Ala Val Gly Pro  
50 55 60  
Cys Leu Ile Ile Trp Ala Ala Cys Gly Val Leu Ala Thr Leu Gly Ala  
65 70 75 80  
Leu Cys Phe Ala Glu Leu Gly Thr Met Ile Thr Lys Ser Gly Gly Glu  
85 90 95  
Tyr Pro Tyr Leu Met Glu Ala Tyr Gly Pro Ile Pro Ala Tyr Leu Phe  
100 105 110  
Ser Trp Ala Ser Leu Ile Val Ile Lys Pro Thr Ser Phe Ala Ile Ile  
115 120 125  
Cys Leu Ser Phe Ser Glu Tyr Val Cys Ala Pro Phe Tyr Val Gly Cys  
130 135 140

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Lys Pro Pro Gln Ile Val Val Lys Cys Leu Ala Ala Ala Ala Ile Leu

145 150 155 160

Phe Ile Ser Thr Val Asn Ser Leu Ser Val Arg Leu Gly Ser Tyr Val

165 170 175

Gln Asn Ile Phe Thr Ala Ala Lys Leu Val Ile Val Ala Ile Ile Ile

180 185 190

Ile Ser Gly Leu Val Leu Leu Ala Gln Gly Asn Thr Lys Asn Phe Asp

195 200 205

Asn Ser Phe Glu Gly Ala Gln Leu Ser Val Gly Ala Ile Ser Leu Ala

210 215 220

Phe Tyr Asn Gly Leu Trp Ala Tyr Asp Gly Trp Asn Gln Leu Asn Tyr

225 230 235 240

Ile Thr Glu Glu Leu Arg Asn Pro Tyr Arg Asn Leu Pro Leu Ala Ile

245 250 255

Ile Ile Gly Ile Pro Leu Val Thr Ala Cys Tyr Ile Leu Met Asn Val

260 265 270

Ser Tyr Phe Thr Val Met Thr Ala Thr Glu Leu Leu Gln Ser Gln Ala

275 280 285

Val Ala Val Thr Phe Gly Asp Arg Val Leu Tyr Pro Ala Ser Trp Ile

290 295 300

Val Pro Leu Phe Val Ala Phe Ser Thr Ile Gly Ala Ala Asn Gly Thr

305 310 315 320

Cys Phe Thr Ala Gly Arg Leu Ile Tyr Val Ala Gly Arg Glu Gly His

325 330 335

Met Leu Lys Val Leu Ser Tyr Ile Ser Val Arg Arg Leu Thr Pro Ala



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340 345 350  
Pro Ala Ile Ile Phe Tyr Gly Ile Ile Ala Thr Ile Tyr Ile Ile Pro  
355 360 365  
Gly Asp Ile Asn Ser Leu Val Asn Tyr Phe Ser Phe Ala Ala Trp Leu  
370 375 380  
Phe Tyr Gly Leu Thr Ile Leu Gly Leu Ile Val Met Arg Phe Thr Arg  
385 390 395 400  
Lys Glu Leu Glu Arg Pro Ile Lys Val Pro Val Val Ile Pro Val Leu  
405 410 415  
Met Thr Leu Ile Ser Val Phe Leu Val Leu Ala Pro Ile Ile Ser Lys  
420 425 430  
Pro Thr Trp Glu Tyr Leu Tyr Cys Val Leu Phe Ile Leu Ser Gly Leu  
435 440 445  
Leu Phe Tyr Phe Leu Phe Val His Tyr Lys Phe Gly Trp Ala Gln Lys  
450 455 460  
Ile Ser Lys Pro Ile Thr Met His Leu Gln Met Leu Met Glu Val Val  
465 470 475 480  
Pro Pro Glu Glu Asp Pro Glu  
485

&lt;210&gt; 34

&lt;211&gt; 375

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 34

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Met Thr Pro Gln Pro Ala Gly Pro Pro Asp Gly Gly Trp Gly Trp Val

1 5 10 15

Val Ala Ala Ala Ala Phe Ala Ile Asn Gly Leu Ser Tyr Gly Leu Leu

20 25 30

Arg Ser Leu Gly Leu Ala Phe Pro Asp Leu Ala Glu His Phe Asp Arg

35 40 45

Ser Ala Gln Asp Thr Ala Trp Ile Ser Ala Leu Ala Leu Ala Val Gln

50 55 60

Gln Ala Ala Ser Pro Val Gly Ser Ala Leu Ser Thr Arg Trp Gly Ala

65 70 75 80

Arg Pro Val Val Met Val Gly Gly Val Leu Ala Ser Leu Gly Phe Val

85 90 95

Phe Ser Ala Phe Ala Ser Gly Leu Leu His Leu Tyr Leu Gly Leu Gly

100 105 110

Leu Leu Ala Gly Phe Gly Trp Ala Leu Val Phe Ala Pro Ala Leu Gly

115 120 125

Thr Leu Ser Arg Tyr Phe Ser Arg Arg Arg Val Leu Ala Val Gly Leu

130 135 140

Ala Leu Thr Gly Asn Gly Ala Ser Ser Leu Leu Leu Ala Pro Ala Leu

145 150 155 160

Gln Leu Leu Leu Asp Thr Phe Gly Trp Arg Gly Ala Leu Leu Leu Leu

165 170 175

Gly Ala Ile Thr Leu His Leu Thr Pro Cys Gly Ala Leu Leu Leu Pro

180 185 190

Leu Val Leu Pro Gly Asp Pro Pro Ala Pro Pro Arg Ser Pro Leu Ala

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195 200 205  
Ala Leu Gly Leu Ser Leu Phe Thr Arg Arg Ala Phe Ser Ile Phe Ala  
210 215 220  
Leu Gly Thr Ala Leu Val Gly Gly Gly Tyr Phe Val Pro Tyr Val His  
225 230 235 240  
Leu Ala Pro Arg Phe Arg Pro Gly Pro Gly Gly Ile Arg Ser Ser Ala  
245 250 255  
Gly Gly Gly Arg Gly Cys Asp Gly Gly Cys Gly Arg Pro Ala Gly Leu  
260 265 270  
Arg Val Ala Gly Arg Pro Arg Leu Gly Ala Pro Pro Ala Ala Ala Gly  
275 280 285  
Arg Ile Arg Gly Ser Asp Trp Ala Gly Ala Val Gly Gly Gly Ala Gly  
290 295 300  
Ala Arg Gly Gly Arg Arg Arg Glu Leu Gly Gly Ser Pro Ala Gly Arg  
305 310 315 320  
Gly Cys Gly Leu Trp Ala Glu Arg Gly Glu Leu Arg Pro Ala Gly Phe  
325 330 335  
Arg Cys Thr Pro Arg Ala Gly Gly Arg Arg Arg Cys Gly Ala Gly His  
340 345 350  
Arg Ala Gly Asp Asp Ala Asp Glu Pro Arg Gly Ala Pro Gly Pro Ser  
355 360 365  
Pro Val Arg Leu Pro Lys Gly  
370 375

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&lt;211&gt; 350

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 35

Met Ala Thr Thr Ala Ala Pro Ala Gly Gly Ala Arg Asn Gly Ala Gly

1 5 10 15

Pro Glu Trp Gly Gly Phe Glu Glu Asn Ile Gln Gly Gly Gly Ser Ala

20 25 30

Val Ile Asp Met Glu Asn Met Asp Asp Thr Ser Gly Ser Ser Phe Glu

35 40 45

Asp Met Gly Glu Leu His Gln Arg Leu Arg Glu Glu Glu Val Asp Ala

50 55 60

Asp Ala Ala Asp Ala Ala Ala Glu Glu Glu Asp Gly Glu Phe Leu

65 70 75 80

Gly Met Lys Gly Phe Lys Gly Gln Leu Ser Arg Gln Val Ala Asp Gln

85 90 95

Met Trp Gln Ala Gly Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr

100 105 110

Ala Asn Ile Asp Ile Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln

115 120 125

Val Arg Ser Arg Leu Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn

130 135 140

Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val

145 150 155 160

Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr

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|   |     |     |     |
|---|-----|-----|-----|
| 165   | 170 | 175 |     |
| Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe |     |     |     |
| 180   | 185 | 190 |     |
| Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu |     |     |     |
| 195   | 200 | 205 |     |
| Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr |     |     |     |
| 210   | 215 | 220 |     |
| Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His |     |     |     |
| 225   | 230 | 235 | 240 |
| Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser |     |     |     |
| 245   | 250 | 255 |     |
| Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr |     |     |     |
| 260   | 265 | 270 |     |
| Gln Arg Leu Leu Leu Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe |     |     |     |
| 275   | 280 | 285 |     |
| Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu |     |     |     |
| 290   | 295 | 300 |     |
| Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg |     |     |     |
| 305   | 310 | 315 | 320 |
| Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu |     |     |     |
| 325   | 330 | 335 |     |
| Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser His         |     |     |     |
| 340   | 345 | 350 |     |

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&lt;211&gt; 667

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 36

Met Ser Ser Gln Pro Ala Gly Asn Gln Thr Ser Pro Gly Ala Thr Glu

1 5 10 15

Asp Tyr Ser Tyr Gly Ser Trp Tyr Ile Asp Glu Pro Gln Gly Gly Glu

20 25 30

Glu Leu Gln Pro Glu Gly Glu Val Pro Ser Cys His Thr Ser Ile Pro

35 40 45

Pro Gly Leu Tyr His Ala Cys Leu Ala Ser Leu Ser Ile Leu Val Leu

50 55 60

Leu Leu Leu Ala Met Leu Val Arg Arg Arg Gln Leu Trp Pro Asp Cys

65 70 75 80

Val Arg Gly Arg Pro Gly Leu Pro Ser Pro Val Asp Phe Leu Ala Gly

85 90 95

Asp Arg Pro Arg Ala Val Pro Ala Ala Val Phe Met Val Leu Leu Ser

100 105 110

Ser Leu Cys Leu Leu Leu Pro Asp Glu Asp Ala Leu Pro Phe Leu Thr

115 120 125

Leu Ala Ser Ala Pro Ser Gln Asp Gly Lys Thr Glu Ala Pro Arg Gly

130 135 140

Ala Trp Lys Ile Leu Gly Leu Phe Tyr Tyr Ala Ala Leu Tyr Tyr Pro

145 150 155 160

Leu Ala Ala Cys Ala Thr Ala Gly His Thr Ala Ala His Leu Leu Gly

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|   |     |     |     |
|---|-----|-----|-----|
| 165   | 170 | 175 |     |
| Ser Thr Leu Ser Trp Ala His Leu Gly Val Gln Val Trp Gln Arg Ala |     |     |     |
| 180   | 185 | 190 |     |
| Glu Cys Pro Gln Val Pro Lys Ile Tyr Lys Tyr Tyr Ser Leu Leu Ala |     |     |     |
| 195   | 200 | 205 |     |
| Ser Leu Pro Leu Leu Leu Gly Leu Gly Phe Leu Ser Leu Trp Tyr Pro |     |     |     |
| 210   | 215 | 220 |     |
| Val Gln Leu Val Arg Ser Phe Ser Arg Arg Thr Gly Ala Gly Ser Lys |     |     |     |
| 225   | 230 | 235 | 240 |
| Gly Leu Gln Ser Ser Tyr Ser Glu Glu Tyr Leu Arg Asn Leu Leu Cys |     |     |     |
| 245   | 250 | 255 |     |
| Arg Lys Lys Leu Gly Ser Ser Tyr His Thr Ser Lys His Gly Phe Leu |     |     |     |
| 260   | 265 | 270 |     |
| Ser Trp Ala Arg Val Cys Leu Arg His Cys Ile Tyr Thr Pro Gln Pro |     |     |     |
| 275   | 280 | 285 |     |
| Gly Phe His Leu Pro Leu Lys Leu Val Leu Ser Ala Thr Leu Thr Gly |     |     |     |
| 290   | 295 | 300 |     |
| Thr Ala Ile Tyr Gln Val Ala Leu Leu Leu Leu Val Gly Val Val Pro |     |     |     |
| 305   | 310 | 315 | 320 |
| Thr Ile Gln Lys Val Arg Ala Gly Val Thr Thr Asp Val Ser Tyr Leu |     |     |     |
| 325   | 330 | 335 |     |
| Leu Ala Gly Phe Gly Ile Val Leu Ser Glu Asp Lys Gln Glu Val Val |     |     |     |
| 340   | 345 | 350 |     |
| Glu Leu Val Lys His His Leu Trp Ala Leu Glu Val Cys Tyr Ile Ser |     |     |     |
| 355   | 360 | 365 |     |

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Ala Leu Val Leu Ser Cys Leu Leu Thr Phe Leu Val Leu Met Arg Ser  
370 375 380  
Leu Val Thr His Arg Thr Asn Leu Arg Ala Leu His Arg Gly Ala Ala  
385 390 395 400  
Leu Asp Leu Ser Pro Leu His Arg Ser Pro His Pro Ser Arg Gln Ala  
405 410 415  
Ile Phe Cys Trp Met Ser Phe Ser Ala Tyr Gln Thr Ala Phe Ile Cys  
420 425 430  
Leu Gly Leu Leu Val Gln Gln Ile Ile Phe Phe Leu Gly Thr Thr Ala  
435 440 445  
Leu Ala Phe Leu Val Leu Met Pro Val Leu His Gly Arg Asn Leu Leu  
450 455 460  
Leu Phe Arg Ser Leu Glu Ser Ser Trp Pro Phe Trp Leu Thr Leu Ala  
465 470 475 480  
Leu Ala Val Ile Leu Gln Asn Met Ala Ala His Trp Val Phe Leu Glu  
485 490 495  
Thr His Asp Gly His Pro Gln Leu Thr Asn Arg Arg Val Leu Tyr Ala  
500 505 510  
Ala Thr Phe Leu Leu Phe Pro Leu Asn Val Leu Val Gly Ala Met Val  
515 520 525  
Ala Thr Trp Arg Val Leu Leu Ser Ala Leu Tyr Asn Ala Ile His Leu  
530 535 540  
Gly Gln Met Asp Leu Ser Leu Leu Pro Pro Arg Ala Ala Thr Leu Asp  
545 550 555 560  
Pro Gly Tyr Tyr Thr Tyr Arg Asn Phe Leu Lys Ile Glu Val Ser Gln



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|   |     |     |     |
|---|-----|-----|-----|
| 565   | 570 | 575 |     |
| Ser His Pro Ala Met Thr Ala Phe Cys Ser Leu Leu Leu Gln Ala Gln |     |     |     |
| 580   | 585 | 590 |     |
| Ser Leu Leu Pro Arg Thr Met Ala Ala Pro Gln Asp Ser Leu Arg Pro |     |     |     |
| 595   | 600 | 605 |     |
| Gly Glu Glu Asp Glu Gly Met Gln Leu Leu Gln Thr Lys Asp Ser Met |     |     |     |
| 610   | 615 | 620 |     |
| Ala Lys Gly Ala Arg Pro Gly Ala Ser Arg Gly Arg Ala Arg Trp Gly |     |     |     |
| 625   | 630 | 635 | 640 |
| Leu Ala Tyr Thr Leu Leu His Asn Pro Thr Leu Gln Val Phe Arg Lys |     |     |     |
| 645   | 650 | 655 |     |
| Thr Ala Leu Leu Gly Ala Asn Gly Ala Gln Pro                     |     |     |     |
| 660   | 665 |     |     |

&lt;210&gt; 37

&lt;211&gt; 464

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 37

|  |
|--|
| Met Ile Val Cys Leu Leu Phe Met Met Ile Leu Leu Ala Lys Glu Val          |
| 1                      5                      10                      15 |
| Gln Leu Val Asp Gln Thr Asp Ser Pro Leu Leu Ser Leu Leu Gly Gln          |
| 20                      25                      30                       |
| Thr Ser Ser Leu Ser Trp His Leu Val Asp Ile Val Ser Tyr Gln Ser          |
| 35                      40                      45                       |

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Val Leu Ser Tyr Phe Ser Ser His Tyr Pro Pro Ser Ile Ile Leu Ala  
50 55 60  
Lys Glu Ser Tyr Ala Glu Leu Ile Met Lys Leu Leu Lys Val Ser Ala  
65 70 75 80  
Gly Leu Ser Ile Pro Thr Asp Ser Gln Lys His Leu Asp Ala Val Pro  
85 90 95  
Lys Cys Gln Ala Phe Thr His Gln Met Val Gln Phe Leu Ser Thr Leu  
100 105 110  
Glu Gln Asn Gly Lys Ile Thr Leu Ala Val Leu Glu Gln Glu Met Ser  
115 120 125  
Lys Leu Leu Asp Asp Ile Ile Val Phe Asn Pro Pro Asp Met Asp Ser  
130 135 140  
Gln Thr Arg His Met Ala Leu Ser Ser Leu Phe Met Glu Val Leu Met  
145 150 155 160  
Met Met Asn Asn Ala Thr Ile Pro Thr Ala Glu Phe Leu Arg Gly Ser  
165 170 175  
Ile Arg Thr Trp Ile Gly Gln Lys Met His Gly Leu Val Val Leu Pro  
180 185 190  
Leu Leu Thr Ala Ala Cys Gln Ser Leu Ala Ser Val Arg His Met Ala  
195 200 205  
Glu Thr Thr Glu Ala Cys Ile Thr Ala Tyr Phe Lys Glu Ser Pro Leu  
210 215 220  
Asn Gln Asn Ser Gly Trp Gly Pro Ile Leu Val Ser Leu Gln Val Pro  
225 230 235 240  
Glu Leu Thr Met Glu Glu Phe Leu Gln Glu Cys Leu Thr Leu Gly Ser

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|   |     |     |     |
|---|-----|-----|-----|
| 245   | 250 | 255 |     |
| Tyr Leu Thr Leu Tyr Val Tyr Leu Leu Gln Cys Leu Asn Ser Glu Gln |     |     |     |
| 260   | 265 | 270 |     |
| Thr Leu Arg Asn Glu Met Lys Val Leu Leu Ile Leu Ser Lys Trp Leu |     |     |     |
| 275   | 280 | 285 |     |
| Glu Gln Val Tyr Pro Ser Ser Val Glu Glu Glu Ala Lys Leu Phe Leu |     |     |     |
| 290   | 295 | 300 |     |
| Trp Trp His Gln Val Leu Gln Leu Ser Leu Ile Gln Thr Glu Gln Asn |     |     |     |
| 305   | 310 | 315 | 320 |
| Asp Ser Val Leu Thr Glu Ser Val Ile Arg Ile Leu Leu Leu Val Gln |     |     |     |
| 325   | 330 | 335 |     |
| Ser Arg Gln Asn Leu Val Ala Glu Glu Arg Leu Ser Ser Gly Ile Leu |     |     |     |
| 340   | 345 | 350 |     |
| Gly Ala Ile Gly Phe Gly Arg Lys Ser Pro Leu Ser Asn Arg Phe Arg |     |     |     |
| 355   | 360 | 365 |     |
| Val Val Ala Arg Ser Met Ala Ala Phe Leu Ser Val Gln Val Pro Met |     |     |     |
| 370   | 375 | 380 |     |
| Glu Asp Gln Ile Arg Leu Arg Pro Gly Ser Glu Leu His Leu Thr Pro |     |     |     |
| 385   | 390 | 395 | 400 |
| Lys Ala Gln Gln Ala Leu Asn Ala Leu Glu Ser Met Ala Ser Ser Lys |     |     |     |
| 405   | 410 | 415 |     |
| Gln Tyr Val Glu Tyr Gln Asp Gln Ile Leu Gln Ala Thr Gln Phe Ile |     |     |     |
| 420   | 425 | 430 |     |
| Arg His Pro Gly His Cys Leu Gln Asp Gly Lys Ser Phe Leu Ala Leu |     |     |     |
| 435   | 440 | 445 |     |

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Leu Val Asn Cys Leu Tyr Pro Glu Val His Tyr Leu Asp His Ile Arg

450

455

460

&lt;210&gt; 38

&lt;211&gt; 470

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 38

Met Ser Arg Leu Gly Ala Leu Gly Gly Ala Arg Ala Gly Leu Gly Leu

1

5

10

15

Leu Leu Gly Thr Ala Ala Gly Leu Gly Phe Leu Cys Leu Leu Tyr Ser

20

25

30

Gln Arg Trp Lys Arg Thr Gln Arg His Gly Arg Ser Gln Ser Leu Pro

35

40

45

Asn Ser Leu Asp Tyr Thr Gln Thr Ser Asp Pro Gly Arg His Val Met

50

55

60

Leu Leu Arg Ala Val Pro Gly Gly Ala Gly Asp Ala Ser Val Leu Pro

65

70

75

80

Ser Leu Pro Arg Glu Gly Gln Glu Lys Val Leu Asp Arg Leu Asp Phe

85

90

95

Val Leu Thr Ser Leu Val Ala Leu Arg Arg Glu Val Glu Glu Leu Arg

100

105

110

Ser Ser Leu Arg Gly Leu Ala Gly Glu Ile Val Gly Glu Val Arg Cys

115

120

125

His Met Glu Glu Asn Gln Arg Val Ala Arg Arg Arg Arg Phe Pro Phe

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|   |     |     |     |
|---|-----|-----|-----|
| 130   | 135 | 140 |     |
| Val Arg Glu Arg Ser Asp Ser Thr Gly Ser Ser Ser Val Tyr Phe Thr |     |     |     |
| 145   | 150 | 155 | 160 |
| Ala Ser Ser Gly Ala Thr Phe Thr Asp Ala Glu Ser Glu Gly Gly Tyr |     |     |     |
|   | 165 | 170 | 175 |
| Thr Thr Ala Asn Ala Glu Ser Asp Asn Glu Arg Asp Ser Asp Lys Glu |     |     |     |
|   | 180 | 185 | 190 |
| Ser Glu Asp Gly Glu Asp Glu Val Ser Cys Glu Thr Val Lys Met Gly |     |     |     |
|   | 195 | 200 | 205 |
| Arg Lys Asp Ser Leu Asp Leu Glu Glu Glu Ala Ala Ser Gly Ala Ser |     |     |     |
|   | 210 | 215 | 220 |
| Ser Ala Leu Glu Ala Gly Gly Ser Ser Gly Leu Glu Asp Val Leu Pro |     |     |     |
| 225   | 230 | 235 | 240 |
| Leu Leu Gln Gln Ala Asp Glu Leu His Arg Gly Asp Glu Gln Gly Lys |     |     |     |
|   | 245 | 250 | 255 |
| Arg Glu Gly Phe Gln Leu Leu Leu Asn Asn Lys Leu Val Tyr Gly Ser |     |     |     |
|   | 260 | 265 | 270 |
| Arg Gln Asp Phe Leu Trp Arg Leu Ala Arg Ala Tyr Ser Asp Met Cys |     |     |     |
|   | 275 | 280 | 285 |
| Glu Leu Thr Glu Glu Val Ser Glu Lys Lys Ser Tyr Ala Leu Asp Gly |     |     |     |
|   | 290 | 295 | 300 |
| Lys Glu Glu Ala Glu Ala Ala Leu Glu Lys Gly Asp Glu Ser Ala Asp |     |     |     |
| 305   | 310 | 315 | 320 |
| Cys His Leu Trp Tyr Ala Val Leu Cys Gly Gln Leu Ala Glu His Glu |     |     |     |
|   | 325 | 330 | 335 |

85 / 307

Ser Ile Gln Arg Arg Ile Gln Ser Gly Phe Ser Phe Lys Glu His Val

340

345

350

Asp Lys Ala Ile Ala Leu Gln Pro Glu Asn Pro Met Ala His Phe Leu

355

360

365

Leu Gly Arg Trp Cys Tyr Gln Val Ser His Leu Ser Trp Leu Glu Lys

370

375

380

Lys Thr Ala Thr Ala Leu Leu Glu Ser Pro Leu Ser Ala Thr Val Glu

385

390

395

400

Asp Ala Leu Gln Ser Phe Leu Lys Ala Glu Glu Leu Gln Pro Gly Phe

405

410

415

Ser Lys Ala Gly Arg Val Tyr Ile Ser Lys Cys Tyr Arg Glu Leu Gly

420

425

430

Lys Asn Ser Glu Ala Arg Trp Trp Met Lys Leu Ala Leu Glu Leu Pro

435

440

445

Asp Val Thr Lys Glu Asp Leu Ala Ile Gln Lys Asp Leu Glu Glu Leu

450

455

460

Glu Val Ile Leu Arg Asp

465

470

&lt;210&gt; 39

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 39

Met Glu Gln Gly Ser Gly Arg Leu Glu Asp Phe Pro Val Asn Val Phe

86 /307

|   |     |     |     |
|---|-----|-----|-----|
| 1   | 5   | 10  | 15  |
| Ser Val Thr Pro Tyr Thr Pro Ser Thr Ala Asp Ile Gln Val Ser Asp |     |     |     |
| 20  | 25  | 30  |     |
| Asp Asp Lys Ala Gly Ala Thr Leu Leu Phe Ser Gly Ile Phe Leu Gly |     |     |     |
| 35  | 40  | 45  |     |
| Leu Val Gly Ile Thr Phe Thr Val Met Gly Trp Ile Lys Tyr Gln Gly |     |     |     |
| 50  | 55  | 60  |     |
| Val Ser His Phe Glu Trp Thr Gln Leu Leu Gly Pro Val Leu Leu Ser |     |     |     |
| 65  | 70  | 75  | 80  |
| Val Gly Val Thr Phe Ile Leu Ile Ala Val Cys Lys Phe Lys Met Leu |     |     |     |
| 85  | 90  | 95  |     |
| Ser Cys Gln Leu Cys Lys Glu Ser Glu Glu Arg Val Pro Asp Ser Glu |     |     |     |
| 100   | 105 | 110 |     |
| Gln Thr Pro Gly Gly Pro Ser Phe Val Phe Thr Gly Ile Asn Gln Pro |     |     |     |
| 115   | 120 | 125 |     |
| Ile Thr Phe His Gly Ala Thr Val Val Gln Tyr Ile Pro Pro Pro Tyr |     |     |     |
| 130   | 135 | 140 |     |
| Gly Ser Pro Glu Pro Met Gly Ile Asn Thr Ser Tyr Leu Gln Ser Val |     |     |     |
| 145   | 150 | 155 | 160 |
| Val Ser Pro Cys Gly Leu Ile Thr Ser Gly Gly Ala Ala Ala Ala Met |     |     |     |
| 165   | 170 | 175 |     |
| Ser Ser Pro Pro Gln Tyr Tyr Thr Ile Tyr Pro Gln Asp Asn Ser Ala |     |     |     |
| 180   | 185 | 190 |     |
| Phe Val Val Asp Glu Gly Cys Leu Ser Phe Thr Asp Gly Gly Asn His |     |     |     |
| 195   | 200 | 205 |     |

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Arg Pro Asn Pro Asp Val Asp Gln Leu Glu Glu Thr Gln Leu Glu Glu

210

215

220

Glu Ala Cys Ala Cys Phe Ser Pro Pro Pro Tyr Glu Glu Ile Tyr Ser

225

230

235

240

Leu Pro Arg

&lt;210&gt; 40

&lt;211&gt; 270

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 40

Met Ala Gly Ala Glu Asp Trp Pro Gly Gln Gln Leu Glu Leu Asp Glu

1

5

10

15

Asp Glu Ala Ser Cys Cys Arg Trp Gly Ala Gln His Ala Gly Ala Arg

20

25

30

Glu Leu Ala Ala Leu Tyr Ser Pro Gly Lys Arg Leu Gln Glu Trp Cys

35

40

45

Ser Val Ile Leu Cys Phe Ser Leu Ile Ala His Asn Leu Val His Leu

50

55

60

Leu Leu Leu Ala Arg Trp Glu Asp Thr Pro Leu Val Ile Leu Gly Val

65

70

75

80

Val Ala Gly Ala Leu Ile Ala Asp Phe Leu Ser Gly Leu Val His Trp

85

90

95

Gly Ala Asp Thr Trp Gly Ser Val Glu Leu Pro Ile Val Gly Lys Ala

100

105

110



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Phe Ile Arg Pro Phe Arg Glu His His Ile Asp Pro Thr Ala Ile Thr

115

120

125

Arg His Asp Phe Ile Glu Thr Asn Gly Asp Asn Cys Leu Val Thr Leu

130

135

140

Leu Pro Leu Leu Asn Met Ala Tyr Lys Phe Arg Thr His Ser Pro Glu

145

150

155

160

Ala Leu Glu Gln Leu Tyr Pro Trp Glu Cys Phe Val Phe Cys Leu Ile

165

170

175

Ile Phe Gly Thr Phe Thr Asn Gln Ile His Lys Trp Ser His Thr Tyr

180

185

190

Phe Gly Leu Pro Arg Trp Val Thr Leu Leu Gln Asp Trp His Val Ile

195

200

205

Leu Pro Arg Lys His His Arg Ile His His Val Ser Pro His Glu Thr

210

215

220

Tyr Phe Cys Ile Thr Thr Gly Trp Leu Asn Tyr Pro Leu Glu Lys Ile

225

230

235

240

Gly Phe Trp Arg Arg Leu Glu Asp Leu Ile Gln Gly Leu Thr Gly Glu

245

250

255

Lys Pro Arg Ala Asp Asp Met Lys Trp Ala Gln Lys Ile Lys

260

265

270

&lt;210&gt; 41

&lt;211&gt; 1131

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

89 / 307

&lt;400&gt; 41

|  |      |
|--|------|
| atggactcgg ccctcagcga tccgcataac ggcaagtgcg aggcaggcgg ccccaaccaac | 60   |
| agcaactacgc ggccgccttc cacgcccagag ggcatcgcg tggectacgg cagcctcctg | 120  |
| ctcatggcgc tgctgcccat ctctctcggc gccctgcgct ccgtacgctg cgcccgcggc  | 180  |
| aagaatgctt cagacatgcc tgaacaatc accagccggg atgccgccg cttccccatc    | 240  |
| atgccagct gcacactctt ggggtcttac ctctttttca aaatattctc ccaggagtac   | 300  |
| atcaacctcc tgctgtccat gtatttcttc gtgctgggaa tcctggccct gtccacacc   | 360  |
| atcagccct tcatgaataa gttttttcca gccagctttc caaatcgaca gtaccagctg   | 420  |
| ctcttcacac agggttctgg ggaaaacaag gaagagatca tcaattatga atttgacacc  | 480  |
| aaggacctgg tgtgcctggg cctgagcagc atcgttggcg tctggtacct gctgaggaag  | 540  |
| cactggattg ccaacaacct ttttggcctg gccttctccc ttaatggagt agagctcctg  | 600  |
| cacctcaaca atgtcagcac tggtgcac cgtctggcg gactcttcac ctacgatgtc     | 660  |
| ttctgggtat ttggcaccaa tgtgatggtg acagtggcca agtccttoga ggcaccaata  | 720  |
| aaattggtgt ttccccagga tctgctggag aaaggcctg aagcaaaca ctttgccatg    | 780  |
| ctgggacttg gagatgtcgt cattccaggg atcttcattg ccttgctgct gcgctttgac  | 840  |
| atcagcttga agaagaatac ccacacctac ttctacacca gctttgcagc ctacatcttc  | 900  |
| ggcctgggcc ttaccatctt catcatgcac atcttcaagc atgtcagcc tgcctccta    | 960  |
| tacctgtcc ccgcctgcac cggttttcct gtctgtgtgg cgctggccaa gggagaagtg   | 1020 |
| acagagatgt tcagttatga ggagtcaaat cctaaggatc cagcggcagt gacagaatcc  | 1080 |
| aaagagggaa cagaggcatc agcatcgaag gggctggaga agaaagagaa a           | 1131 |

&lt;210&gt; 42

&lt;211&gt; 243

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

90 / 307

&lt;400&gt; 42

|   |     |
|---|-----|
| atgacggcgc actcattcgc cctccccgtc atcatcttca ccacgttctg gggcctcgtc   | 60  |
| ggcatcgccg ggccctgggt cgtgccgaag ggaccaacc gcggagtgat catcaccatg    | 120 |
| ctggtcgcca ccgccgtctg ctgttacctc ttctggctca tcgccatcct ggcgcagctg   | 180 |
| aacccccctgt tcgggccccca gctgaagaat gagaccatct ggtacgtgcg cttcctgtgg | 240 |
| gag   | 243 |

&lt;210&gt; 43

&lt;211&gt; 1461

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 43

|  |     |
|--|-----|
| atgggggata ctggcctgag aaagcggaga gaggatgaga agtcgatcca gagccaagag  | 60  |
| cctaagacca ccagtctcca aaaggagctg ggcctcatca gtggcatctc catcatcgtg  | 120 |
| ggcaccatca ttggctctgg gatcttcgtt tcccccaagt ctgtgctcag caacacggaa  | 180 |
| gctgtggggc cctgcctcat catatgggcg gcttgccggg tcctcgcgac gctgggtgcc  | 240 |
| ctgtgctttg cggagcttgg cacaatgatc accaagtcag ggggagagta tccctacctg  | 300 |
| atggaggcct acggggcccat cccgcctac ctcttctcct gggccagcct gatcgtcatt  | 360 |
| aagcccacgt ccttcgccat catctgctc agcttctccg agtatgtgtg tgcgcccttc   | 420 |
| tatgtgggct gcaagcctcc tcaaatcgtt gtgaaatgcc tggccgccgc cgccatcttg  | 480 |
| ttcatctcga cagtgaactc actgagcgtg cggctgggaa gctacgtcca gaacatcttc  | 540 |
| accgcggcca agctggtgat cgtggccatc atcatcatca gcgggctggt gtccttggcc  | 600 |
| caaggaaaca caaagaattt tgataattct ttcgagggcg cccagctgtc tgtgggagcc  | 660 |
| atcagcctgg cgttttaciaa tggactctgg gcctatgatg gatggaatca actcaattac | 720 |
| atcacagaag aacttagaaa cccttacaga aacctgcctt tgccattat catcgggac    | 780 |

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cccctggtga cggcgtgcta catcctcatg aacgtgtcct acttcaccgt gatgactgcc 840  
 accgaactcc tgcagtccca ggcggtggct gtgacatttg gtgaccgtgt tctctatcct 900  
 gcttcttgga tcgttcact ttttgtggca tttcaacca tcggtgctgc taacgggacc 960  
 tgcttcacag cgggcagact catttacgtg gcgggcggg agggtcacat gctcaaagtg 1020  
 ctttcttaca tcagcgtcag gcgcctcact ccagcccccg ccatcatctt ttatggtatc 1080  
 atagcaacga tttatatcat ccctggtgac ataaactcgt tagtcaatta tttcagcttt 1140  
 gccgcatggc tgttttatgg cctgacgatt ctaggactca tcgtgatgag atttacaagg 1200  
 aaagagctgg aaaggcctat caaggtgccc gtagtcattc ccgtcttgat gacactcatc 1260  
 tctgtgtttt tggttctggc tccaatcacc agcaagccca cctgggagta cctctactgt 1320  
 gtgctgttta tattaagcgg ccttttattt tacttctgtt ttgtccacta caagtttgga 1380  
 tgggctcaga aaatctcaaa gccgattacc atgcaccttc agatgctaata ggaagtggtc 1440  
 ccaccggagg aagaccctga g 1461

&lt;210&gt; 44

&lt;211&gt; 1125

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 44

atgaccccc agcccgccgg acccccgat gggggctggg gctgggtggt ggcgccgca 60  
 gccttcgca taaacgggt gtcctacggg ctgctgcgt cgctgggcct tgccttcct 120  
 gaccttgccg agcactttga ccgaagcgc caggacactg cgtggatcag cgccctggcc 180  
 ctggccgtgc agcaggcagc cagccccgtg ggcagcgccc tgagcacgcg ctggggggcc 240  
 cgccccgtgg tgatggttg gggcgctctc gcctcgtgg gcttcgtctt ctcggctttc 300  
 gccagcggtc tctgcatct ctacctggc ctgggcctcc tcgtggctt tggttgggcc 360  
 ctggtgttcg cccccgcct aggcacctc tcgcgttact tctccgcgc tcgagtcttg 420

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gcggtggggc tggcgctcac cggcaacggg gcctcctcgc tgctcctggc gcccgcttg 480  
cagcttctcc tcgatacttt cggctggcgg ggcgctctgc tcctcctcgg cgcgatcacc 540  
ctccacctca cccctgtgg cgcctgtctg ctacccttg tccttcttg agacccccca 600  
gccccaccgc gtagtccct agctgccctc ggctgagtc tgtcacacg ccgggccttc 660  
tcaatctttg ctctaggcac agccctggtt gggggcgggt acttcgttcc ttacgtcac 720  
ttggctcccc gctttagacc ggggcctggg gggatacga gcagcgttg tggtgccgt 780  
ggctgcgatg ggggatgcgg gcgccggct ggtctgcggg tggctggcag accaaggctg 840  
ggtgccctc ccggcgctgc tggcgtatt cggggctctg actgggctgg ggctgtgggt 900  
ggtggggctg gtgccgttg tggcgggcga agagagctgg gggggtcccc tgctggccgc 960  
ggctgtggcc tatgggctga gcgcggggag ttacgccccg ctggttttcg gtgtactccc 1020  
cgggctggtg ggcgtcggag gtgtggtgca gccacaggg ctggtgatga tgctgatgag 1080  
cctcgggggg ctctgggcc ctccctgtc aggttctta aggga 1125

&lt;210&gt; 45

&lt;211&gt; 1050

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 45

atggcaacta cagcggcgcc ggcggcgcc gcccgaaatg gagctggccc ggaatgggga 60  
gggttcgaag aaaacatcca gggcggaggc tcagctgtga ttgacatgga gaacatggat 120  
gatacctcag gctctagctt cgaggatatg ggtgagctgc atcagcgcct gcgcaggaa 180  
gaagtagacg ctgatgcagc tgatgcagct gctgctgaag aggaggatgg agagttcctg 240  
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tactttgatg tggagcctgc tcaggtgcga agcaggctcc tggagtccat gatccctatc 420

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aagatggtca acttccccca gaaaattgca ggtgaactct atggacctct catgctggtc 480  
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ttcatttact tccttgccca cctgtgcaac gccagatca ccatgctgca gatgttgga 660  
ctgctgggct atggcctctt tgggcattgc attgtcctgt tcacaccta taatatccac 720  
ctccacgccc tcttctacct cttctggctg ttggtgggtg gactgtccac actgcgcatg 780  
gtagcagtgt tgggtgtctg gaccgtgggc ccacacagc ggctgctcct ctgtggcacc 840  
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aaagctgttg cggtgacct gcagtcacac 1050

&lt;210&gt; 46

&lt;211&gt; 2001

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 46

atgtcgtccc agccagcagg gaaccagacc tccccgggg ccacagagga ctactctat 60  
ggcagctggt acatcgatga gcccagggg ggcgaggagc tccagccaga gggggaagtg 120  
cctcctgcc acaccagcat accaccggc ctgtaccacg cctgctggc ctgctgtca 180  
atccttgtgc tgctgctcct ggccatgctg gtgaggcgcc gccagctctg gcctgactgt 240  
gtgcgtggca ggcccggcct gccagccct gtggatttct tggctgggga caggccccgg 300  
gcagtgcctg ctgctgtttt catggtcctc ttgagctccc tgtgtttgct gctccccgac 360  
gaggacgcat tgcccttctt gactctgcc tcagcaccca gccaatgg gaaaactgag 420  
gctccaagag gggcctggaa gatactggga ctgttctatt atgctgcct ctactaccct 480

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ctggctgcct gtgccacggc tggccacaca gctgcacacc tgctcggcag cacgctgtcc 540  
tgggcccacc ttgggggtcca ggtctggcag agggcagagt gtccccaggt gccaagatc 600  
tacaagtact actccctgct ggcctccctg cctctcctgc tgggcctcgg attcctgagc 660  
ctttggtacc ctgtgcagct ggtgagaagc ttcagccgta ggacaggagc aggctccaag 720  
gggctgcaga gcagctactc tgaggaatat ctgaggaacc tcctttgcag gaagaagctg 780  
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cactgcatct acactccaca gccaggattc catctcccgc tgaagctggt gctttcagct 900  
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caccacagc tgaccaaccg gcgagtgtc tatgcagcca ctttcttct cttccccctc 1560  
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gccccccagg acagcctcag accaggggag gaagacgaag ggatgcagct gctacagaca 1860  
aaggactcca tggccaaggg agctaggccc ggggccagcc gcggcagggc tcgctggggt 1920  
ctggcctaca cgctgctgca caaccaacc ctgcaggtct tccgcaagac ggccctgttg 1980

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gggtgccaatg gtgcccagcc c

2001

&lt;210&gt; 47

&lt;211&gt; 1392

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 47

|  |      |
|--|------|
| atgattgtct gcctcctttt catgatgatt ttattggcaa aggaagttca actggtagac  | 60   |
| caaacagatt cacctttact tagtctcctt ggacagacaa gtcactttc atggcatctt   | 120  |
| gtggatattg tgctgtacca gagtgtgcta agttatttca gcagccatta cccgccgtcc  | 180  |
| atcatcctgg caaaagaatc ttatgtctgaa ttaatcatga agctcctaaa agtgtctgcg | 240  |
| ggccttttcta ttctactga cagccagaag catcttgatg cagttccaaa atgccaagct  | 300  |
| tttactcadc agatggttca attcctcagc accctggaac aaaatggaaa aatcacctta  | 360  |
| gcagtcttag aacaggaaat gtctaagctc ttagacgata tcattgtctt taaccgccc   | 420  |
| gacatggaca gccagaccg ccacatggcc ctcagcagcc tctttatgga agtcctgatg   | 480  |
| atgatgaaca acgcgactat tccaacagca gagttccttc ggggcagtat ccggacctgg  | 540  |
| attggccaaa aaatgcatgg gctggtggtg ctgccccttt taacagcagc ctgccagagc  | 600  |
| ctggcgctccg tccgccacat ggctgagact acagaagcct gcactactgc ctacttcaaa | 660  |
| gaaagccctc tcaatcagaa ttcaggatgg ggaccattc tggatatcct tcaggttccc   | 720  |
| gagctcacca tggaagagtt cctgcaggag tgcctcacct tgggcagtta cttgactctt  | 780  |
| tacgtctact tgcttcagtg tttaaacagc gaacagactt taaggaatga aatgaaagtg  | 840  |
| ctgctcatct taagcaagtg gctggaacag gtgtacccaa gctccgtgga ggaagaggca  | 900  |
| aagctgtttt tgtggtggca ccaagtcctt cagctctccc tcattcagac agagcagaat  | 960  |
| gactccgtcc tgacagaatc tgctattcga attctgctct tggttcagag caggcagaac  | 1020 |
| ctcgtggctg aggagagact cagctctggg atcctggggg caattgggtt tggccggaag  | 1080 |



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tcgcctttgt ctaacagggt ccgagtgggt gccgaagca tggctgcctt cctttcagtt 1140  
 caggttccta tggaagatca gatccgtttg aggcctggct ctgaattaca tctgaccccc 1200  
 aaagctcagc aggcctctgaa tgctcttgaa tccatggcat caagtaagca gtatgttgaa 1260  
 taccaggatc aaatattgca agccacccaa tttataaggc atcctggcca ttgccttcaa 1320  
 gatgggaaaa gcttcttggc tcttctcggt aactgtctgt atccagaagt gcattatttg 1380  
 gaccacatac ga 1392

&lt;210&gt; 48

&lt;211&gt; 1410

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 48

atgtctagac tgggagccct ggggtggtgcc cgtgccgggc tgggactggt gctgggtacc 60  
 gccgccggcc ttggattcct gtgcctcctt tacagccagc gatggaaacg gaccacagct 120  
 catggccgca gccagagcct gcccaactcc ctggactata cgcagacttc agatcccga 180  
 cgccacgtga tgctctgcg ggctgtccca ggtggggctg gagatgcctc agtctgccc 240  
 agccttccac gggaaggaca ggagaagggt ctggaccgcc tggactttgt gctgaccagc 300  
 cttgtggcgc tgcggcggga ggtggaggag ctgagaagca gcctgcgagg gcttgcgggg 360  
 gagattgttg gggaggtccg atgccacatg gaagagaacc agagagtggc tcggcggcga 420  
 aggtttccgt ttgtccggga gaggagtgc tccactggct ccagctctgt ctacttcacg 480  
 gcctctcgg gagccacgtt cacagatgct gagagtgaag ggggttacac aacagccaat 540  
 gcggagtctg acaatgagcg ggactctgac aaagaaagtg aggacgggga agatgaagtg 600  
 agctgtgaga ctgtgaagat ggggagaaag gattctcttg acttgaggga agaggcagct 660  
 tcaggtgcct ccagtgcct ggaggttgga ggttcctcag gcttggaggga tgtgtgccc 720  
 ctctgcagc aggccgacga gctgcacagg ggtgatgagc aaggcaagcg ggagggttc 780

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cagctgctgc tcaacaacaa gctggtgtat ggaagccggc aggactttct ctggcgccctg 840  
 gcccgagcct acagtacat gtgtgagctc actgaggagg tgagcgagaa gaagtcatat 900  
 gccctagatg gaaaagaaga agcagaggct gctctggaga agggggatga gagtgtgac 960  
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 cgcattccaga gtggcttttag cttcaaggag catgtggaca aagccattgc tctccagcca 1080  
 gaaaacccca tggctcactt tcttcttggc aggtggtgct atcaggtctc tcacctgagc 1140  
 tggctagaaa aaaaaactgc tacagccttg cttgaaagcc ctctcagtgc cactgtggaa 1200  
 gatgcctcc agagcttcct aaaggctgaa gaactacagc caggattttc caaagcagga 1260  
 agggatatata tttccaagtg ctacagagaa ctagggaaaa actctgaagc tagatggtgg 1320  
 atgaagttgg ccttgagct gccagatgtc acgaaggagg atttggtat ccagaaggac 1380  
 ctggaagaac tggaagtcatt ttacgagac 1410

&lt;210&gt; 49

&lt;211&gt; 729

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 49

atggagcagg gcagcgccg cttggaggac ttccctgtca atgtgttctc cgtcactcct 60  
 tacacacca gcaccgtga catccagggtg tccgatgatg acaaggcggg ggccaccttg 120  
 ctcttctcag gcatctttct gggactggtg gggatcacat tcactgtcat gggctggatc 180  
 aaataccaag gtgtctcca ctttgaatgg acccagctcc ttgggcccggt cctgtgtca 240  
 gttggggtga cattcatcct gattgtgtg tgcaagtcca aaatgtctc ctgccagttg 300  
 tgcaaagaaa gtgaggaaag ggtcccggac tcggaacaga caccaggagg accatcattt 360  
 gttttcactg gcatcaacca acccatcacc ttccatgggg cactgtggt gcagtacatc 420  
 cctcctcctt atggttctcc agagcctatg gggataaata ccagctacct gcagtctgtg 480

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gtgagcccct gggcctcat aacctctgga ggggcagcag ccgcatgtc aagtcctcct 540  
 caatactaca ccatctaccc tcaagataac tctgcatttg tggttgatga gggctgcctt 600  
 tctttcacgg acggtggaaa tcacaggccc aatcctgatg ttgaccagct agaagagaca 660  
 cagctggaag aggaggcctg tgccctgctt tctcctcccc cttatgaaga aatatactct 720  
 ctccctcgc 729

&lt;210&gt; 50

&lt;211&gt; 810

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 50

atggcgggcg ccgaggactg gccgggccag cagctggagc tggacgagga cgaggcgtct 60  
 tgttgccgct ggggcgcgca gcacgccggg gcccgcgagc tggctgcgct ctactcgcca 120  
 ggcaagcgcc tccaggagtg gtgctctgtg atcctgtgct tcagcctcat cgcccacaac 180  
 ctggtccatc tctgtctgct ggcccgttg gaggacacac ccctcgtcat actcggtgtt 240  
 gttgcagggg ctctcattgc tgacttcttg tctggcctgg tacactgggg tgctgacaca 300  
 tggggctctg tggagctgcc cattgtgggg aaggtttca tccgaccctt ccgggagcac 360  
 cacattgacc caacagctat cacacggcac gacttcacg agaccaacgg ggacaactgc 420  
 ctggtgacac tgctgccgct gctaaacatg gcctacaagt tccgcacca cagccctgaa 480  
 gccctggagc agctataccc ctgggagtgc ttcgttctt gcctgatcat ctteggcacc 540  
 ttcaccaacc agatccacaa gtggtcgcac acgtactttg ggctgccacg ctgggtcacc 600  
 ctctgcagg actggcatgt catcctgcc cgtaaacc atcgatcca ccacgtctca 660  
 cccacgaga cctacttctg catcaccaca ggctggetca actaccctct ggagaagata 720  
 ggcttctggc gacgcctgga ggacctcatc cagggcctga cgggcgagaa gcctcgggca 780  
 gatgacatga aatgggcccc gaagatcaaa 810

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&lt;210&gt; 51

&lt;211&gt; 1551

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (98)... (1231)

&lt;400&gt; 51

caaggggaac gtggetttcc ctgcagagcc ggtgtctccg cctgcgtccc tgetgcagca 60

accggagctg gagtcggatc ccgaacgcac cctcgcc atg gac tcg gcc ctc agc 115

Met Asp Ser Ala Leu Ser

1 5

gat ccg cat aac ggc agt gcc gag gca ggc ggc ccc acc aac agc act 163

Asp Pro His Asn Gly Ser Ala Glu Ala Gly Gly Pro Thr Asn Ser Thr

10 15 20

acg cgg ccg cct tcc acg ccc gag ggc atc gcg ctg gcc tac ggc agc 211

Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile Ala Leu Ala Tyr Gly Ser

25 30 35

ctc ctg ctc atg gcg ctg ctg ccc atc ttc ttc ggc gcc ctg cgc tcc 259

Leu Leu Leu Met Ala Leu Leu Pro Ile Phe Phe Gly Ala Leu Arg Ser

40 45 50

gta cgc tgc gcc cgc ggc aag aat gct tca gac atg cct gaa aca atc 307

Val Arg Cys Ala Arg Gly Lys Asn Ala Ser Asp Met Pro Glu Thr Ile

55 60 65 70

100/307

|   |     |
|---|-----|
| acc agc cgg gat gcc gcc cgc ttc ccc atc atc gcc agc tgc aca ctc | 355 |
| Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile Ile Ala Ser Cys Thr Leu |     |
| 75 80 85  |     |
| ttg ggg ctc tac ctc ttt ttc aaa ata ttc tcc cag gag tac atc aac | 403 |
| Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe Ser Gln Glu Tyr Ile Asn |     |
| 90 95 100   |     |
| ctc ctg ctg tcc atg tat ttc ttc gtg ctg gga atc ctg gcc ctg tcc | 451 |
| Leu Leu Leu Ser Met Tyr Phe Phe Val Leu Gly Ile Leu Ala Leu Ser |     |
| 105 110 115   |     |
| cac acc atc agc ccc ttc atg aat aag ttt ttt cca gcc agc ttt cca | 499 |
| His Thr Ile Ser Pro Phe Met Asn Lys Phe Phe Pro Ala Ser Phe Pro |     |
| 120 125 130   |     |
| aat cga cag tac cag ctg ctc ttc aca cag ggt tct ggg gaa aac aag | 547 |
| Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln Gly Ser Gly Glu Asn Lys |     |
| 135 140 145 150   |     |
| gaa gag atc atc aat tat gaa ttt gac acc aag gac ctg gtg tgc ctg | 595 |
| Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr Lys Asp Leu Val Cys Leu |     |
| 155 160 165   |     |
| ggc ctg agc agc atc gtt ggc gtc tgg tac ctg ctg agg aag cac tgg | 643 |
| Gly Leu Ser Ser Ile Val Gly Val Trp Tyr Leu Leu Arg Lys His Trp |     |
| 170 175 180   |     |
| att gcc aac aac ctt ttt ggc ctg gcc ttc tcc ctt aat gga gta gag | 691 |
| Ile Ala Asn Asn Leu Phe Gly Leu Ala Phe Ser Leu Asn Gly Val Glu |     |
| 185 190 195   |     |
| ctc ctg cac ctc aac aat gtc agc act ggc tgc atc ctg ctg ggc gga | 739 |

101/307

Leu Leu His Leu Asn Asn Val Ser Thr Gly Cys Ile Leu Leu Gly Gly  
 200 205 210  
 ctc ttc atc tac gat gtc ttc tgg gta ttt ggc acc aat gtg atg gtg 787  
 Leu Phe Ile Tyr Asp Val Phe Trp Val Phe Gly Thr Asn Val Met Val  
 215 220 225 230  
 aca gtg gcc aag tcc ttc gag gca cca ata aaa ttg gtg ttt ccc cag 835  
 Thr Val Ala Lys Ser Phe Glu Ala Pro Ile Lys Leu Val Phe Pro Gln  
 235 240 245  
 gat ctg ctg gag aaa ggc ctc gaa gca aac aac ttt gcc atg ctg gga 883  
 Asp Leu Leu Glu Lys Gly Leu Glu Ala Asn Asn Phe Ala Met Leu Gly  
 250 255 260  
 ctt gga gat gtc gtc att cca ggg atc ttc att gcc ttg ctg ctg cgc 931  
 Leu Gly Asp Val Val Ile Pro Gly Ile Phe Ile Ala Leu Leu Leu Arg  
 265 270 275  
 ttt gac atc agc ttg aag aag aat acc cac acc tac ttc tac acc agc 979  
 Phe Asp Ile Ser Leu Lys Lys Asn Thr His Thr Tyr Phe Tyr Thr Ser  
 280 285 290  
 ttt gca gcc tac atc ttc ggc ctg ggc ctt acc atc ttc atc atg cac 1027  
 Phe Ala Ala Tyr Ile Phe Gly Leu Gly Leu Thr Ile Phe Ile Met His  
 295 300 305 310  
 atc ttc aag cat gct cag cct gcc ctc cta tac ctg gtc ccc gcc tgc 1075  
 Ile Phe Lys His Ala Gln Pro Ala Leu Leu Tyr Leu Val Pro Ala Cys  
 315 320 325  
 atc ggt ttt cct gtc ctg gtg gcg ctg gcc aag gga gaa gtg aca gag 1123  
 Ile Gly Phe Pro Val Leu Val Ala Leu Ala Lys Gly Glu Val Thr Glu

102/307

|   |     |     |      |
|---|-----|-----|------|
| 330   | 335 | 340 |      |
| atg ttc agt tat gag gag tca aat cct aag gat cca gcg gca gtg aca   |     |     | 1171 |
| Met Phe Ser Tyr Glu Glu Ser Asn Pro Lys Asp Pro Ala Ala Val Thr   |     |     |      |
| 345   | 350 | 355 |      |
| gaa tcc aaa gag gga aca gag gca tca gca tcg aag ggg ctg gag aag   |     |     | 1219 |
| Glu Ser Lys Glu Gly Thr Glu Ala Ser Ala Ser Lys Gly Leu Glu Lys   |     |     |      |
| 360   | 365 | 370 |      |
| aaa gag aaa tg atgcagctgg tgcccgagcc tctcagggcc agaccagaca        |     |     | 1270 |
| Lys Glu Lys   |     |     |      |
| 375   |     |     |      |
| gatgggggct gggcccacac aggcgtgcac cggtagaggg cacaggaggc caagggcagc |     |     | 1330 |
| tccaggacag ggcagggggc agcaggatac ctccagccag gcctctgtgg cctctgtttc |     |     | 1390 |
| cttctccctt tcttgccct cctctgctcc tccccacacc ctgcaggcaa aagaaacccc  |     |     | 1450 |
| cagcttcccc cctccccggg agccaggtgg gaaaagtggg tgtgattttt agattttgta |     |     | 1510 |
| ttgtggactg attttgctc acattaataaa ctcacccat g                      |     |     | 1551 |

&lt;210&gt; 52

&lt;211&gt; 1713

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (89)... (334)

&lt;400&gt; 52

|  |    |
|--|----|
| tctcagcgcg ctgcccggct ggggacccgc gcacctgcag cgcccgtgc tcggccctgc | 60 |
|--|----|

103/307

atcctgcctg ggcatacctgc gcccggcc atg acg gcg cac tca ttc gcc ctc 112

Met Thr Ala His Ser Phe Ala Leu

1

5

ccg gtc atc atc ttc acc acg ttc tgg ggc ctc gtc ggc atc gcc ggg 160

Pro Val Ile Ile Phe Thr Thr Phe Trp Gly Leu Val Gly Ile Ala Gly

10

15

20

ccc tgg ttc gtg ccg aag gga ccc aac cgc gga gtg atc atc acc atg 208

Pro Trp Phe Val Pro Lys Gly Pro Asn Arg Gly Val Ile Ile Thr Met

25

30

35

40

ctg gtc gcc acc gcc gtc tgc tgt tac ctc ttc tgg ctc atc gcc atc 256

Leu Val Ala Thr Ala Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile

45

50

55

ctg gcg cag ctg aac ccc ctg ttc ggg ccc cag ctg aag aat gag acc 304

Leu Ala Gln Leu Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr

60

65

70

atc tgg tac gtg cgc ttc ctg tgg gag tgacccgcc gcccccgacc 350

Ile Trp Tyr Val Arg Phe Leu Trp Glu

75

80

caggtgccca gctctcgga tgactgtggc tccactgtcc ctgacaaccc cttegtccgg 410

accctcccc acacaactat gtctggtcac cagctccctc ctgctggcac ccagagaccc 470

ggacccgcag ggctgcctg gttcctggaa gtcttccag tcttccagc cagcccgggc 530

cctggggagc cctgggcaca gcagcgccg aggggatgtc ctgctccaat accgcactg 590

ctctggagtt tgccctcttt cccaaggaga tgctgctggg gagctggtat ggggtggggtc 650

tttcccttta cagacggggc agatgccagg actcagccca tcctgaggag gacacgtgtc 710

ctcatggaga ggggtgtccg gcccaggcgg gggagtcagt gccagtcag cagctctgcc 770



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accatcctgc tgggaactgg gggggcctct attgggttat aggcaaggcc ttttctctgg 830  
catggaattg ttaattttct gacacgtcta gatgtgaaat ttctgaaaat gttgaagcag 890  
agaaacattc acacacaaaa agcaacatag tcatgtgggt ccagatggcc tcagtcctag 950  
atgttggcac ctttgetgt gtctectcag agtatectgt tccgcctcct gccacctgga 1010  
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tgggacgggc cagccctgct cctgagccag ccccgccctc tgccccctgg ccctgggctc 1250  
tgtgctaggg atggtgaaga atgggggcgt gccagcctgg caggagtggg aagcaacacg 1310  
caggggtccc ggacctctcc agccttgccc tcacgcttac ccgagctccc agtgtgttta 1370  
gcacagagct caccacactt gcctggctcc cagctggggc ctgtctcac tgggtgtcca 1430  
ggggaagaaa cgacagcctc acttctgtat ggactgctga tgtggcctgc catcctgttc 1490  
agcgggcatt gtctttggag cagcaggaga ataggatgcc tctcactcac atgccagttc 1550  
ctggctggcc agctgctcag ggctcaggt ggggcctccc attgacatcc tccccctaca 1610  
ctccctctct gagcctccgt cggccctcct gttgggtaag ggtgttgagt gtgacttgtg 1670  
ctgaaaacct ggttcatata taataaataa tggatgatgaa aag 1713

&lt;210&gt; 53

&lt;211&gt; 1758

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (190)... (1653)

&lt;400&gt; 53

105/307

tttctagggt tggaccgtgc aggcacgggc ggtcagctgg gccgcagctc ctccggctct 60  
gcagggtcac ggaggaagcc agtccccta gtccaggccg agcttgcaact tgcgtcttgt 120  
ctgctgctgc tgaaccaaga tttagctgtg cgcctcctt gcagtctcct ggaaccagca 180  
ggaggaaac atg ggg gat act ggc ctg aga aag cgg aga gag gat gag 228

Met Gly Asp Thr Gly Leu Arg Lys Arg Arg Glu Asp Glu

1 5 10

aag tcg atc cag agc caa gag cct aag acc acc agt ctc caa aag gag 276  
Lys Ser Ile Gln Ser Gln Glu Pro Lys Thr Thr Ser Leu Gln Lys Glu

15 20 25

ctg ggc ctc atc agt ggc atc tcc atc atc gtg ggc acc atc att ggc 324  
Leu Gly Leu Ile Ser Gly Ile Ser Ile Ile Val Gly Thr Ile Ile Gly

30 35 40 45

tct ggg atc ttc gtt tcc ccc aag tct gtg ctc agc aac acg gaa gct 372  
Ser Gly Ile Phe Val Ser Pro Lys Ser Val Leu Ser Asn Thr Glu Ala

50 55 60

gtg ggg ccc tgc ctc atc ata tgg gcg gct tgc ggg gtc ctc gcg acg 420  
Val Gly Pro Cys Leu Ile Ile Trp Ala Ala Cys Gly Val Leu Ala Thr

65 70 75

ctg ggt gcc ctg tgc ttt gcg gag ctt ggc aca atg atc acc aag tca 468  
Leu Gly Ala Leu Cys Phe Ala Glu Leu Gly Thr Met Ile Thr Lys Ser

80 85 90

ggg gga gag tat ccc tac ctg atg gag gcc tac ggg ccc atc ccc gcc 516  
Gly Gly Glu Tyr Pro Tyr Leu Met Glu Ala Tyr Gly Pro Ile Pro Ala

95 100 105

tac ctc ttc tcc tgg gcc agc ctg atc gtc att aag ccc acg tcc ttc 564

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Tyr Leu Phe Ser Trp Ala Ser Leu Ile Val Ile Lys Pro Thr Ser Phe  
 110 115 120 125  
 gcc atc atc tgc ctc agc ttc tcc gag tat gtg tgt gcg ccc ttc tat 612  
 Ala Ile Ile Cys Leu Ser Phe Ser Glu Tyr Val Cys Ala Pro Phe Tyr  
 130 135 140  
 gtg ggc tgc aag cct cct caa atc gtt gtg aaa tgc ctg gcc gcc gcc 660  
 Val Gly Cys Lys Pro Pro Gln Ile Val Val Lys Cys Leu Ala Ala Ala  
 145 150 155  
 gcc atc ttg ttc atc tcg aca gtg aac tca ctg agc gtg cgg ctg gga 708  
 Ala Ile Leu Phe Ile Ser Thr Val Asn Ser Leu Ser Val Arg Leu Gly  
 160 165 170  
 agc tac gtc cag aac atc ttc acc gcg gcc aag ctg gtg atc gtg gcc 756  
 Ser Tyr Val Gln Asn Ile Phe Thr Ala Ala Lys Leu Val Ile Val Ala  
 175 180 185  
 atc atc atc atc agc ggg ctg gtg ctc ctg gcc caa gga aac aca aag 804  
 Ile Ile Ile Ile Ser Gly Leu Val Leu Leu Ala Gln Gly Asn Thr Lys  
 190 195 200 205  
 aat ttt gat aat tct ttc gag ggc gcc cag ctg tct gtg gga gcc atc 852  
 Asn Phe Asp Asn Ser Phe Glu Gly Ala Gln Leu Ser Val Gly Ala Ile  
 210 215 220  
 agc ctg gcg ttt tac aat gga ctc tgg gcc tat gat gga tgg aat caa 900  
 Ser Leu Ala Phe Tyr Asn Gly Leu Trp Ala Tyr Asp Gly Trp Asn Gln  
 225 230 235  
 ctc aat tac atc aca gaa gaa ctt aga aac cct tac aga aac ctg cct 948  
 Leu Asn Tyr Ile Thr Glu Glu Leu Arg Asn Pro Tyr Arg Asn Leu Pro

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|  |     |     |      |
|--|-----|-----|------|
| 240  | 245 | 250 |      |
| ttg gcc att atc atc ggg atc ccc ctg gtg acg gcg tgc tac atc ctc  |     |     | 996  |
| Leu Ala Ile Ile Ile Gly Ile Pro Leu Val Thr Ala Cys Tyr Ile Leu  |     |     |      |
| 255  | 260 | 265 |      |
| atg aac gtg tcc tac ttc acc gtg atg act gcc acc gaa ctc ctg cag  |     |     | 1044 |
| Met Asn Val Ser Tyr Phe Thr Val Met Thr Ala Thr Glu Leu Leu Gln  |     |     |      |
| 270  | 275 | 280 | 285  |
| tcc cag gcg gtg gct gtg aca ttt ggt gac cgt gtt ctc tat cct gct  |     |     | 1092 |
| Ser Gln Ala Val Ala Val Thr Phe Gly Asp Arg Val Leu Tyr Pro Ala  |     |     |      |
| 290  | 295 | 300 |      |
| tct tgg atc gtt cca ctt ttt gtg gca ttt tca acc atc ggt gct gct  |     |     | 1140 |
| Ser Trp Ile Val Pro Leu Phe Val Ala Phe Ser Thr Ile Gly Ala Ala  |     |     |      |
| 305  | 310 | 315 |      |
| aac ggg acc tgc ttc aca gcg ggc aga ctc att tac gtg gcg ggc cgg  |     |     | 1188 |
| Asn Gly Thr Cys Phe Thr Ala Gly Arg Leu Ile Tyr Val Ala Gly Arg  |     |     |      |
| 320  | 325 | 330 |      |
| gag ggt cac atg ctc aaa. gtg ctt tct tac atc agc gtc agg cgc ctc |     |     | 1236 |
| Glu Gly His Met Leu Lys Val Leu Ser Tyr Ile Ser Val Arg Arg Leu  |     |     |      |
| 335  | 340 | 345 |      |
| act cca gcc ccc gcc atc atc ttt tat ggt atc ata gca acg att tat  |     |     | 1284 |
| Thr Pro Ala Pro Ala Ile Ile Phe Tyr Gly Ile Ile Ala Thr Ile Tyr  |     |     |      |
| 350  | 355 | 360 | 365  |
| atc atc cct ggt gac ata aac tcg tta gtc aat tat ttc agc ttt gcc  |     |     | 1332 |
| Ile Ile Pro Gly Asp Ile Asn Ser Leu Val Asn Tyr Phe Ser Phe Ala  |     |     |      |
| 370  | 375 | 380 |      |

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gca tgg ctg ttt tat ggc ctg acg att cta gga ctc atc gtg atg aga 1380  
 Ala Trp Leu Phe Tyr Gly Leu Thr Ile Leu Gly Leu Ile Val Met Arg  
 385 390 395  
 ttt aca agg aaa gag ctg gaa agg cct atc aag gtg ccc gta gtc att 1428  
 Phe Thr Arg Lys Glu Leu Glu Arg Pro Ile Lys Val Pro Val Val Ile  
 400 405 410  
 ccc gtc ttg atg aca ctc atc tct gtg ttt ttg gtt ctg gct cca atc 1476  
 Pro Val Leu Met Thr Leu Ile Ser Val Phe Leu Val Leu Ala Pro Ile  
 415 420 425  
 atc agc aag ccc acc tgg gag tac ctc tac tgt gtg ctg ttt ata tta 1524  
 Ile Ser Lys Pro Thr Trp Glu Tyr Leu Tyr Cys Val Leu Phe Ile Leu  
 430 435 440 445  
 agc ggc ctt tta ttt tac ttc ctg ttt gtc cac tac aag ttt gga tgg 1572  
 Ser Gly Leu Leu Phe Tyr Phe Leu Phe Val His Tyr Lys Phe Gly Trp  
 450 455 460  
 gct cag aaa atc tca aag ccg att acc atg cac ctt cag atg cta atg 1620  
 Ala Gln Lys Ile Ser Lys Pro Ile Thr Met His Leu Gln Met Leu Met  
 465 470 475  
 gaa gtg gtc cca ccg gag gaa gac cct gag taacaagctc cgtctcttgt 1670  
 Glu Val Val Pro Pro Glu Glu Asp Pro Glu  
 480 485  
 agccaagtca gctgaattta ttttcttaag caatatttgt gggtatttct tccttttttt 1730  
 cttacgaata aaatatactc agatgttt 1758

109/307

&lt;211&gt; 1550

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (154)... (1281)

&lt;400&gt; 54

ctctgtttac cgagagagcc cgtccaagtt gggctccatc gctgccctcg ctccccttcg 60

gggcctccgc ccgcctggga agcagagaga aagccgggcc cagcccttcc tcacccttcc 120

cctccccgca ccgccggag aggtcggacg gcg atg acc ccc cag ccc gcc gga 174

Met Thr Pro Gln Pro Ala Gly

1

5

ccc ccg gat ggg ggc tgg ggc tgg gtg gtg gcg gcc gca gcc ttc gcg 222

Pro Pro Asp Gly Gly Trp Gly Trp Val Val Ala Ala Ala Ala Phe Ala

10

15

20

ata aac ggg ctg tcc tac ggg ctg ctg cgc tcg ctg ggc ctt gcc ttc 270

Ile Asn Gly Leu Ser Tyr Gly Leu Leu Arg Ser Leu Gly Leu Ala Phe

25

30

35

cct gac ctt gcc gag cac ttt gac cga agc gcc cag gac act gcg tgg 318

Pro Asp Leu Ala Glu His Phe Asp Arg Ser Ala Gln Asp Thr Ala Trp

40

45

50

55

atc agc gcc ctg gcc ctg gcc gtg cag cag gca gcc agc ccc gtg ggc 366

Ile Ser Ala Leu Ala Leu Ala Val Gln Gln Ala Ala Ser Pro Val Gly

60

65

70

agc gcc ctg agc acg cgc tgg ggg gcc cgc ccc gtg gtg atg gtt ggg 414

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Ser Ala Leu Ser Thr Arg Trp Gly Ala Arg Pro Val Val Met Val Gly  
 75 80 85  
 ggc gtc ctc gcc tcg ctg ggc ttc gtc ttc tcg gct ttc gcc agc ggt 462  
 Gly Val Leu Ala Ser Leu Gly Phe Val Phe Ser Ala Phe Ala Ser Gly  
 90 95 100  
 ctg ctg cat ctc tac ctc ggc ctg ggc ctc ctc gct ggc ttt ggt tgg 510  
 Leu Leu His Leu Tyr Leu Gly Leu Gly Leu Leu Ala Gly Phe Gly Trp  
 105 110 115  
 gcc ctg gtg ttc gcc ccc gcc cta ggc acc ctc tcg cgt tac ttc tcc 558  
 Ala Leu Val Phe Ala Pro Ala Leu Gly Thr Leu Ser Arg Tyr Phe Ser  
 120 125 130 135  
 cgc cgt cga gtc ttg gcg gtg ggg ctg gcg ctc acc ggc aac ggg gcc 606  
 Arg Arg Arg Val Leu Ala Val Gly Leu Ala Leu Thr Gly Asn Gly Ala  
 140 145 150  
 tcc tcg ctg ctc ctg gcg ccc gcc ttg cag ctt ctc ctc gat act ttc 654  
 Ser Ser Leu Leu Leu Ala Pro Ala Leu Gln Leu Leu Leu Asp Thr Phe  
 155 160 165  
 ggc tgg cgg ggc gct ctg ctc ctc ctc ggc gcg atc acc ctc cac ctc 702  
 Gly Trp Arg Gly Ala Leu Leu Leu Leu Gly Ala Ile Thr Leu His Leu  
 170 175 180  
 acc ccc tgt ggc gcc ctg ctg cta ccc ctg gtc ctt cct gga gac ccc 750  
 Thr Pro Cys Gly Ala Leu Leu Leu Pro Leu Val Leu Pro Gly Asp Pro  
 185 190 195  
 cca gcc cca ccg cgt agt ccc cta gct gcc ctc ggc ctg agt ctg ttc 798  
 Pro Ala Pro Pro Arg Ser Pro Leu Ala Ala Leu Gly Leu Ser Leu Phe

111/307

|   |     |     |     |      |
|---|-----|-----|-----|------|
| 200   | 205 | 210 | 215 |      |
| aca cgc cgg gcc ttc tca atc ttt gct cta ggc aca gcc ctg gtt ggg |     |     |     | 846  |
| Thr Arg Arg Ala Phe Ser Ile Phe Ala Leu Gly Thr Ala Leu Val Gly |     |     |     |      |
|   | 220 | 225 | 230 |      |
| ggc ggg tac ttc gtt cct tac gtg cac ttg gct ccc cgc ttt aga ccg |     |     |     | 894  |
| Gly Gly Tyr Phe Val Pro Tyr Val His Leu Ala Pro Arg Phe Arg Pro |     |     |     |      |
|   | 235 | 240 | 245 |      |
| ggg cct ggg ggg ata cgg agc agc gct ggt ggt ggc cgt ggc tgc gat |     |     |     | 942  |
| Gly Pro Gly Gly Ile Arg Ser Ser Ala Gly Gly Gly Arg Gly Cys Asp |     |     |     |      |
|   | 250 | 255 | 260 |      |
| ggg gga tgc ggg cgc ccg gct ggt ctg cgg gtg gct ggc aga cca agg |     |     |     | 990  |
| Gly Gly Cys Gly Arg Pro Ala Gly Leu Arg Val Ala Gly Arg Pro Arg |     |     |     |      |
|   | 265 | 270 | 275 |      |
| ctg ggt gcc cct ccc gcg gct gct ggc cgt att cgg ggc tct gac tgg |     |     |     | 1038 |
| Leu Gly Ala Pro Pro Ala Ala Ala Gly Arg Ile Arg Gly Ser Asp Trp |     |     |     |      |
| 280   | 285 | 290 | 295 |      |
| gct ggg gct gtg ggt ggt ggg gct ggt gcc cgt ggt ggg cgg cga aga |     |     |     | 1086 |
| Ala Gly Ala Val Gly Gly Gly Ala Gly Ala Arg Gly Gly Arg Arg Arg |     |     |     |      |
|   | 300 | 305 | 310 |      |
| gag ctg ggg ggg tcc cct gct ggc cgc ggc tgt ggc cta tgg gct gag |     |     |     | 1134 |
| Glu Leu Gly Gly Ser Pro Ala Gly Arg Gly Cys Gly Leu Trp Ala Glu |     |     |     |      |
|   | 315 | 320 | 325 |      |
| cgc ggg gag tta cgc ccc gct ggt ttt cgg tgt act ccc cgg gct ggt |     |     |     | 1182 |
| Arg Gly Glu Leu Arg Pro Ala Gly Phe Arg Cys Thr Pro Arg Ala Gly |     |     |     |      |
|   | 330 | 335 | 340 |      |



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ggg cgt cgg agg tgt ggt gca ggc cac agg gct ggt gat gat gct gat 1230

Gly Arg Arg Arg Cys Gly Ala Gly His Arg Ala Gly Asp Asp Ala Asp

345

350

355

gag cct cgg ggg gct cct ggg ccc tcc cct gtc agg ctt cct aag gga 1278

Glu Pro Arg Gly Ala Pro Gly Pro Ser Pro Val Arg Leu Pro Lys Gly

360

365

370

375

tg agacaggaga cttcacgccc tctttcctcc tgtctggttc ttgatcctc 1330

tccggcagct tcactacat aggggtgccc agggcgctgc cctcctgtgg tccagcctcc 1390

cctccagcca cgctccccc agagacgggg gagctgcttc ccgtcccca ggcagtcttg 1450

ctgtccccag gaggcctgg ctccactctg gacaccactt gttgattatt ttcttgttg 1510

agccccctccc ccaataaaga atttttatcg ggttttcctg 1550

<210> 55

<211> 1485

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (101)... (1153)

<400> 55

ctctcctcga ccctggacgt ctaccttcg gagggccaca tcttgccac tccgcgcgcg 60

gggctagcgc gggtttcagc gacgggagcc ctcaaggac atg gca act aca gcg 115

Met Ala Thr Thr Ala

1

5

gcg ccg gcg ggc ggc gcc cga aat gga gct ggc ccg gaa tgg gga ggg 163

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|   |     |
|---|-----|
| Ala Pro Ala Gly Gly Ala Arg Asn Gly Ala Gly Pro Glu Trp Gly Gly |     |
| 10 15 20  |     |
| ttc gaa gaa aac atc cag ggc gga ggc tca gct gtg att gac atg gag | 211 |
| Phe Glu Glu Asn Ile Gln Gly Gly Gly Ser Ala Val Ile Asp Met Glu |     |
| 25 30 35  |     |
| aac atg gat gat acc tca ggc tct agc ttc gag gat atg ggt gag ctg | 259 |
| Asn Met Asp Asp Thr Ser Gly Ser Ser Phe Glu Asp Met Gly Glu Leu |     |
| 40 45 50  |     |
| cat cag cgc ctg cgc gag gaa gaa gta gac gct gat gca gct gat gca | 307 |
| His Gln Arg Leu Arg Glu Glu Glu Val Asp Ala Asp Ala Ala Asp Ala |     |
| 55 60 65  |     |
| gct gct gct gaa gag gag gat gga gag ttc ctg ggc atg aag ggc ttt | 355 |
| Ala Ala Ala Glu Glu Glu Asp Gly Glu Phe Leu Gly Met Lys Gly Phe |     |
| 70 75 80 85   |     |
| aag gga cag ctg agc cgg cag gtg gca gat cag atg tgg cag gct ggg | 403 |
| Lys Gly Gln Leu Ser Arg Gln Val Ala Asp Gln Met Trp Gln Ala Gly |     |
| 90 95 100   |     |
| aaa aga caa gcc tcc agg gcc ttc agc ttg tac gcc aac atc gac atc | 451 |
| Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr Ala Asn Ile Asp Ile |     |
| 105 110 115   |     |
| ctc aga ccc tac ttt gat gtg gag cct gct cag gtg cga agc agg ctc | 499 |
| Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln Val Arg Ser Arg Leu |     |
| 120 125 130   |     |
| ctg gag tcc atg atc cct atc aag atg gtc aac ttc ccc cag aaa att | 547 |
| Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn Phe Pro Gln Lys Ile |     |

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|   |     |     |     |
|---|-----|-----|-----|
| 135   | 140 | 145 |     |
| gca ggt gaa ctc tat gga cct ctc atg ctg gtc ttc act ctg gtt gct |     |     | 595 |
| Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val Phe Thr Leu Val Ala |     |     |     |
| 150   | 155 | 160 | 165 |
| atc cta ctc cat ggg atg aag acg tct gac act att atc cgg gag ggc |     |     | 643 |
| Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr Ile Ile Arg Glu Gly |     |     |     |
|   | 170 | 175 | 180 |
| acc ctg atg ggc aca gcc att ggc acc tgc ttc ggc tac tgg ctg gga |     |     | 691 |
| Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe Gly Tyr Trp Leu Gly |     |     |     |
|   | 185 | 190 | 195 |
| gtc tca tcc ttc att tac ttc ctt gcc tac ctg tgc aac gcc cag atc |     |     | 739 |
| Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu Cys Asn Ala Gln Ile |     |     |     |
| 200   | 205 | 210 |     |
| acc atg ctg cag atg ttg gca ctg ctg ggc tat ggc ctc ttt ggg cat |     |     | 787 |
| Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr Gly Leu Phe Gly His |     |     |     |
| 215   | 220 | 225 |     |
| tgc att gtc ctg ttc atc acc tat aat atc cac ctc cac gcc ctc ttc |     |     | 835 |
| Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His Leu His Ala Leu Phe |     |     |     |
| 230   | 235 | 240 | 245 |
| tac ctc ttc tgg ctg ttg gtg ggt gga ctg tcc aca ctg cgc atg gta |     |     | 883 |
| Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser Thr Leu Arg Met Val |     |     |     |
|   | 250 | 255 | 260 |
| gca gtg ttg gtg tct cgg acc gtg ggc ccc aca cag cgg ctg ctc ctc |     |     | 931 |
| Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr Gln Arg Leu Leu Leu |     |     |     |
| 265   | 270 | 275 |     |

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|   |      |
|---|------|
| tgt ggc acc ctg gct gcc cta cac atg ctc ttc ctg ctc tat ctg cat     | 979  |
| Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe Leu Leu Tyr Leu His     |      |
| 280 285 290   |      |
| ttt gcc tac cac aaa gtg gta gag ggg atc ctg gac aca ctg gag ggc     | 1027 |
| Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu Asp Thr Leu Glu Gly     |      |
| 295 300 305   |      |
| ccc aac atc ccg ccc atc cag agg gtc ccc aga gac atc cct gcc atg     | 1075 |
| Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg Asp Ile Pro Ala Met     |      |
| 310 315 320 325   |      |
| ctc cct gct gct cgg ctt ccc acc acc gtc ctc aac gcc aca gcc aaa     | 1123 |
| Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu Asn Ala Thr Ala Lys     |      |
| 330 335 340   |      |
| gct gtt gcg gtg acc ctg cag tca cac tgacccacc tgaaattctt            | 1170 |
| Ala Val Ala Val Thr Leu Gln Ser His                                 |      |
| 345 350   |      |
| ggccagtccct ctttcccgca gctgcagaga ggaggaagac tattaaagga cagtccctgat | 1230 |
| gacatgtttc gtagatgggg ttgacagctg ccactgagct gtagctgcgt aagtacctcc   | 1290 |
| ttgatgcctg tcggcacttc tgaaaggcac aaggccaaga actcctggcc aggactgcaa   | 1350 |
| ggctctgcag ccaatgcaga aaatgggtca gctcctttga gaaccctcc ccacctaccc    | 1410 |
| cttccttccct ctttatctct cccacattgt cttgctaaat atagacttgg taattaaaat  | 1470 |
| gttgattgaa gtctg  | 1485 |

&lt;210&gt; 56

&lt;211&gt; 2694

&lt;212&gt; DNA

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&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (80)... (2083)

&lt;400&gt; 56

gtagactctg cggatcccga gaccagcgcc actcatcctg cagcactggg gacagacaga 60

gcaggagaag ggccagaga atg tcg tcc cag cca gca ggg aac cag acc tcc 112

Met Ser Ser Gln Pro Ala Gly Asn Gln Thr Ser

1 5 10

ccc ggg gcc aca gag gac tac tcc tat ggc agc tgg tac atc gat gag 160

Pro Gly Ala Thr Glu Asp Tyr Ser Tyr Gly Ser Trp Tyr Ile Asp Glu

15 20 25

ccc cag ggg ggc gag gag ctc cag cca gag ggg gaa gtg ccc tcc tgc 208

Pro Gln Gly Gly Glu Glu Leu Gln Pro Glu Gly Glu Val Pro Ser Cys

30 35 40

cac acc agc ata cca ccc ggc ctg tac cac gcc tgc ctg gcc tcg ctg 256

His Thr Ser Ile Pro Pro Gly Leu Tyr His Ala Cys Leu Ala Ser Leu

45 50 55

tca atc ctt gtg ctg ctg ctc ctg gcc atg ctg gtg agg cgc cgc cag 304

Ser Ile Leu Val Leu Leu Leu Leu Ala Met Leu Val Arg Arg Arg Gln

60 65 70 75

ctc tgg cct gac tgt gtg cgt ggc agg ccc ggc ctg ccc agc cct gtg 352

Leu Trp Pro Asp Cys Val Arg Gly Arg Pro Gly Leu Pro Ser Pro Val

80 85 90

gat ttc ttg gct ggg gac agg ccc cgg gca gtg cct gct gct gtt ttc 400

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Asp Phe Leu Ala Gly Asp Arg Pro Arg Ala Val Pro Ala Ala Val Phe  
 95 100 105  
 atg gtc ctc ttg agc tcc ctg tgt ttg ctg ctc ccc gac gag gac gca 448  
 Met Val Leu Leu Ser Ser Leu Cys Leu Leu Leu Pro Asp Glu Asp Ala  
 110 115 120  
 ttg ccc ttc ctg act ctc gcc tca gca ccc agc caa gat ggg aaa act 496  
 Leu Pro Phe Leu Thr Leu Ala Ser Ala Pro Ser Gln Asp Gly Lys Thr  
 125 130 135  
 gag gct cca aga ggg gcc tgg aag ata ctg gga ctg ttc tat tat gct 544  
 Glu Ala Pro Arg Gly Ala Trp Lys Ile Leu Gly Leu Phe Tyr Tyr Ala  
 140 145 150 155  
 gcc ctc tac tac cct ctg gct gcc tgt gcc acg gct ggc cac aca gct 592  
 Ala Leu Tyr Tyr Pro Leu Ala Ala Cys Ala Thr Ala Gly His Thr Ala  
 160 165 170  
 gca cac ctg ctc ggc agc acg ctg tcc tgg gcc cac ctt ggg gtc cag 640  
 Ala His Leu Leu Gly Ser Thr Leu Ser Trp Ala His Leu Gly Val Gln  
 175 180 185  
 gtc tgg cag agg gca gag tgt ccc cag gtg ccc aag atc tac aag tac 688  
 Val Trp Gln Arg Ala Glu Cys Pro Gln Val Pro Lys Ile Tyr Lys Tyr  
 190 195 200  
 tac tcc ctg ctg gcc tcc ctg cct ctc ctg ctg ggc ctc gga ttc ctg 736  
 Tyr Ser Leu Leu Ala Ser Leu Pro Leu Leu Leu Gly Leu Gly Phe Leu  
 205 210 215  
 agc ctt tgg tac cct gtg cag ctg gtg aga agc ttc agc cgt agg aca 784  
 Ser Leu Trp Tyr Pro Val Gln Leu Val Arg Ser Phe Ser Arg Arg Thr

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|   |     |     |     |      |
|---|-----|-----|-----|------|
| 220   | 225 | 230 | 235 |      |
| gga gca ggc tcc aag ggg ctg cag agc agc tac tct gag gaa tat ctg |     |     |     | 832  |
| Gly Ala Gly Ser Lys Gly Leu Gln Ser Ser Tyr Ser Glu Glu Tyr Leu |     |     |     |      |
|   | 240 | 245 | 250 |      |
| agg aac ctc ctt tgc agg aag aag ctg gga agc agc tac cac acc tcc |     |     |     | 880  |
| Arg Asn Leu Leu Cys Arg Lys Lys Leu Gly Ser Ser Tyr His Thr Ser |     |     |     |      |
|   | 255 | 260 | 265 |      |
| aag cat ggc ttc ctg tcc tgg gcc cgc gtc tgc ttg aga cac tgc atc |     |     |     | 928  |
| Lys His Gly Phe Leu Ser Trp Ala Arg Val Cys Leu Arg His Cys Ile |     |     |     |      |
|   | 270 | 275 | 280 |      |
| tac act cca cag cca gga ttc cat ctc ccg ctg aag ctg gtg ctt tca |     |     |     | 976  |
| Tyr Thr Pro Gln Pro Gly Phe His Leu Pro Leu Lys Leu Val Leu Ser |     |     |     |      |
|   | 285 | 290 | 295 |      |
| gct aca ctg aca ggg acg gcc att tac cag gtg gcc ctg ctg ctg ctg |     |     |     | 1024 |
| Ala Thr Leu Thr Gly Thr Ala Ile Tyr Gln Val Ala Leu Leu Leu Leu |     |     |     |      |
| 300   | 305 | 310 | 315 |      |
| gtg ggc gtg gta ccc act atc cag aag gtg agg gca ggg gtc acc acg |     |     |     | 1072 |
| Val Gly Val Val Pro Thr Ile Gln Lys Val Arg Ala Gly Val Thr Thr |     |     |     |      |
|   | 320 | 325 | 330 |      |
| gat gtc tcc tac ctg ctg gcc ggc ttt gga atc gtg ctc tcc gag gac |     |     |     | 1120 |
| Asp Val Ser Tyr Leu Leu Ala Gly Phe Gly Ile Val Leu Ser Glu Asp |     |     |     |      |
|   | 335 | 340 | 345 |      |
| aag cag gag gtg gtg gag ctg gtg aag cac cat ctg tgg gct ctg gaa |     |     |     | 1168 |
| Lys Gln Glu Val Val Glu Leu Val Lys His His Leu Trp Ala Leu Glu |     |     |     |      |
| 350   | 355 | 360 |     |      |

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gtg tgc tac atc tca gcc ttg gtc ttg tcc tgc tta ctc acc ttc ctg 1216

Val Cys Tyr Ile Ser Ala Leu Val Leu Ser Cys Leu Leu Thr Phe Leu

365

370

375

gtc ctg atg cgc tca ctg gtg aca cac agg acc aac ctt cga gct ctg 1264

Val Leu Met Arg Ser Leu Val Thr His Arg Thr Asn Leu Arg Ala Leu

380

385

390

395

cac cga gga gct gcc ctg gac ttg agt ccc ttg cat cgg agt ccc cat 1312

His Arg Gly Ala Ala Leu Asp Leu Ser Pro Leu His Arg Ser Pro His

400

405

410

ccc tcc cgc caa gcc ata ttc tgt tgg atg agc ttc agt gcc tac cag 1360

Pro Ser Arg Gln Ala Ile Phe Cys Trp Met Ser Phe Ser Ala Tyr Gln

415

420

425

aca gcc ttt atc tgc ctt ggg ctc ctg gtg cag cag atc atc ttc ttc 1408

Thr Ala Phe Ile Cys Leu Gly Leu Leu Val Gln Gln Ile Ile Phe Phe

430

435

440

ctg gga acc acg gcc ctg gcc ttc ctg gtg ctc atg cct gtg ctc cat 1456

Leu Gly Thr Thr Ala Leu Ala Phe Leu Val Leu Met Pro Val Leu His

445

450

455

ggc agg aac ctc ctg ctc ttc cgt tcc ctg gag tcc tcg tgg ccc ttc 1504

Gly Arg Asn Leu Leu Leu Phe Arg Ser Leu Glu Ser Ser Trp Pro Phe

460

465

470

475

tgg ctg act ttg gcc ctg gct gtg atc ctg cag aac atg gca gcc cat 1552

Trp Leu Thr Leu Ala Leu Ala Val Ile Leu Gln Asn Met Ala Ala His

480

485

490

tgg gtc ttc ctg gag act cat gat gga cac cca cag ctg acc aac cgg 1600



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|   |      |
|---|------|
| Trp Val Phe Leu Glu Thr His Asp Gly His Pro Gln Leu Thr Asn Arg |      |
| 495 500 505   |      |
| cga gtg ctc tat gca gcc acc ttt ctt ctc ttc ccc ctc aat gtg ctg | 1648 |
| Arg Val Leu Tyr Ala Ala Thr Phe Leu Leu Phe Pro Leu Asn Val Leu |      |
| 510 515 520   |      |
| gtg ggt gcc atg gtg gcc acc tgg cga gtg ctc ctc tct gcc ctc tac | 1696 |
| Val Gly Ala Met Val Ala Thr Trp Arg Val Leu Leu Ser Ala Leu Tyr |      |
| 525 530 535   |      |
| aac gcc atc cac ctt ggc cag atg gac ctc agc ctg ctg cca ccg aga | 1744 |
| Asn Ala Ile His Leu Gly Gln Met Asp Leu Ser Leu Leu Pro Pro Arg |      |
| 540 545 550 555   |      |
| gcc gcc act ctc gac ccc ggc tac tac acg tac cga aac ttc ttg aag | 1792 |
| Ala Ala Thr Leu Asp Pro Gly Tyr Tyr Thr Tyr Arg Asn Phe Leu Lys |      |
| 560 565 570   |      |
| att gaa gtc agc cag tcg cat cca gcc atg aca gcc ttc tgc tcc ctg | 1840 |
| Ile Glu Val Ser Gln Ser His Pro Ala Met Thr Ala Phe Cys Ser Leu |      |
| 575 580 585   |      |
| ctc ctg caa gcg cag agc ctc cta ccc agg acc atg gca gcc ccc cag | 1888 |
| Leu Leu Gln Ala Gln Ser Leu Leu Pro Arg Thr Met Ala Ala Pro Gln |      |
| 590 595 600   |      |
| gac agc ctc aga cca ggg gag gaa gac gaa ggg atg cag ctg cta cag | 1936 |
| Asp Ser Leu Arg Pro Gly Glu Glu Asp Glu Gly Met Gln Leu Leu Gln |      |
| 605 610 615   |      |
| aca aag gac tcc atg gcc aag gga gct agg ccc ggg gcc agc cgc ggc | 1984 |
| Thr Lys Asp Ser Met Ala Lys Gly Ala Arg Pro Gly Ala Ser Arg Gly |      |

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|  |     |     |     |      |
|--|-----|-----|-----|------|
| 620  | 625 | 630 | 635 |      |
| agg gct cgc tgg ggt ctg gcc tac acg ctg ctg cac aac cca acc ctg    |     |     |     | 2032 |
| Arg Ala Arg Trp Gly Leu Ala Tyr Thr Leu Leu His Asn Pro Thr Leu    |     |     |     |      |
|  | 640 | 645 | 650 |      |
| cag gtc ttc cgc aag acg gcc ctg ttg ggt gcc aat ggt gcc cag ccc    |     |     |     | 2080 |
| Gln Val Phe Arg Lys Thr Ala Leu Leu Gly Ala Asn Gly Ala Gln Pro    |     |     |     |      |
|  | 655 | 660 | 665 |      |
| tgagggcagg gaaggtcaac ccacctgccc atctgtgctg aggcattgttc            |     |     |     | 2130 |
| ctgcctacca tctcctccc tccccggctc tctcccagc atcacaccag ccatgcagcc    |     |     |     | 2190 |
| agcaggctcct ccggatcacc gtggttggtt ggaggtctgt ctgcactggg agcctcagga |     |     |     | 2250 |
| gggctctgct ccaccactt ggctatggga gagccagcag gggttctgga gaaagaaact   |     |     |     | 2310 |
| ggtgggtag ggccttggtc caggagccag ttgagccagg gcagccacat ccaggcgtct   |     |     |     | 2370 |
| ccctaccctg gctctgcat cagccttgaa gggcctcgat gaagccttct ctggaaccac   |     |     |     | 2430 |
| tccagcccag ctccacctca gccttggcct tcacgctgtg gaagcagcca aggcaattcc  |     |     |     | 2490 |
| tcacccctc agcgccacgg acctctctgg ggagtggccg gaaagctccc gggcctctgg   |     |     |     | 2550 |
| cctgcagggc agcccaagtc atgactcaga ccaggtecca cactgagctg cccacactcg  |     |     |     | 2610 |
| agagccagat atttttgtag tttttatgcc tttggctatt atgaaagagg ttagtgtgtt  |     |     |     | 2670 |
| ccctgcaata aacttggtcc tgag   |     |     |     | 2694 |

&lt;210&gt; 57

&lt;211&gt; 3297

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

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&lt;222&gt; (83)... (1477)

&lt;400&gt; 57

|   |     |
|---|-----|
| gggggtctgta ctcgtgaag tcaactgggt tagtgtgctc tctgatgcct ggaattccag | 60  |
| tccccaccca gaaaccgcga gc atg att gtc tgc ctc ctt ttc atg atg att  | 112 |
| Met Ile Val Cys Leu Leu Phe Met Met Ile                           |     |
| 1 5 10  |     |
| tta ttg gca aag gaa gtt caa ctg gta gac caa aca gat tca cct tta   | 160 |
| Leu Leu Ala Lys Glu Val Gln Leu Val Asp Gln Thr Asp Ser Pro Leu   |     |
| 15 20 25  |     |
| ctt agt ctc ctt gga cag aca agc tca ctt tca tgg cat ctt gtg gat   | 208 |
| Leu Ser Leu Leu Gly Gln Thr Ser Ser Leu Ser Trp His Leu Val Asp   |     |
| 30 35 40  |     |
| att gtg tcg tac cag agt gtg cta agt tat ttc agc agc cat tac ccg   | 256 |
| Ile Val Ser Tyr Gln Ser Val Leu Ser Tyr Phe Ser Ser His Tyr Pro   |     |
| 45 50 55  |     |
| ccg tcc atc atc ctg gca aaa gaa tct tat gct gaa tta atc atg aag   | 304 |
| Pro Ser Ile Ile Leu Ala Lys Glu Ser Tyr Ala Glu Leu Ile Met Lys   |     |
| 60 65 70  |     |
| ctc cta aaa gtg tct gcg ggc ctt tct att cct act gac agc cag aag   | 352 |
| Leu Leu Lys Val Ser Ala Gly Leu Ser Ile Pro Thr Asp Ser Gln Lys   |     |
| 75 80 85 90   |     |
| cat ctt gat gca gtt cca aaa tgc caa gct ttt act cat cag atg gtt   | 400 |
| His Leu Asp Ala Val Pro Lys Cys Gln Ala Phe Thr His Gln Met Val   |     |
| 95 100 105  |     |
| caa ttc ctc agc acc ctg gaa caa aat gga aaa atc acc tta gca gtc   | 448 |

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Gln Phe Leu Ser Thr Leu Glu Gln Asn Gly Lys Ile Thr Leu Ala Val  
 110 115 120  
 cta gaa cag gaa atg tct aag ctc tta gac gat atc att gtc ttt aac 496  
 Leu Glu Gln Glu Met Ser Lys Leu Leu Asp Asp Ile Ile Val Phe Asn  
 125 130 135  
 ccg ccc gac atg gac agc cag acc cgc cac atg gcc ctc agc agc ctc 544  
 Pro Pro Asp Met Asp Ser Gln Thr Arg His Met Ala Leu Ser Ser Leu  
 140 145 150  
 ttt atg gaa gtc ctg atg atg atg aac aac gcg act att cca aca gca 592  
 Phe Met Glu Val Leu Met Met Met Asn Asn Ala Thr Ile Pro Thr Ala  
 155 160 165 170  
 gag ttc ctt cgg ggc agt atc cgg acc tgg att ggc caa aaa atg cat 640  
 Glu Phe Leu Arg Gly Ser Ile Arg Thr Trp Ile Gly Gln Lys Met His  
 175 180 185  
 ggg ctg gtg gtg ctg ccc ctt tta aca gca gcc tgc cag agc ctg gcg 688  
 Gly Leu Val Val Leu Pro Leu Leu Thr Ala Ala Cys Gln Ser Leu Ala  
 190 195 200  
 tcc gtc cgc cac atg gct gag act aca gaa gcc tgc atc act gcc tac 736  
 Ser Val Arg His Met Ala Glu Thr Thr Glu Ala Cys Ile Thr Ala Tyr  
 205 210 215  
 ttc aaa gaa agc cct ctc aat cag aat tca gga tgg gga ccc att ctg 784  
 Phe Lys Glu Ser Pro Leu Asn Gln Asn Ser Gly Trp Gly Pro Ile Leu  
 220 225 230  
 gta tcc ctt cag gtt ccc gag ctc acc atg gaa gag ttc ctg cag gag 832  
 Val Ser Leu Gln Val Pro Glu Leu Thr Met Glu Glu Phe Leu Gln Glu

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|   |     |     |     |      |
|---|-----|-----|-----|------|
| 235   | 240 | 245 | 250 |      |
| tgc ctc acc ttg ggc agt tac ttg act ctt tac gtc tac ttg ctt cag |     |     |     | 880  |
| Cys Leu Thr Leu Gly Ser Tyr Leu Thr Leu Tyr Val Tyr Leu Leu Gln |     |     |     |      |
|   | 255 | 260 | 265 |      |
| tgt tta aac agc gaa cag act tta agg aat gaa atg aaa gtg ctg ctc |     |     |     | 928  |
| Cys Leu Asn Ser Glu Gln Thr Leu Arg Asn Glu Met Lys Val Leu Leu |     |     |     |      |
|   | 270 | 275 | 280 |      |
| atc tta agc aag tgg ctg gaa cag gtg tac cca agc tcc gtg gag gaa |     |     |     | 976  |
| Ile Leu Ser Lys Trp Leu Glu Gln Val Tyr Pro Ser Ser Val Glu Glu |     |     |     |      |
|   | 285 | 290 | 295 |      |
| gag gca aag ctg ttt ttg tgg tgg cac caa gtc ctt cag ctc tcc ctc |     |     |     | 1024 |
| Glu Ala Lys Leu Phe Leu Trp Trp His Gln Val Leu Gln Leu Ser Leu |     |     |     |      |
|   | 300 | 305 | 310 |      |
| att cag aca gag cag aat gac tcc gtc ctg aca gaa tct gtc att cga |     |     |     | 1072 |
| Ile Gln Thr Glu Gln Asn Asp Ser Val Leu Thr Glu Ser Val Ile Arg |     |     |     |      |
|   | 315 | 320 | 325 | 330  |
| att ctg ctc ttg gtt cag agc agg cag aac ctc gtg gct gag gag aga |     |     |     | 1120 |
| Ile Leu Leu Leu Val Gln Ser Arg Gln Asn Leu Val Ala Glu Glu Arg |     |     |     |      |
|   | 335 | 340 | 345 |      |
| ctc agc tct ggg atc ctg ggg gca att ggg ttt ggc cgg aag tcg cct |     |     |     | 1168 |
| Leu Ser Ser Gly Ile Leu Gly Ala Ile Gly Phe Gly Arg Lys Ser Pro |     |     |     |      |
|   | 350 | 355 | 360 |      |
| ttg tct aac agg ttc cga gtg gtt gcc cga agc atg gct gcc ttc ctt |     |     |     | 1216 |
| Leu Ser Asn Arg Phe Arg Val Val Ala Arg Ser Met Ala Ala Phe Leu |     |     |     |      |
|   | 365 | 370 | 375 |      |

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tca gtt cag gtt cct atg gaa gat cag atc cgt ttg agg cct ggc tct 1264  
 Ser Val Gln Val Pro Met Glu Asp Gln Ile Arg Leu Arg Pro Gly Ser  
 380 385 390  
 gaa tta cat ctg acc ccc aaa gct cag cag gct ctg aat gct ctt gaa 1312  
 Glu Leu His Leu Thr Pro Lys Ala Gln Gln Ala Leu Asn Ala Leu Glu  
 395 400 405 410  
 tcc atg gca tca agt aag cag tat gtt gaa tac cag gat caa ata ttg 1360  
 Ser Met Ala Ser Ser Lys Gln Tyr Val Glu Tyr Gln Asp Gln Ile Leu  
 415 420 425  
 caa gcc acc caa ttt ata agg cat cct ggc cat tgc ctt caa gat ggg 1408  
 Gln Ala Thr Gln Phe Ile Arg His Pro Gly His Cys Leu Gln Asp Gly  
 430 435 440  
 aaa agc ttc ttg gct ctt ctc gtt aac tgt ctg tat cca gaa gtg cat 1456  
 Lys Ser Phe Leu Ala Leu Leu Val Asn Cys Leu Tyr Pro Glu Val His  
 445 450 455  
 tat ttg gac cac ata cga tagtta acactgaggc tcttgaaaaa cccattgctg 1510  
 Tyr Leu Asp His Ile Arg  
 460  
 tttatgttta catttaactt tgctgttgca caagtaactt tgctcaattg cactgtagag 1570  
 ctcagtttgg ccaatgtgta gttgactgag atgcaagttg ggaggcgta gatattagat 1630  
 aattttgggg tgtgtgtgtg tgtgtgtgtg tgttttctta gctcttaaga ccttctgggg 1690  
 actctttaag tttttatatt tatccacaag agaaacttac taagttccac ttgggtgcag 1750  
 agccactcac agttgccgaa tgtcccagtc atctcacaag acctccagat ggagttcttt 1810  
 gtatgtttcc acttctgtct ctgttttatg taaatgttcc agatctgaca accttggaag 1870  
 tcactcagta cccttacttt taaaccccat ttgtgttcct ccaaagtaaa gaagtcaatt 1930

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|  |      |
|--|------|
| ttgaaaaatt tctgcatttc tcaaatgtgg acaaatacaa tagttttaaa gtattgtttt  | 1990 |
| tctcagaagg gagataaaaa tgccgagtta gttaaagtgg gtcattgtga aaatacgacc  | 2050 |
| acttgatcgt gattatagtg ggcagtagag atgatgacaa gtcaatttcc atccagccgt  | 2110 |
| gtatcctcat ggagaagctg cctgtctgaa tcaggatggc aagctggcag tctgggagga  | 2170 |
| gcatgttttg cacagatgtt ttgtttggc cacttggtga ggagtgcaga cagggctgcc   | 2230 |
| tctctctagt cgggagagtc tgtgcattcc ctctgggccct gaccctagcc tcattcacat | 2290 |
| cacttgcccc tgcgacacc taagtttgca ccctttgata gacaccatgt tcgatatctg   | 2350 |
| aaaggctcag tgcaggaga cagagactga gggagactga agacctgatt ctctgttccc   | 2410 |
| tgcttgtttt ttaacttcaa actcagatga agccaatgga cctgctgaaa cacttgtctg  | 2470 |
| tggaaactgg gtcaggtcgg gagatctact gaaatttggc tttttttcca tagccacgtg  | 2530 |
| ccttctgttg ttgacagttc attcattacc aaagcctgtg tgtaactttg ccttgttctg  | 2590 |
| tggccatctt cttgctcatg ttatttctcc tgggaatgag cagtttgact tctgttccca  | 2650 |
| cgttcctcat tctatcagct ctagatggat ttgacctgca tagctggctt aatatgtctt  | 2710 |
| tgtgtatggg tagtctgtag cctgagaata ttacctaata aatgtctaaa cagccaccaa  | 2770 |
| gaatgtttat aggggtatag gaatatagtt aacagagtgc taatctctcc tcaaatgtcc  | 2830 |
| ttttggaatg cttcccccaa aattgggaag ttggtaggag cttttcttta ctttgaattt  | 2890 |
| ctttacttgg acagaacgat tctgccttaa agacacgctt tgcagctctg ataaagaaca  | 2950 |
| tcctgttta gtctcttgag ttttacaggc cacaaaatgt ccgtctcaga gggatctgtc   | 3010 |
| tcagcttttc ttatTTTTgc ttctctccgt ttcaaaaatt aatcatcttg ttctctgtat  | 3070 |
| aagaaaattt gagaagctgt ggacaattta atagtctgat ctggcaacag cgatttttgt  | 3130 |
| ttggaaatat ttgtgtttt ctttgaggag gatataatta ctgatctctt aggatgtgaa   | 3190 |
| atTTTTgagt gacagtatgc acattttaaa gaaaattatg attaactctgt ataattgttt | 3250 |
| ttggctctga aaaattataa aaaataaaat catttatctt tggttgt                | 3297 |

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&lt;211&gt; 2126

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (61)... (1473)

&lt;400&gt; 58

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aacactgaca gcgtgagccc gcggcggctg ctgccatggt ggctggcggc cgggtgcagc      60
atg tct aga ctg gga gcc ctg ggt ggt gcc cgt gcc ggg ctg gga ctg      108
Met Ser Arg Leu Gly Ala Leu Gly Gly Ala Arg Ala Gly Leu Gly Leu
      1              5              10              15
ttg ctg ggt acc gcc gcc ggc ctt gga ttc ctg tgc ctc ctt tac agc      156
Leu Leu Gly Thr Ala Ala Gly Leu Gly Phe Leu Cys Leu Leu Tyr Ser
      20              25              30
cag cga tgg aaa cgg acc cag cgt cat ggc cgc agc cag agc ctg ccc      204
Gln Arg Trp Lys Arg Thr Gln Arg His Gly Arg Ser Gln Ser Leu Pro
      35              40              45
aac tcc ctg gac tat acg cag act tca gat ccc gga cgc cac gtg atg      252
Asn Ser Leu Asp Tyr Thr Gln Thr Ser Asp Pro Gly Arg His Val Met
      50              55              60
ctc ctg cgg gct gtc cca ggt ggg gct gga gat gcc tca gtg ctg ccc      300
Leu Leu Arg Ala Val Pro Gly Gly Ala Gly Asp Ala Ser Val Leu Pro
      65              70              75              80
agc ctt cca cgg gaa gga cag gag aag gtg ctg gac cgc ctg gac ttt      348
Ser Leu Pro Arg Glu Gly Gln Glu Lys Val Leu Asp Arg Leu Asp Phe

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|   |     |     |     |
|---|-----|-----|-----|
| 85  | 90  | 95  |     |
| gtg ctg acc agc ctt gtg gcg ctg cgg cgg gag gtg gag gag ctg aga |     |     | 396 |
| Val Leu Thr Ser Leu Val Ala Leu Arg Arg Glu Val Glu Glu Leu Arg |     |     |     |
| 100   | 105 | 110 |     |
| agc agc ctg cga ggg ctt gcg ggg gag att gtt ggg gag gtc cga tgc |     |     | 444 |
| Ser Ser Leu Arg Gly Leu Ala Gly Glu Ile Val Gly Glu Val Arg Cys |     |     |     |
| 115   | 120 | 125 |     |
| cac atg gaa gag aac cag aga gtg gct cgg cgg cga agg ttt ccg ttt |     |     | 492 |
| His Met Glu Glu Asn Gln Arg Val Ala Arg Arg Arg Arg Phe Pro Phe |     |     |     |
| 130   | 135 | 140 |     |
| gtc cgg gag agg agt gac tcc act ggc tcc agc tct gtc tac ttc acg |     |     | 540 |
| Val Arg Glu Arg Ser Asp Ser Thr Gly Ser Ser Ser Val Tyr Phe Thr |     |     |     |
| 145   | 150 | 155 | 160 |
| gcc tcc tcg gga gcc acg ttc aca gat gct gag agt gaa ggg ggt tac |     |     | 588 |
| Ala Ser Ser Gly Ala Thr Phe Thr Asp Ala Glu Ser Glu Gly Gly Tyr |     |     |     |
| 165   | 170 | 175 |     |
| aca aca gcc aat gcg gag tct gac aat gag cgg gac tct gac aaa gaa |     |     | 636 |
| Thr Thr Ala Asn Ala Glu Ser Asp Asn Glu Arg Asp Ser Asp Lys Glu |     |     |     |
| 180   | 185 | 190 |     |
| agt gag gac ggg gaa gat gaa gtg agc tgt gag act gtg aag atg ggg |     |     | 684 |
| Ser Glu Asp Gly Glu Asp Glu Val Ser Cys Glu Thr Val Lys Met Gly |     |     |     |
| 195   | 200 | 205 |     |
| aga aag gat tct ctt gac ttg gag gaa gag gca gct tca ggt gcc tcc |     |     | 732 |
| Arg Lys Asp Ser Leu Asp Leu Glu Glu Glu Ala Ala Ser Gly Ala Ser |     |     |     |
| 210   | 215 | 220 |     |

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|  |      |
|--|------|
| agt gcc ctg gag gct gga ggt tcc tca ggc ttg gag gat gtg ctg ccc                | 780  |
| Ser Ala Leu Glu Ala Gly Gly Ser Ser Gly Leu Glu Asp Val Leu Pro                |      |
| 225                      230                      235                      240 |      |
| ctc ctg cag cag gcc gac gag ctg cac agg ggt gat gag caa ggc aag                | 828  |
| Leu Leu Gln Gln Ala Asp Glu Leu His Arg Gly Asp Glu Gln Gly Lys                |      |
| 245                      250                      255                          |      |
| cgg gag ggc ttc cag ctg ctg ctc aac aac aag ctg gtg tat gga agc                | 876  |
| Arg Glu Gly Phe Gln Leu Leu Leu Asn Asn Lys Leu Val Tyr Gly Ser                |      |
| 260                      265                      270                          |      |
| cgg cag gac ttt ctc tgg cgc ctg gcc cga gcc tac agt gac atg tgt                | 924  |
| Arg Gln Asp Phe Leu Trp Arg Leu Ala Arg Ala Tyr Ser Asp Met Cys                |      |
| 275                      280                      285                          |      |
| gag ctc act gag gag gtg agc gag aag aag tca tat gcc cta gat gga                | 972  |
| Glu Leu Thr Glu Glu Val Ser Glu Lys Lys Ser Tyr Ala Leu Asp Gly                |      |
| 290                      295                      300                          |      |
| aaa gaa gaa gca gag gct gct ctg gag aag ggg gat gag agt gct gac                | 1020 |
| Lys Glu Glu Ala Glu Ala Ala Leu Glu Lys Gly Asp Glu Ser Ala Asp                |      |
| 305                      310                      315                      320 |      |
| tgt cac ctg tgg tat gcg gtg ctt tgt ggt cag ctg gct gag cat gag                | 1068 |
| Cys His Leu Trp Tyr Ala Val Leu Cys Gly Gln Leu Ala Glu His Glu                |      |
| 325                      330                      335                          |      |
| agc atc cag agg cgc atc cag agt ggc ttt agc ttc aag gag cat gtg                | 1116 |
| Ser Ile Gln Arg Arg Ile Gln Ser Gly Phe Ser Phe Lys Glu His Val                |      |
| 340                      345                      350                          |      |
| gac aaa gcc att gct ctc cag cca gaa aac ccc atg gct cac ttt ctt                | 1164 |

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Asp Lys Ala Ile Ala Leu Gln Pro Glu Asn Pro Met Ala His Phe Leu  
 355 360 365  
 ctt ggc agg tgg tgc tat cag gtc tct cac ctg agc tgg cta gaa aaa 1212  
 Leu Gly Arg Trp Cys Tyr Gln Val Ser His Leu Ser Trp Leu Glu Lys  
 370 375 380  
 aaa act gct aca gcc ttg ctt gaa agc cct ctc agt gcc act gtg gaa 1260  
 Lys Thr Ala Thr Ala Leu Leu Glu Ser Pro Leu Ser Ala Thr Val Glu  
 385 390 395 400  
 gat gcc ctc cag agc ttc cta aag gct gaa gaa cta cag cca gga ttt 1308  
 Asp Ala Leu Gln Ser Phe Leu Lys Ala Glu Glu Leu Gln Pro Gly Phe  
 405 410 415  
 tcc aaa gca gga agg gta tat att tcc aag tgc tac aga gaa cta ggg 1356  
 Ser Lys Ala Gly Arg Val Tyr Ile Ser Lys Cys Tyr Arg Glu Leu Gly  
 420 425 430  
 aaa aac tct gaa gct aga tgg tgg atg aag ttg gcc ctg gag ctg cca 1404  
 Lys Asn Ser Glu Ala Arg Trp Trp Met Lys Leu Ala Leu Glu Leu Pro  
 435 440 445  
 gat gtc acg aag gag gat ttg gct atc cag aag gac ctg gaa gaa ctg 1452  
 Asp Val Thr Lys Glu Asp Leu Ala Ile Gln Lys Asp Leu Glu Glu Leu  
 450 455 460  
 gaa gtc att tta cga gac taaccacgtt tcaactggcct tcatgacttg 1500  
 Glu Val Ile Leu Arg Asp  
 465 470  
 atgccactat ttaaggtggg ggggcgggga ggcttttttc cttagacctt gctgagatca 1560  
 ggaaaccaca caaatctgtc tcctgggtct gactgctacc cactaccact cccattagt 1620

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taatttatc taacctctaa cctaattctag aattggggca gtactcatgg ctcccgtttc 1680  
 tgttggtctc tcccttgagt aatctcttaa aaaaatcaag attcacacct gccccaggat 1740  
 tacacatggg tagagcctgc aagacctgag accttccaat tgctgggtgag gtggatgaac 1800  
 ttcaaagcta taggaacaaa gcacataact tgtcacttta atctttttca ctgactaata 1860  
 ggactcagta catatagtct taagatcata ccttacctac caaggtaaaa agagggatca 1920  
 gagtggccca cagacattgc tttcttatca cctatcatgt gaattctacc tgtattcctg 1980  
 ggctggacca ctigataact tccagtgtcc tggcagcttt tggaatgaca gcagtggat 2040  
 ggggtttatg atgctataaa acaatgtctg aaaagttgcc tagaatatat ttgtttacaa 2100  
 acttgaaata aaccaaattt gatgtt 2126

&lt;210&gt; 59

&lt;211&gt; 1781

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (74)... (805)

&lt;400&gt; 59

aatttggacc tgtgattcct tggttctcac aatcctctcc actctaagaa gcagggtgag 60  
 cccacaagga gca atg gag cag ggc agc ggc cgc ttg gag gac ttc cct 109

Met Glu Gln Gly Ser Gly Arg Leu Glu Asp Phe Pro

1

5

10

gtc aat gtg ttc tcc gtc act cct tac aca ccc agc acc gct gac atc 157

Val Asn Val Phe Ser Val Thr Pro Tyr Thr Pro Ser Thr Ala Asp Ile

15

20

25

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|   |     |
|---|-----|
| cag gtg tcc gat gat gac aag gcg ggg gcc acc ttg ctc ttc tca ggc | 205 |
| Gln Val Ser Asp Asp Asp Lys Ala Gly Ala Thr Leu Leu Phe Ser Gly |     |
| 30 35 40  |     |
| atc ttt ctg gga ctg gtg ggg atc aca ttc act gtc atg ggc tgg atc | 253 |
| Ile Phe Leu Gly Leu Val Gly Ile Thr Phe Thr Val Met Gly Trp Ile |     |
| 45 50 55 60   |     |
| aaa tac caa ggt gtc tcc cac ttt gaa tgg acc cag ctc ctt ggg ccc | 301 |
| Lys Tyr Gln Gly Val Ser His Phe Glu Trp Thr Gln Leu Leu Gly Pro |     |
| 65 70 75  |     |
| gtc ctg ctg tca gtt ggg gtg aca ttc atc ctg att gct gtg tgc aag | 349 |
| Val Leu Leu Ser Val Gly Val Thr Phe Ile Leu Ile Ala Val Cys Lys |     |
| 80 85 90  |     |
| ttc aaa atg ctc tcc tgc cag ttg tgc aaa gaa agt gag gaa agg gtc | 397 |
| Phe Lys Met Leu Ser Cys Gln Leu Cys Lys Glu Ser Glu Glu Arg Val |     |
| 95 100 105  |     |
| ccg gac tcg gaa cag aca cca gga gga cca tca ttt gtt ttc act ggc | 445 |
| Pro Asp Ser Glu Gln Thr Pro Gly Gly Pro Ser Phe Val Phe Thr Gly |     |
| 110 115 120   |     |
| atc aac caa ccc atc acc ttc cat ggg gcc act gtg gtg cag tac atc | 493 |
| Ile Asn Gln Pro Ile Thr Phe His Gly Ala Thr Val Val Gln Tyr Ile |     |
| 125 130 135 140   |     |
| cct cct cct tat ggt tct cca gag cct atg ggg ata aat acc agc tac | 541 |
| Pro Pro Pro Tyr Gly Ser Pro Glu Pro Met Gly Ile Asn Thr Ser Tyr |     |
| 145 150 155   |     |
| ctg cag tct gtg gtg agc ccc tgc ggc ctc ata acc tct gga ggg gca | 589 |

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Leu Gln Ser Val Val Ser Pro Cys Gly Leu Ile Thr Ser Gly Gly Ala  
 160 165 170  
 gca gcc gcc atg tca agt cct cct caa tac tac acc atc tac cct caa 637  
 Ala Ala Ala Met Ser Ser Pro Pro Gln Tyr Tyr Thr Ile Tyr Pro Gln  
 175 180 185  
 gat aac tct gca ttt gtg gtt gat gag ggc tgc ctt tct ttc acg gac 685  
 Asp Asn Ser Ala Phe Val Val Asp Glu Gly Cys Leu Ser Phe Thr Asp  
 190 195 200  
 ggt gga aat cac agg ccc aat cct gat gtt gac cag cta gaa gag aca 733  
 Gly Gly Asn His Arg Pro Asn Pro Asp Val Asp Gln Leu Glu Glu Thr  
 205 210 215 220  
 cag ctg gaa gag gag gcc tgt gcc tgc ttc tct cct ccc cct tat gaa 781  
 Gln Leu Glu Glu Glu Ala Cys Ala Cys Phe Ser Pro Pro Pro Tyr Glu  
 225 230 235  
 gaa ata tac tct ctc cct cgc tagaggct attctgatat aataacacaa 830  
 Glu Ile Tyr Ser Leu Pro Arg  
 240  
 tgctcagctc agggagcaag tgtttccgtc attgttacct gacaaccgtg gtgttctatg 890  
 ttgtaacctt cagaagttac agcagcgccc aggcagcctg acagagatca ttcaaggggg 950  
 gaaaggggaa gtgggaggtg caatttctca gatttggtaaa aattaggctg ggctggggaa 1010  
 atttctctcc ggaacagttt caaatccct cgggtaagaa atctctgta taaggttcag 1070  
 gagcaggaat ttcaattttt catccaccac cctccccctt ctctgtagga aggcattggt 1130  
 ggctcaattt taaccccagc agccaatgga aaaatcacga cttctgagac ttggggagtt 1190  
 tccacagagg tgagagtcgg gtgggaagga agcaggggaag agaaagcagg cccagctgga 1250  
 gatttctggt tggctgtcct tggcccaaaa gcagactcac taatcccaaa caactcagct 1310

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gccatctggc ctctctgagg actctgggta ccttaaagac tataaaacaa aacaaaacaa 1370  
 aaacatcaaa ccaatgaaat aaaataaatc atgtctcctg ctagaatagt attggatacc 1430  
 tgactaaatt acacaaaata gaccataata ggatagcact gtgaatacat ccttcccgat 1490  
 cactgagtca cagtgaccct tggctgctgc agttctcgtc tgcaagggtg aagcttgacg 1550  
 tgtgatgaac atgggtgggc tcttgggtcca cccaggtg gggcctgcgc caagcatgaa 1610  
 ctagctggga ccagtggctg acagaacaca ggacttcct aagtaccgt aggtccgtgg 1670  
 agcaagacag agcagagttg ccatgtcaac acatggggaa tgatatgata gaaacaatct 1730  
 ttatgactaa aagaaactca tcttcttcat taaaaaact ttggtgtcct t 1781

&lt;210&gt; 60

&lt;211&gt; 1788

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (87)... (899)

&lt;400&gt; 60

attggcgggc gtgatctcgc cgcggttccg cggccctgcc gccgccgccg ccagcagagc 60  
 gcaccggggc gatcgggcga gtggcc atg gcg ggc gcc gag gac tgg ccg ggc 113

Met Ala Gly Ala Glu Asp Trp Pro Gly

1

5

cag cag ctg gag ctg gac gag gac gag gcg tct tgt tgc cgc tgg ggc 161

Gln Gln Leu Glu Leu Asp Glu Asp Glu Ala Ser Cys Cys Arg Trp Gly

10

15

20

25

gcg cag cac gcc ggg gcc cgc gag ctg gct gcg ctc tac tcg cca ggc 209

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|   |     |
|---|-----|
| Ala Gln His Ala Gly Ala Arg Glu Leu Ala Ala Leu Tyr Ser Pro Gly |     |
| 30 35 40  |     |
| aag cgc ctc cag gag tgg tgc tct gtg atc ctg tgc ttc agc ctc atc | 257 |
| Lys Arg Leu Gln Glu Trp Cys Ser Val Ile Leu Cys Phe Ser Leu Ile |     |
| 45 50 55  |     |
| gcc cac aac ctg gtc cat ctc ctg ctg ctg gcc cgc tgg gag gac aca | 305 |
| Ala His Asn Leu Val His Leu Leu Leu Leu Ala Arg Trp Glu Asp Thr |     |
| 60 65 70  |     |
| ccc ctc gtc ata ctc ggt gtt gtt gca ggg gct ctc att gct gac ttc | 353 |
| Pro Leu Val Ile Leu Gly Val Val Ala Gly Ala Leu Ile Ala Asp Phe |     |
| 75 80 85  |     |
| ttg tct ggc ctg gta cac tgg ggt gct gac aca tgg ggc tct gtg gag | 401 |
| Leu Ser Gly Leu Val His Trp Gly Ala Asp Thr Trp Gly Ser Val Glu |     |
| 90 95 100 105   |     |
| ctg ccc att gtg ggg aag gct ttc atc cga ccc ttc cgg gag cac cac | 449 |
| Leu Pro Ile Val Gly Lys Ala Phe Ile Arg Pro Phe Arg Glu His His |     |
| 110 115 120   |     |
| att gac cca aca gct atc aca cgg cac gac ttc atc gag acc aac ggg | 497 |
| Ile Asp Pro Thr Ala Ile Thr Arg His Asp Phe Ile Glu Thr Asn Gly |     |
| 125 130 135   |     |
| gac aac tgc ctg gtg aca ctg ctg ccg ctg cta aac atg gcc tac aag | 545 |
| Asp Asn Cys Leu Val Thr Leu Leu Pro Leu Leu Asn Met Ala Tyr Lys |     |
| 140 145 150   |     |
| ttc cgc acc cac agc cct gaa gcc ctg gag cag cta tac ccc tgg gag | 593 |
| Phe Arg Thr His Ser Pro Glu Ala Leu Glu Gln Leu Tyr Pro Trp Glu |     |



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|   |     |     |      |
|---|-----|-----|------|
| 155   | 160 | 165 |      |
| tgc ttc gtc ttc tgc ctg atc atc ttc ggc acc ttc acc aac cag atc   |     |     | 641  |
| Cys Phe Val Phe Cys Leu Ile Ile Phe Gly Thr Phe Thr Asn Gln Ile   |     |     |      |
| 170   | 175 | 180 | 185  |
| cac aag tgg tgc cac acg tac ttt ggg ctg cca cgc tgg gtc acc ctc   |     |     | 689  |
| His Lys Trp Ser His Thr Tyr Phe Gly Leu Pro Arg Trp Val Thr Leu   |     |     |      |
|   | 190 | 195 | 200  |
| ctg cag gac tgg cat gtc atc ctg cca cgt aaa cac cat cgc atc cac   |     |     | 737  |
| Leu Gln Asp Trp His Val Ile Leu Pro Arg Lys His His Arg Ile His   |     |     |      |
|   | 205 | 210 | 215  |
| cac gtc tca ccc cac gag acc tac ttc tgc atc acc aca ggc tgg ctc   |     |     | 785  |
| His Val Ser Pro His Glu Thr Tyr Phe Cys Ile Thr Thr Gly Trp Leu   |     |     |      |
|   | 220 | 225 | 230  |
| aac tac cct ctg gag aag ata ggc ttc tgg cga cgc ctg gag gac ctc   |     |     | 833  |
| Asn Tyr Pro Leu Glu Lys Ile Gly Phe Trp Arg Arg Leu Glu Asp Leu   |     |     |      |
|   | 235 | 240 | 245  |
| atc cag ggc ctg acg ggc gag aag cct cgg gca gat gac atg aaa tgg   |     |     | 881  |
| Ile Gln Gly Leu Thr Gly Glu Lys Pro Arg Ala Asp Asp Met Lys Trp   |     |     |      |
| 250   | 255 | 260 | 265  |
| gcc cag aag atc aaa taac ttctcgcgagc ctgctacctg gttgccaacc        |     |     | 930  |
| Ala Gln Lys Ile Lys   |     |     |      |
|   | 270 |     |      |
| ttccctagcc cccaaaccga agccatctgc caaattccag cctctttgag ctggcccctc |     |     | 990  |
| cagatggaga ggacatctcc tgggctgggc ccaggtaccc cagcccaccc ctcatgacac |     |     | 1050 |
| agaatacttg agccactgat ttttcatttc tttttttttt ttttctctcg gccctcctc  |     |     | 1110 |

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agccacctga gttgctctat ctgcaagcct gactctgccca gcctccccctg gtagagagga 1170  
 ggtttaccca ctccctgcac gcctgccgtc cctgccccgc tgggcagccc ttcagtgtgg 1230  
 ctggcggttg ggccagtga ttgcctcttt cctccttgt ctggccccag tggctctgggg 1290  
 agccccagg cacacctaag cgtcgtggag cattgttctg ccacagccct gcatactgac 1350  
 cccgggaggc tgggcaggtg gacagcccca gccaccacct tcagcctagc ctgtcccca 1410  
 aggatggtga agctcagcag gggctctgagg gtagccggcc agaagaggct ggaacctcct 1470  
 gctcaagtct agaccctac ttctctgctg cccccacct gccagagctg atgtttccaa 1530  
 taccaagatg tcttcacagg gcacagcccc tgcagagcat cttggtcatt tggaagagga 1590  
 cacggtatcc cctctggcca gagtatgtca gagaaggaag agtagggctt tttgttttg 1650  
 ttttttttta aaggtgcttg cttgtttaat gtaaataata gaaagcctta atatcttttc 1710  
 tgtaacacgg agtaatat ttatgtcatg ttttgatgt acataatata tttataacaa 1770  
 agcagcaaga gtctactt 1788

&lt;210&gt; 61

&lt;211&gt; 389

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 61

Met Asp Arg Gly Glu Lys Ile Gln Leu Lys Arg Val Phe Gly Tyr Trp

1

5

10

15

Trp Gly Thr Ser Phe Leu Leu Ile Asn Ile Ile Gly Ala Gly Ile Phe

20

25

30

Val Ser Pro Lys Gly Val Leu Ala Tyr Ser Cys Met Asn Val Gly Val

35

40

45

Ser Leu Cys Val Trp Ala Gly Cys Ala Ile Leu Ala Met Thr Ser Thr

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|   |     |     |     |
|---|-----|-----|-----|
| 50  | 55  | 60  |     |
| Leu Cys Ser Ala Glu Ile Ser Ile Ser Phe Pro Cys Ser Gly Ala Gln |     |     |     |
| 65  | 70  | 75  | 80  |
| Tyr Tyr Phe Leu Lys Arg Tyr Phe Gly Ser Thr Val Ala Phe Leu Asn |     |     |     |
| 85  | 90  | 95  |     |
| Leu Trp Thr Ser Leu Phe Leu Gly Ser Gly Val Val Ala Gly Gln Ala |     |     |     |
| 100   | 105 | 110 |     |
| Leu Leu Leu Ala Glu Tyr Ser Ile Gln Pro Phe Phe Pro Ser Cys Ser |     |     |     |
| 115   | 120 | 125 |     |
| Val Pro Lys Leu Pro Lys Lys Cys Leu Ala Leu Ala Met Leu Trp Ile |     |     |     |
| 130   | 135 | 140 |     |
| Val Gly Ile Leu Thr Ser Arg Gly Val Lys Glu Val Thr Trp Leu Gln |     |     |     |
| 145   | 150 | 155 | 160 |
| Ile Ala Ser Ser Val Leu Lys Val Ser Ile Leu Ser Phe Ile Ser Leu |     |     |     |
| 165   | 170 | 175 |     |
| Thr Gly Val Val Phe Leu Ile Arg Gly Lys Lys Glu Asn Val Glu Arg |     |     |     |
| 180   | 185 | 190 |     |
| Phe Gln Asn Ala Phe Asp Ala Glu Leu Pro Asp Ile Ser His Leu Ile |     |     |     |
| 195   | 200 | 205 |     |
| Gln Ala Ile Phe Gln Gly Tyr Phe Ala Tyr Ser Gly Glu Leu Lys Lys |     |     |     |
| 210   | 215 | 220 |     |
| Pro Arg Thr Thr Ile Pro Lys Cys Ile Phe Thr Ala Leu Pro Leu Val |     |     |     |
| 225   | 230 | 235 | 240 |
| Thr Val Val Tyr Leu Leu Val Asn Ile Ser Tyr Leu Thr Val Leu Thr |     |     |     |
| 245   | 250 | 255 |     |

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Pro Arg Glu Ile Leu Ser Ser Asp Ala Val Ala Ile Thr Trp Ala Asp

260

265

270

Arg Ala Phe Pro Ser Leu Ala Trp Ile Met Pro Phe Ala Ile Ser Thr

275

280

285

Ser Leu Phe Ser Asn Leu Leu Ile Ser Ile Phe Lys Ser Ser Arg Pro

290

295

300

Ile Tyr Leu Ala Ser Gln Glu Gly Gln Leu Pro Leu Leu Phe Asn Thr

305

310

315

320

Leu Asn Ser His Ser Ser Pro Phe Thr Ala Val Leu Leu Leu Val Thr

325

330

335

Leu Gly Ser Leu Ala Ile Ile Leu Thr Ser Leu Ile Asp Leu Ile Asn

340

345

350

Tyr Ile Phe Phe Thr Gly Ser Leu Trp Ser Ile Leu Leu Met Ile Gly

355

360

365

Ile Leu Arg Arg Arg Tyr Gln Glu Pro Asn Leu Ser Ile Pro Tyr Lys

370

375

380

Val Lys Leu Asp Phe

385

&lt;210&gt; 62

&lt;211&gt; 348

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 62

Met Ala Ala Thr Leu Gly Pro Leu Gly Ser Trp Gln Gln Trp Arg Arg

140/307

|   |     |     |     |
|---|-----|-----|-----|
| 1   | 5   | 10  | 15  |
| Cys Leu Ser Ala Arg Asp Gly Ser Arg Met Leu Leu Leu Leu Leu Leu |     |     |     |
| 20  | 25  | 30  |     |
| Leu Gly Ser Gly Gln Gly Pro Gln Gln Val Gly Ala Gly Gln Thr Phe |     |     |     |
| 35  | 40  | 45  |     |
| Glu Tyr Leu Lys Arg Glu His Ser Leu Ser Lys Pro Tyr Gln Gly Val |     |     |     |
| 50  | 55  | 60  |     |
| Gly Thr Gly Ser Ser Ser Leu Trp Asn Leu Met Gly Asn Ala Met Val |     |     |     |
| 65  | 70  | 75  | 80  |
| Met Thr Gln Tyr Ile Arg Leu Thr Pro Asp Met Gln Ser Lys Gln Gly |     |     |     |
| 85  | 90  | 95  |     |
| Ala Leu Trp Asn Arg Val Pro Cys Phe Leu Arg Asp Trp Glu Leu Gln |     |     |     |
| 100   | 105 | 110 |     |
| Val His Phe Lys Ile His Gly Gln Gly Lys Lys Asn Leu His Gly Asp |     |     |     |
| 115   | 120 | 125 |     |
| Gly Leu Ala Ile Trp Tyr Thr Lys Asp Arg Met Gln Pro Gly Pro Val |     |     |     |
| 130   | 135 | 140 |     |
| Phe Gly Asn Met Asp Lys Phe Val Gly Leu Gly Val Phe Val Asp Thr |     |     |     |
| 145   | 150 | 155 | 160 |
| Tyr Pro Asn Glu Glu Lys Gln Gln Glu Arg Val Phe Pro Tyr Ile Ser |     |     |     |
| 165   | 170 | 175 |     |
| Ala Met Val Asn Asn Gly Ser Leu Ser Tyr Asp His Glu Arg Asp Gly |     |     |     |
| 180   | 185 | 190 |     |
| Arg Pro Thr Glu Leu Gly Gly Cys Thr Ala Ile Val Arg Asn Leu His |     |     |     |
| 195   | 200 | 205 |     |

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Tyr Asp Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His Leu Thr Ile

210

215

220

Met Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys Ile Glu Val

225

230

235

240

Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr Ser Ser Ile

245

250

255

Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys Leu Phe

260

265

270

Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu His Arg Asp

275

280

285

Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro Glu Met Thr Ala

290

295

300

Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe Leu Ile Val Phe Phe

305

310

315

320

Ser Leu Val Phe Ser Val Phe Ala Ile Val Ile Gly Ile Ile Leu Tyr

325

330

335

Asn Lys Trp Gln Glu Gln Ser Arg Lys Arg Phe Tyr

340

345

&lt;210&gt; 63

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 63

Met Glu Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys

142/307

|   |     |     |     |
|---|-----|-----|-----|
| 1   | 5   | 10  | 15  |
| Ser Ser Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val |     |     |     |
| 20  | 25  | 30  |     |
| Val Thr Thr Thr Lys Pro Ser Ile Thr Thr Pro Asn Thr Glu Ser Leu |     |     |     |
| 35  | 40  | 45  |     |
| Gln Lys Asn Val Val Thr Pro Thr Thr Gly Thr Thr Pro Lys Gly Thr |     |     |     |
| 50  | 55  | 60  |     |
| Ile Thr Asn Glu Leu Leu Lys Met Ser Leu Met Ser Thr Ala Thr Phe |     |     |     |
| 65  | 70  | 75  | 80  |
| Leu Thr Ser Lys Asp Glu Gly Leu Lys Ala Thr Thr Thr Asp Val Arg |     |     |     |
| 85  | 90  | 95  |     |
| Lys Asn Asp Ser Ile Ile Ser Asn Val Thr Val Thr Ser Val Thr Leu |     |     |     |
| 100   | 105 | 110 |     |
| Pro Asn Ala Val Ser Thr Leu Gln Ser Ser Lys Pro Lys Thr Glu Thr |     |     |     |
| 115   | 120 | 125 |     |
| Gln Ser Ser Ile Lys Thr Thr Glu Ile Pro Gly Ser Val Leu Gln Pro |     |     |     |
| 130   | 135 | 140 |     |
| Asp Ala Ser Pro Ser Lys Thr Gly Thr Leu Thr Ser Ile Pro Val Thr |     |     |     |
| 145   | 150 | 155 | 160 |
| Ile Pro Glu Asn Thr Ser Gln Ser Gln Val Ile Gly Thr Glu Gly Gly |     |     |     |
| 165   | 170 | 175 |     |
| Lys Asn Ala Ser Thr Ser Ala Thr Ser Arg Ser Tyr Ser Ser Ile Ile |     |     |     |
| 180   | 185 | 190 |     |
| Leu Pro Val Val Ile Ala Leu Ile Val Ile Thr Leu Ser Val Phe Val |     |     |     |
| 195   | 200 | 205 |     |

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Leu Val Gly Leu Tyr Arg Met Cys Trp Lys Ala Asp Pro Gly Thr Pro

210

215

220

Glu Asn Gly Asn Asp Gln Pro Gln Ser Asp Lys Glu Ser Val Lys Leu

225

230

235

240

Leu Thr Val Lys Thr Ile Ser His Glu Ser Gly Glu His Ser Ala Gln

245

250

255

Gly Lys Thr Lys Asn

260

&lt;210&gt; 64

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 64

Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala Glu Leu

1

5

10

15

Cys Gln Pro Gly Ala Glu Asn Ala Phe Lys Val Arg Leu Ser Ile Arg

20

25

30

Thr Ala Leu Gly Asp Lys Ala Tyr Ala Trp Asp Thr Asn Glu Glu Tyr

35

40

45

Leu Phe Lys Ala Met Val Ala Phe Ser Met Arg Lys Val Pro Asn Arg

50

55

60

Glu Ala Thr Glu Ile Ser His Val Leu Leu Cys Asn Val Thr Gln Arg

65

70

75

80

Val Ser Phe Trp Phe Val Val Thr Asp Pro Ser Lys Asn His Thr Leu



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|   |     |     |     |
|---|-----|-----|-----|
| 85  | 90  | 95  |     |
| Pro Ala Val Glu Val Gln Ser Ala Ile Arg Met Asn Lys Asn Arg Ile |     |     |     |
| 100   | 105 | 110 |     |
| Asn Asn Ala Phe Phe Leu Asn Asp Gln Thr Leu Glu Phe Leu Lys Ile |     |     |     |
| 115   | 120 | 125 |     |
| Pro Ser Thr Leu Ala Pro Pro Met Asp Pro Ser Val Pro Ile Trp Ile |     |     |     |
| 130   | 135 | 140 |     |
| Ile Ile Phe Gly Val Ile Phe Cys Ile Ile Ile Val Ala Ile Ala Leu |     |     |     |
| 145   | 150 | 155 | 160 |
| Leu Ile Leu Ser Gly Ile Trp Gln Arg Arg Arg Lys Asn Lys Glu Pro |     |     |     |
| 165   | 170 | 175 |     |
| Ser Glu Val Asp Asp Ala Glu Asp Lys Cys Glu Asn Met Ile Thr Ile |     |     |     |
| 180   | 185 | 190 |     |
| Glu Asn Gly Ile Pro Ser Asp Pro Leu Asp Met Lys Gly Gly His Ile |     |     |     |
| 195   | 200 | 205 |     |
| Asn Asp Ala Phe Met Thr Glu Asp Glu Arg Leu Thr Pro Leu         |     |     |     |
| 210   | 215 | 220 |     |

&lt;210&gt; 65

&lt;211&gt; 183

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 65

Met Gly Val Arg Val His Val Val Ala Ala Ser Ala Leu Leu Tyr Phe

1

5

10

15

145/307

Ile Leu Leu Ser Gly Thr Arg Cys Glu Glu Asn Cys Gly Asn Pro Glu

20

25

30

His Cys Leu Thr Thr Asp Trp Val His Leu Trp Tyr Ile Trp Leu Leu

35

40

45

Val Val Ile Gly Ala Leu Leu Leu Leu Cys Gly Leu Thr Ser Leu Cys

50

55

60

Phe Arg Cys Cys Cys Leu Ser Arg Gln Gln Asn Gly Glu Asp Gly Gly

65

70

75

80

Pro Pro Pro Cys Glu Val Thr Val Ile Ala Phe Asp His Asp Ser Thr

85

90

95

Leu Gln Ser Thr Ile Thr Ser Leu Gln Ser Val Phe Gly Pro Ala Ala

100

105

110

Arg Arg Ile Leu Ala Val Ala His Ser His Ser Ser Leu Gly Gln Leu

115

120

125

Pro Ser Ser Leu Asp Thr Leu Pro Gly Tyr Glu Glu Ala Leu His Met

130

135

140

Ser Arg Phe Thr Val Ala Met Cys Gly Gln Lys Ala Pro Asp Leu Pro

145

150

155

160

Pro Val Pro Glu Glu Lys Gln Leu Pro Pro Thr Glu Lys Glu Ser Thr

165

170

175

Arg Ile Val Asp Ser Trp Asn

180

&lt;210&gt; 66

&lt;211&gt; 262

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&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 66

Met Gly Lys Thr Phe Ser Gln Leu Gly Ser Trp Arg Glu Asp Glu Asn

1 5 10 15

Lys Ser Ile Leu Ser Ser Lys Pro Ala Ile Gly Ser Lys Ala Val Asn

20 25 30

Tyr Ser Ser Thr Gly Ser Ser Lys Ser Phe Cys Ser Cys Val Pro Cys

35 40 45

Glu Gly Thr Ala Asp Ala Ser Phe Val Thr Cys Pro Thr Cys Gln Gly

50 55 60

Ser Gly Lys Ile Pro Gln Glu Leu Glu Lys Gln Leu Val Ala Leu Ile

65 70 75 80

Pro Tyr Gly Asp Gln Arg Leu Lys Pro Lys His Thr Lys Leu Phe Val

85 90 95

Phe Leu Ala Val Leu Ile Cys Leu Val Thr Ser Ser Phe Ile Val Phe

100 105 110

Phe Leu Phe Pro Arg Ser Val Ile Val Gln Pro Ala Gly Leu Asn Ser

115 120 125

Ser Thr Val Ala Phe Asp Glu Ala Asp Ile Tyr Leu Asn Ile Thr Asn

130 135 140

Ile Leu Asn Ile Ser Asn Gly Asn Tyr Tyr Pro Ile Met Val Thr Gln

145 150 155 160

Leu Thr Leu Glu Val Leu His Leu Ser Leu Val Val Gly Gln Val Ser

165 170 175

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Asn Asn Leu Leu Leu His Ile Gly Pro Leu Ala Ser Glu Gln Met Phe

180

185

190

Tyr Ala Val Ala Thr Lys Ile Arg Asp Glu Asn Thr Tyr Lys Ile Cys

195

200

205

Thr Trp Leu Glu Ile Lys Val His His Val Leu Leu His Ile Gln Gly

210

215

220

Thr Leu Thr Cys Ser Tyr Leu Ser His Ser Glu Gln Leu Val Phe Gln

225

230

235

240

Ser Tyr Glu Tyr Val Asp Cys Arg Gly Asn Ala Ser Val Pro His Gln

245

250

255

Leu Thr Pro His Pro Pro

260

&lt;210&gt; 67

&lt;211&gt; 168

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 67

Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly Ser

1

5

10

15

Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Lys Asp Ala Pro

20

25

30

Ser Asn Cys Val Val Tyr Pro Ser Ser Ser Gln Glu Ser Glu Asn Ile

35

40

45

Thr Ala Ala Ala Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys

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50                      55                      60  
 Leu Pro Leu Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser  
 65                      70                      75                      80  
 Asn Arg Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly  
                          85                      90                      95  
 Ile Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro  
                          100                      105                      110  
 Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln Pro  
                          115                      120                      125  
 Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro Leu Ser  
                          130                      135                      140  
 Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp Pro Val Pro  
 145                      150                      155                      160  
 Asp Ser Pro Asn Phe Glu Val Ile  
                          165

&lt;210&gt; 68

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 68

Met Ser Ser Gly Thr Glu Leu Leu Trp Pro Gly Ala Ala Leu Leu Val  
 1                      5                      10                      15  
 Leu Leu Gly Val Ala Ala Ser Leu Cys Val Arg Cys Ser Arg Pro Gly  
                          20                      25                      30

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Ala Lys Arg Ser Glu Lys Ile Tyr Gln Gln Arg Ser Leu Arg Glu Asp  
35 40 45  
Gln Gln Ser Phe Thr Gly Ser Arg Thr Tyr Ser Leu Val Gly Gln Ala  
50 55 60  
Trp Pro Gly Pro Leu Ala Asp Met Ala Pro Thr Arg Lys Asp Lys Leu  
65 70 75 80  
Leu Gln Phe Tyr Pro Ser Leu Glu Asp Pro Ala Ser Ser Arg Tyr Gln  
85 90 95  
Asn Phe Ser Lys Gly Ser Arg His Gly Ser Glu Glu Ala Tyr Ile Asp  
100 105 110  
Pro Ile Ala Met Glu Tyr Tyr Asn Trp Gly Arg Phe Ser Lys Pro Pro  
115 120 125  
Glu Asp Asp Asp Ala Asn Ser Tyr Glu Asn Val Leu Ile Cys Lys Gln  
130 135 140  
Lys Thr Thr Glu Thr Gly Ala Gln Gln Glu Gly Ile Gly Gly Leu Cys  
145 150 155 160  
Arg Gly Asp Leu Ser Leu Ser Leu Ala Leu Lys Thr Gly Pro Thr Ser  
165 170 175  
Gly Leu Cys Pro Ser Ala Ser Pro Glu Glu Asp Glu Glu Ser Glu Asp  
180 185 190  
Tyr Gln Asn Ser Ala Ser Ile His Gln Trp Arg Glu Ser Arg Lys Val  
195 200 205  
Met Gly Gln Leu Gln Arg Glu Ala Ser Pro Gly Pro Val Gly Ser Pro  
210 215 220  
Asp Glu Glu Asp Gly Glu Pro Asp Tyr Val Asn Gly Glu Val Ala Ala

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225                      230                      235                      240

Thr Glu Ala

<210> 69

<211> 428

<212> PRT

<213> Homo sapiens

<400> 69

Met Ala Arg Ser Leu Cys Pro Gly Ala Trp Leu Arg Lys Pro Tyr Tyr

1                      5                      10                      15

Leu Gln Ala Arg Phe Ser Tyr Val Arg Met Lys Tyr Leu Phe Phe Ser

20                      25                      30

Trp Leu Val Val Phe Val Gly Ser Trp Ile Ile Tyr Val Gln Tyr Ser

35                      40                      45

Thr Tyr Thr Glu Leu Cys Arg Gly Lys Asp Cys Lys Lys Ile Ile Cys

50                      55                      60

Asp Lys Tyr Lys Thr Gly Val Ile Asp Gly Pro Ala Cys Asn Ser Leu

65                      70                      75                      80

Cys Val Thr Glu Thr Leu Tyr Phe Gly Lys Cys Leu Ser Thr Lys Pro

85                      90                      95

Asn Asn Gln Met Tyr Leu Gly Ile Trp Asp Asn Leu Pro Gly Val Val

100                      105                      110

Lys Cys Gln Met Glu Gln Ala Leu His Leu Asp Phe Gly Thr Glu Leu

115                      120                      125

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Glu Pro Arg Lys Glu Ile Val Leu Phe Asp Lys Pro Thr Arg Gly Thr

130

135

140

Thr Val Gln Lys Phe Lys Glu Met Val Tyr Ser Leu Phe Lys Ala Lys

145

150

155

160

Leu Gly Asp Gln Gly Asn Leu Ser Glu Leu Val Asn Leu Ile Leu Thr

165

170

175

Val Ala Asp Gly Asp Lys Asp Gly Gln Val Ser Leu Gly Glu Ala Lys

180

185

190

Ser Ala Trp Ala Leu Leu Gln Leu Asn Glu Phe Leu Leu Met Val Ile

195

200

205

Leu Gln Asp Lys Glu His Thr Pro Lys Leu Met Gly Phe Cys Gly Asp

210

215

220

Leu Tyr Val Met Glu Ser Val Glu Tyr Thr Ser Leu Tyr Gly Ile Ser

225

230

235

240

Leu Pro Trp Val Ile Glu Leu Phe Ile Pro Ser Gly Phe Arg Arg Ser

245

250

255

Met Asp Gln Leu Phe Thr Pro Ser Trp Pro Arg Lys Ala Lys Ile Ala

260

265

270

Ile Gly Leu Leu Glu Phe Val Glu Asp Val Phe His Gly Pro Tyr Gly

275

280

285

Asn Phe Leu Met Cys Asp Thr Ser Ala Lys Asn Leu Gly Tyr Asn Asp

290

295

300

Lys Tyr Asp Leu Lys Met Val Asp Met Arg Lys Ile Val Pro Glu Thr

305

310

315

320

Asn Leu Lys Glu Leu Ile Lys Asp Arg His Cys Glu Ser Asp Leu Asp



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|   |     |     |     |
|---|-----|-----|-----|
| 325   | 330 | 335 |     |
| Cys Val Tyr Gly Thr Asp Cys Arg Thr Ser Cys Asp Gln Ser Thr Met |     |     |     |
| 340   | 345 | 350 |     |
| Lys Cys Thr Ser Glu Val Ile Gln Pro Asn Leu Ala Lys Ala Cys Gln |     |     |     |
| 355   | 360 | 365 |     |
| Leu Leu Lys Asp Tyr Leu Leu Arg Gly Ala Pro Ser Glu Ile Arg Glu |     |     |     |
| 370   | 375 | 380 |     |
| Glu Leu Glu Lys Gln Leu Tyr Ser Cys Ile Ala Leu Lys Val Thr Ala |     |     |     |
| 385   | 390 | 395 | 400 |
| Asn Gln Met Glu Met Glu His Ser Leu Ile Leu Asn Asn Leu Lys Thr |     |     |     |
| 405   | 410 | 415 |     |
| Leu Leu Trp Lys Lys Ile Ser Tyr Thr Asn Asp Ser                 |     |     |     |
| 420   | 425 |     |     |

&lt;210&gt; 70

&lt;211&gt; 283

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 70

|  |
|--|
| Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His          |
| 1                      5                      10                      15 |
| Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr          |
| 20                      25                      30                       |
| Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val          |
| 35                      40                      45                       |

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Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys

50

55

60

Ser Leu Ala Glu Glu Leu His His Ile His Ser Arg Tyr Arg Gly Ser

65

70

75

80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly

85

90

95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala

100

105

110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln

115

120

125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile

130

135

140

Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala

145

150

155

160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln

165

170

175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly

180

185

190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val

195

200

205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys

210

215

220

Leu Pro Gln Gln Thr Ala Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr

225

230

235

240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Asn Leu Gln

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|   |     |     |
|---|-----|-----|
| 245   | 250 | 255 |
| Met Thr Ala Ala Ser Arg Cys Pro Arg Arg Phe Ser Gly Thr Cys Gly |     |     |
| 260   | 265 | 270 |
| Arg Arg Lys Arg Lys Arg Leu Leu Trp Ala Ala                     |     |     |
| 275   | 280 |     |

&lt;210&gt; 71

&lt;211&gt; 1167

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 71

```

atggatagag gggagaaaat acagctcaag agagtgtttg gatattggtg gggcacaagt      60
tttttgctta ttaatatcat tgggtgcagga atttttgtgt cccccaaagg tgtgttgga      120
tactcttgca tgaacgtggg agtctccctg tgcgtttggg ctggctgtgc catactggcc      180
atgacatcaa ctctttgctc tgcagagata agtataagct tcccatgcag tggagctcaa      240
tactattttc tcaagagata ctttggtccc acggttgctt tttgaatct ctggacatcc      300
ttgtttctgg ggtcaggggt agttgctggc caagctctgc tccttctga gtacagcatc      360
cagccttttt ttcccagctg ctctgtccca aagctgccta agaaatgtct ggcattggcc      420
atgttggtga ttgtaggaat tctgacttct cgtggtgtga aagaagtga tggccttcag      480
atagctagct cagtgtgaa agtgtccata cttagcttca ttccctaac tggagtagtg      540
ttcctgataa gagggaaaaa ggagaatgta gaacatttc agaatgcttt tgatgtgaa      600
cttcagata tctctcacct tatacaagcc atctccaag gatattttgc atattcaggg      660
gagctgaaga agcccagaac aacaattccc aaatgcata tttactgcgtt acctctggtg      720
actgtagttt atttactggt taacatttcc tatctgactg ttctgacacc cagggaatt      780
ctctcttcag atgctgtagc tatcacatgg gctgatcgag cttttccctc attagcatgg      840

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attatgcctt ttgctatttc tacctcatta tttagcaacc ttctgatttc tatatttaaa 900  
 tcttcgagac caatatatct tgcaagccaa gagggccagc tgcctttgct atttaataca 960  
 cttaatagtc actcttctcc atttacagct gtgctactac ttgtcacttt gggatccctt 1020  
 gcaattatct taacaagtct aattgatttg ataaactata tttttttcac gggttcatta 1080  
 tggctctatat tattaatgat aggaatacta aggcggagat accaggaacc caatctatct 1140  
 ataccttata aggtaaaatt ggatttc 1167

&lt;210&gt; 72

&lt;211&gt; 1044

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

atggcggcga ctctgggacc ccttgggtcg tggcagcagt ggccggcgatg tttgtcggct 60  
 cgggatgggt ccaggatgtt actccttctt cttttgttgg ggtctgggca ggggccacag 120  
 caagtcgggg cggttcaaac gtctgagtac ttgaaacggg agcactcgct gtcgaagccc 180  
 taccagggtg tgggcacagg cagttcctca ctgtggaatc tgatgggcaa tgccatgggtg 240  
 atgacccagt atatccgctt taccacagat atgcaaagta aacagggtgc cttgtggaac 300  
 cgggtgccat gtttctgag agactgggag ttgcagggtgc acttcaaaat ccatggacaa 360  
 ggaaagaaga atctgcatgg ggatggcttg gcaatctggg acacaaagga tcggatgcag 420  
 ccagggcctg tgtttgaaa catggacaaa tttgtggggc tgggagtatt tgtagacacc 480  
 taccccaatg aggagaagca gcaagagcgg gtattccctt acatctcagc catggtgaac 540  
 aacggctccc tcagctatga tcatgagcgg gatgggcggc ctacagagct gggaggctgc 600  
 acagccattg tccgcaatct tcattacgac accttccttg tgattcgcta cgtcaagagg 660  
 catttgacga taatgatgga tattgatggc aagcatgagt ggagggactg cattgaagtg 720  
 cccggagtcc gcctgccccg cggtactactac ttccgcacct cctccatcac tggggatctc 780

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|  |      |
|--|------|
| tcagataatc atgatgtcat ttccttgaag ttgtttgaac tgacagtgga gagaacccca  | 840  |
| gaagaggaaa agctccatcg agatgtgttc ttgccctcag tggacaatat gaagctgcct  | 900  |
| gagatgacag ctccactgcc gccctgagt ggcctggccc tcttccatcat cgtctttttc  | 960  |
| tccctgggtgt tttctgtatt tgccatagtc attggtatca tactctacaa caaatggcag | 1020 |
| gaacagagcc gaaagcgctt ctac   | 1044 |

&lt;210&gt; 73

&lt;211&gt; 783

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

|   |     |
|---|-----|
| atggaactgc ttcaagtgc cattcttttt cttctgccc gtatttgag cagtaacagc      | 60  |
| acagggtgtt tagaggcagc taataattca cttgttgta ctacaacaaa accatctata    | 120 |
| acaacaccaa acacagaatc attacagaaa aatgttgtca caccaacaac tggaacaact   | 180 |
| cctaaaggaa caatcaccaa tgaattactt aaaatgtctc tgatgtcaac agctactttt   | 240 |
| ttaacaagta aagatgaagg attgaaagcc acaaccactg atgtcaggaa gaatgactcc   | 300 |
| atcatttcaa acgtaacagt aacaagtgtt acacttccaa atgctgtttc aacattacaa   | 360 |
| agttccaaac ccaagactga aactcagagt tcaattaaaa caacagaaat accaggtagt   | 420 |
| gttctacaac cagatgcac accttctaaa actggtacat taacctcaat accagttaca    | 480 |
| attccagaaa acacctcaca gtctcaagta ataggcactg aggggtggaaa aatgcaagc   | 540 |
| acttcagcaa ccagccggtc ttattccagt attattttgc cgggtggttat tgctttgatt  | 600 |
| gtaataacac tttcagtatt tgttctgggtg gggttggtacc gaatgtgctg gaaggcagat | 660 |
| ccgggcacac cagaaaatgg aatgatcaa cctcagctctg ataaagagag cgtgaagctt   | 720 |
| cttaccgtta agacaatttc tcatgagtct ggtgagcact ctgcacaagg aaaaaccaag   | 780 |
| aac   | 783 |

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&lt;210&gt; 74

&lt;211&gt; 666

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 74

```
atgttggtggc tgctcttttt tctggtgact gccattcatg ctgaactctg tcaaccaggt. 60
gcagaaaatg cttttaaaagt gagacttagt atcagaacag ctctgggaga taaagcatat 120
gcctgggata ccaatgaaga atacctcttc aaagcgatgg tagctttctc catgagaaaa 180
gttcccaaca gagaagcaac agaaatttcc catgtcctac ttgcaatgt aaccagagg 240
gtatcattct ggtttggtgt tacagaccct tcaaaaaatc acacccttcc tgctgttgag 300
gtgcaatcag ccataagaat gaacaagaac cggatcaaca atgccttctt tctaaatgac 360
caaactctgg aatttttaaa aatcccttcc acacttgac caccatgga cccatctgtg 420
cccatctgga ttattatatt tgggtgata ttttgcata tcatagttgc aattgcacta 480
ctgattttat cagggatctg gcaacgtaga agaaagaaca aagaaccatc tgaagtggat 540
gacgctgaag ataagtgtga aaacatgatc acaattgaaa atggcatccc ctctgatccc 600
ctggacatga agggagggca tattaatgat gccttcatga cagaggatga gaggtcacc 660
cctctc 666
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&lt;210&gt; 75

&lt;211&gt; 549

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 75

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atgggagtcc gagttcatgt cgtggcggcc tcagccctgc tgtatttcat cctgctttct 60
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gggacgagat gtgaggaaaa ctgtggtaat cctgaacatt gcctgaccac agactgggta 120  
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 gctcttcaca tgagtcgctt cacagtagcc atgtgcgggc agaaagcacc tgatctaccc 480  
 ccagtacctg aagaaaagca gctgcctcca acagagaagg agtcgactcg aatagttgac 540  
 tcttggaaac 549

&lt;210&gt; 76

&lt;211&gt; 786

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 76

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 tctttttgtt cctgtgtgcc ttgtgaagga actgctgatg ccagcttcgt gacttgtecc 180  
 acctgccagg gcagtggcaa gattccccaa gagctggaga agcagttggt ggctctcatt 240  
 ccctatgggg accagaggct gaagcccaag cacacgaagc tctttgtgtt cctggccgtg 300  
 ctcatctgcc tggtgacctc ctcttcacg gtctttttcc tgtttccccg gtccgtcatt 360  
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 aacataacga atatcttaaa catctccaat ggcaactact accccattat ggtgacacag 480  
 ctgaccctcg aggttctgca cctgtccctc gtggtggggc aggtttccaa caaccttctc 540  
 ctacacattg gccctttggc cagtgaacag atgttttacg cagtagctac caagatacgg 600

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gatgaaaaca catacaaaat ctgtacctgg ctggaaatca aagtccacca tgtgcttttg 660  
cacatccagg gcacctgac ctgttcatac ctgagccatt cagagcagct ggtctttcag 720  
agctatgaat atgtggactg ccgaggaaac gcattctgtgc cccaccagct gacccctcac 780  
ccacca 786

&lt;210&gt; 77

&lt;211&gt; 504

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 77

atgggcgtcc ccacggccct ggaggccggc agctggcgt ggggatccct gctcttctgct 60  
ctcttctctgg ctgcgtccct aggcaaagat gcaccatcca actgtgtggt gtacccatcc 120  
tcctcccagg agagtgaata catcacggct gcagccctgg ctacgggtgc ctgcatcgta 180  
ggaatcctct gcctcccct catcctgtct ctggtctaca agcaaaggca ggcagcctcc 240  
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ggctttgaag cctcaccacc tgcccagggg atacccgagg ccaaagtcag gcaccccctg 360  
tcctatgtgg cccagcggca gccttctgag tctggcggc atctgctttc ggagcccagc 420  
acccccctgt ctctccagg ccccgagac gtcttcttcc catcctgga ccctgtccct 480  
gactctccaa actttgaggt catc 504

&lt;210&gt; 78

&lt;211&gt; 729

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 78



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 cagcagagaa gtctgcgtga ggaccaacag agctttacgg ggtcccggac ctactccttg 180  
 gtccggcagg catggccagg acccctggcg gacatggcac ccacaaggaa ggacaagctg 240  
 ttgcaattct accccagcct ggaggatcca gcatcttcca ggtaccagaa cttcagcaaa 300  
 ggaagcagac acgggtcggg ggaagcctac atagacccca ttgccatgga gtattacaac 360  
 tgggggcggg tctcgaagcc cccagaagat gatgatgcca attcctacga gaatgtgctc 420  
 atttgcaagc agaaaaccac agagacaggt gccagcagg agggcatagg tggcctctgc 480  
 agaggggacc tcagcctgtc actggccctg aagactggcc ccacttctgg tctctgtccc 540  
 tctgcctccc cggaagaaga tgaggaatct gaggattatc agaactcagc atccatccat 600  
 cagtggcgcg agtccaggaa ggtcatgggg caactccaga gagaagcatc ccctggcccg 660  
 gtgggaagcc cagacgagga ggacggggaa ccggattacg tgaatgggga ggtggcagcc 720  
 acagaagcc 729

&lt;210&gt; 79

&lt;211&gt; 1284

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 79

atggcgagga gtctctgtcc gggggcctgg ctaaggaaac cctattacct ccaggctcgc 60  
 ttctcatatg tgcggatgaa atatcttttc ttttctgggt tagtggtttt tggttgaagc 120  
 tggattatat atgtgcagta ttctacctat acagaattat gcagaggaaa ggactgtaag 180  
 aaaataatat gtgacaagta caagactgga gttattgatg ggcctgcatg taacagcctt 240  
 tgtgttacag aaactcttta ctttggaaaa tgtttatcca ccaagcccaa caatcagatg 300  
 tatttaggga tttgggataa tctaccaggt gttgtgaaat gtcaaatgga acaagcgctt 360

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catcttgatt ttggaactga attggaacca agaaaagaaa tagtgctatt tgataagcca 420  
actagaggaa ctactgtaca aaaatttaaa gaaatggctct atagtctctt taaggcaaaa 480  
ttgggtgacc aaggaaacct ctctgaactg gttaatctca tcttgacggt ggctgatgga 540  
gacaaagatg gccaggtttc cttgggagaa gcaaagtcgg catgggcact tcttcaactg 600  
aatgaatttc ttctcatggt gatacttcaa gataaagaac ataccccaa attaatggga 660  
ttctgtggtg acctctatgt gatggaaagt gttgaatata cctctcttta tggaataagc 720  
cttccttggg tcattgaact tttattcca tctgggttca gaagaagcat ggatcagctg 780  
ttcacaccat catggccaag aaaggccaaa atagccatag gacttctaga atttgtggaa 840  
gatgttttcc atggccccta cggaaatttc ctcatgtgcg atactagtgc caaaaaccta 900  
ggatataatg ataagtatga tttgaaaatg gtggatatga gaaaaattgt gccagagaca 960  
aacctgaaag aacttattaa ggatcgtcac tgtgagtctg atttggactg tgtctatggc 1020  
acagattgta gaactagctg tgatcagagt acaatgaagt gtacttcaga agtgatacaa 1080  
ccaaacttgg caaaagcttg tcagttactc aaagactacc tactgctgg tgctccaagt 1140  
gaaattcgtg agaattaga aaagcagctt tattcttgta ttgctctcaa agtcacagca 1200  
aatcaaattg aatggaaca ttctttgata ctaaataacc taaaaacatt attgtggaag 1260  
aaaatttcct acactaatga ctct 1284

&lt;210&gt; 80

&lt;211&gt; 849

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 80

atgccccact ccagcctgca tccatccatc ccgtgtccca ggggtcacgg ggcccagaag 60  
gcagccttgg ttctgctgag tgcctgcctg gtgacccttt gggggctagg agagccacca 120  
gagcacactc tccgtacct ggtgctccac ctagcctccc tgcagctggg actgctgtta 180

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```

aacggggtct gcagcctggc tgaggagctg caccacatcc actccaggta ccggggcagc 240
tactggagga ctgtgcgggc ctgcctgggc tgccccctcc gccgtggggc cctgttgctg 300
ctgtccatct atttctacta ctcctccca aatgcggtcg gcccgccctt cacttggatg 360
cttgccctcc tgggcctctc gcaggcactg aacatcctcc tgggcctcaa gggcctggcc 420
ccagctgaga tctctgcagt gtgtgaaaaa gggaatttca acgtggccca tgggctggca 480
tggtcatatt acatcggata tctgcggtg atcctgccag agctccaggc ccggattcga 540
acttacaatc agcattacaa caacctgcta cggggtgcag tgagccagcg gctgtatatt 600
ctcctcccat tggactgtgg ggtgcctgat aacctgagta tggctgacct caacattcgc 660
ttcctggata aactgcccc aagaccgct gaccgtgctg gcatcaagga tcgggtttac 720
agcaacagca tctatgagct tctggagaac gggcagcgga acctgcagat gacagcagct 780
tctcgtgtc ccaggagggt ctcgggcacc tgcggcagga ggaaaaggaa gaggttactg 840
tgggcagct 849

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&lt;210&gt; 81

&lt;211&gt; 1376

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (100)... (1269)

&lt;400&gt; 81

```

atTTTTatTT caggaatcca tcaacatcct ttgcagctac ataggcagga aaatctagaa 60
attgtaattt atatagaatt ttaaaactct tcaattaca atg gat aga ggg gag 114

```

Met Asp Arg Gly Glu

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|   |     |
|---|-----|
| aaa ata cag ctc aag aga gtg ttt gga tat tgg tgg ggc aca agt ttt | 162 |
| Lys Ile Gln Leu Lys Arg Val Phe Gly Tyr Trp Trp Gly Thr Ser Phe |     |
| 10 15 20  |     |
| ttg ctt att aat atc att ggt gca gga att ttt gtg tcc ccc aaa ggt | 210 |
| Leu Leu Ile Asn Ile Ile Gly Ala Gly Ile Phe Val Ser Pro Lys Gly |     |
| 25 30 35  |     |
| gtg ttg gca tac tct tgc atg aac gtg gga gtc tcc ctg tgc gtt tgg | 258 |
| Val Leu Ala Tyr Ser Cys Met Asn Val Gly Val Ser Leu Cys Val Trp |     |
| 40 45 50  |     |
| gct ggc tgt gcc ata ctg gcc atg aca tca act ctt tgc tct gca gag | 306 |
| Ala Gly Cys Ala Ile Leu Ala Met Thr Ser Thr Leu Cys Ser Ala Glu |     |
| 55 60 65  |     |
| ata agt ata agc ttc cca tgc agt gga gct caa tac tat ttt ctc aag | 354 |
| Ile Ser Ile Ser Phe Pro Cys Ser Gly Ala Gln Tyr Tyr Phe Leu Lys |     |
| 70 75 80 85   |     |
| aga tac ttt ggc tcc acg gtt gct ttt ttg aat ctc tgg aca tcc ttg | 402 |
| Arg Tyr Phe Gly Ser Thr Val Ala Phe Leu Asn Leu Trp Thr Ser Leu |     |
| 90 95 100   |     |
| ttt ctg ggg tca ggg gta gtt gct ggc caa gct ctg ctc ctt gct gag | 450 |
| Phe Leu Gly Ser Gly Val Val Ala Gly Gln Ala Leu Leu Leu Ala Glu |     |
| 105 110 115   |     |
| tac agc atc cag cct ttt ttt ccc agc tgc tct gtc cca aag ctg cct | 498 |
| Tyr Ser Ile Gln Pro Phe Phe Pro Ser Cys Ser Val Pro Lys Leu Pro |     |
| 120 125 130   |     |
| aag aaa tgt ctg gca ttg gcc atg ttg tgg att gta gga att ctg act | 546 |

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Lys Lys Cys Leu Ala Leu Ala Met Leu Trp Ile Val Gly Ile Leu Thr  
 135 140 145  
 tct cgt ggt gtg aaa gaa gtg act tgg ctt cag ata gct agc tca gtg 594  
 Ser Arg Gly Val Lys Glu Val Thr Trp Leu Gln Ile Ala Ser Ser Val  
 150 155 160 165  
 ctg aaa gtg tcc ata ctt agc ttc att tcc cta act gga gta gtg ttc 642  
 Leu Lys Val Ser Ile Leu Ser Phe Ile Ser Leu Thr Gly Val Val Phe  
 170 175 180  
 ctg ata aga ggg aaa aag gag aat gta gaa cga ttt cag aat gct ttt 690  
 Leu Ile Arg Gly Lys Lys Glu Asn Val Glu Arg Phe Gln Asn Ala Phe  
 185 190 195  
 gat gct gaa ctt cca gat atc tct cac ctt ata caa gcc atc ttc caa 738  
 Asp Ala Glu Leu Pro Asp Ile Ser His Leu Ile Gln Ala Ile Phe Gln  
 200 205 210  
 gga tat ttt gca tat tca ggg gag ctg aag aag ccc aga aca aca att 786  
 Gly Tyr Phe Ala Tyr Ser Gly Glu Leu Lys Lys Pro Arg Thr Thr Ile  
 215 220 225  
 ccc aaa tgc ata ttt act gcg tta cct ctg gtg act gta gtt tat tta 834  
 Pro Lys Cys Ile Phe Thr Ala Leu Pro Leu Val Thr Val Val Tyr Leu  
 230 235 240 245  
 ctg gtt aac att tcc tat ctg act gtt ctg aca ccc agg gaa att ctc 882  
 Leu Val Asn Ile Ser Tyr Leu Thr Val Leu Thr Pro Arg Glu Ile Leu  
 250 255 260  
 tct tca gat gct gta gct atc aca tgg gct gat cga gct ttt ccc tca 930  
 Ser Ser Asp Ala Val Ala Ile Thr Trp Ala Asp Arg Ala Phe Pro Ser

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|   |     |     |      |
|---|-----|-----|------|
| 265   | 270 | 275 |      |
| tta gca tgg att atg cct ttt gct att tct acc tca tta ttt agc aac |     |     | 978  |
| Leu Ala Trp Ile Met Pro Phe Ala Ile Ser Thr Ser Leu Phe Ser Asn |     |     |      |
| 280   | 285 | 290 |      |
| ctt ctg att tct ata ttt aaa tct tcg aga cca ata tat ctt gca agc |     |     | 1026 |
| Leu Leu Ile Ser Ile Phe Lys Ser Ser Arg Pro Ile Tyr Leu Ala Ser |     |     |      |
| 295   | 300 | 305 |      |
| caa gag ggc cag ctg cct ttg cta ttt aat aca ctt aat agt cac tct |     |     | 1074 |
| Gln Glu Gly Gln Leu Pro Leu Leu Phe Asn Thr Leu Asn Ser His Ser |     |     |      |
| 310   | 315 | 320 | 325  |
| tct cca ttt aca gct gtg cta cta ctt gtc act ttg gga tcc ctt gca |     |     | 1122 |
| Ser Pro Phe Thr Ala Val Leu Leu Leu Val Thr Leu Gly Ser Leu Ala |     |     |      |
| 330   | 335 | 340 |      |
| att atc tta aca agt cta att gat ttg ata aac tat att ttt ttc acg |     |     | 1170 |
| Ile Ile Leu Thr Ser Leu Ile Asp Leu Ile Asn Tyr Ile Phe Phe Thr |     |     |      |
| 345   | 350 | 355 |      |
| ggt tca tta tgg tct ata tta tta atg ata gga ata cta agg cgg aga |     |     | 1218 |
| Gly Ser Leu Trp Ser Ile Leu Leu Met Ile Gly Ile Leu Arg Arg Arg |     |     |      |
| 360   | 365 | 370 |      |
| tac cag gaa ccc aat cta tct ata cct tat aag gta aaa ttg gat ttc |     |     | 1266 |
| Tyr Gln Glu Pro Asn Leu Ser Ile Pro Tyr Lys Val Lys Leu Asp Phe |     |     |      |
| 375   | 380 | 385 |      |
| taat tcttttctgt gtgaaataac agatattgag tataactgta tttaagatta     |     |     | 1320 |
| taatcagagc atctataagt agatcttctg aatctcagt tactgtgaaa cacatg    |     |     | 1376 |

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&lt;210&gt; 82

&lt;211&gt; 2392

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (22)... (1068)

&lt;400&gt; 82

```

gaagggtcgt tgggtgggaaa g atg gcg gcg act ctg gga ccc ctt ggg tcg      51
                               Met Ala Ala Thr Leu Gly Pro Leu Gly Ser
                               1           5           10

tgg cag cag tgg cgg cga tgt ttg tcg gct cgg gat ggg tcc agg atg      99
Trp Gln Gln Trp Arg Arg Cys Leu Ser Ala Arg Asp Gly Ser Arg Met
                               15           20           25

tta ctc ctt ctt ctt ttg ttg ggg tct ggg cag ggg cca cag caa gtc      147
Leu Leu Leu Leu Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln Val
                               30           35           40

ggg gcg ggt caa acg ttc gag tac ttg aaa cgg gag cac tcg ctg tcg      195
Gly Ala Gly Gln Thr Phe Glu Tyr Leu Lys Arg Glu His Ser Leu Ser
                               45           50           55

aag ccc tac cag ggt gtg ggc aca ggc agt tcc tca ctg tgg aat ctg      243
Lys Pro Tyr Gln Gly Val Gly Thr Gly Ser Ser Ser Leu Trp Asn Leu
                               60           65           70

atg ggc aat gcc atg gtg atg acc cag tat atc cgc ctt acc cca gat      291
Met Gly Asn Ala Met Val Met Thr Gln Tyr Ile Arg Leu Thr Pro Asp

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|   |     |     |     |     |
|---|-----|-----|-----|-----|
| 75  | 80  | 85  | 90  |     |
| atg caa agt aaa cag ggt gcc ttg tgg aac cgg gtg cca tgt ttc ctg |     |     |     | 339 |
| Met Gln Ser Lys Gln Gly Ala Leu Trp Asn Arg Val Pro Cys Phe Leu |     |     |     |     |
|   | 95  | 100 | 105 |     |
| aga gac tgg gag ttg cag gtg cac ttc aaa atc cat gga caa gga aag |     |     |     | 387 |
| Arg Asp Trp Glu Leu Gln Val His Phe Lys Ile His Gly Gln Gly Lys |     |     |     |     |
|   | 110 | 115 | 120 |     |
| aag aat ctg cat ggg gat ggc ttg gca atc tgg tac aca aag gat cgg |     |     |     | 435 |
| Lys Asn Leu His Gly Asp Gly Leu Ala Ile Trp Tyr Thr Lys Asp Arg |     |     |     |     |
|   | 125 | 130 | 135 |     |
| atg cag cca ggg cct gtg ttt gga aac atg gac aaa ttt gtg ggg ctg |     |     |     | 483 |
| Met Gln Pro Gly Pro Val Phe Gly Asn Met Asp Lys Phe Val Gly Leu |     |     |     |     |
|   | 140 | 145 | 150 |     |
| gga gta ttt gta gac acc tac ccc aat gag gag aag cag caa gag cgg |     |     |     | 531 |
| Gly Val Phe Val Asp Thr Tyr Pro Asn Glu Glu Lys Gln Gln Glu Arg |     |     |     |     |
|   | 155 | 160 | 165 | 170 |
| gta ttc ccc tac atc tca gcc atg gtg aac aac ggc tcc ctc agc tat |     |     |     | 579 |
| Val Phe Pro Tyr Ile Ser Ala Met Val Asn Asn Gly Ser Leu Ser Tyr |     |     |     |     |
|   | 175 | 180 | 185 |     |
| gat cat gag cgg gat ggg cgg cct aca gag ctg gga ggc tgc aca gcc |     |     |     | 627 |
| Asp His Glu Arg Asp Gly Arg Pro Thr Glu Leu Gly Gly Cys Thr Ala |     |     |     |     |
|   | 190 | 195 | 200 |     |
| att gtc cgc aat ctt cat tac gac acc ttc ctg gtg att cgc tac gtc |     |     |     | 675 |
| Ile Val Arg Asn Leu His Tyr Asp Thr Phe Leu Val Ile Arg Tyr Val |     |     |     |     |
|   | 205 | 210 | 215 |     |



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|   |      |
|---|------|
| aag agg cat ttg acg ata atg atg gat att gat ggc aag cat gag tgg | 723  |
| Lys Arg His Leu Thr Ile Met Met Asp Ile Asp Gly Lys His Glu Trp |      |
| 220 225 230   |      |
| agg gac tgc att gaa gtg ccc gga gtc cgc ctg ccc cgc ggc tac tac | 771  |
| Arg Asp Cys Ile Glu Val Pro Gly Val Arg Leu Pro Arg Glv Tyr Tyr |      |
| 235 240 245 250   |      |
| ttc ggc acc tcc tcc atc act ggg gat ctc tca gat aat cat gat gtc | 819  |
| Phe Gly Thr Ser Ser Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val |      |
| 255 260 265   |      |
| att tcc ttg aag ttg ttt gaa ctg aca gtg gag aga acc cca gaa gag | 867  |
| Ile Ser Leu Lys Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu |      |
| 270 275 280   |      |
| gaa aag ctc cat cga gat gtg ttc ttg ccc tca gtg gac aat atg aag | 915  |
| Glu Lys Leu His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys |      |
| 285 290 295   |      |
| ctg cct gag atg aca gct cca ctg ccg ccc ctg agt ggc ctg gcc ctc | 963  |
| Leu Pro Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu |      |
| 300 305 310   |      |
| ttc ctc atc gtc ttt ttc tcc ctg gtg ttt tct gta ttt gcc ata gtc | 1011 |
| Phe Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val |      |
| 315 320 325 330   |      |
| att ggt atc ata ctc tac aac aaa tgg cag gaa cag agc cga aag cgc | 1059 |
| Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys Arg |      |
| 335 340 345   |      |
| ttc tac tgagc cctcctgctg ccaccacttt tgtgactgtc acccatgagg       | 1110 |

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Phe Tyr

|  |      |
|--|------|
| tatggaagga gcaggcactg gcctgagcat gcagcctgga gagggttctt gtctctagca  | 1170 |
| gctggttggg gactatattc tgtcactgga gttttgaatg cagggaacccc gcattcccat | 1230 |
| ggttgtgcat ggggacatct aactctggtc tgggaagcca cccaccccag ggcaatgctg  | 1290 |
| ctgtgatgtg cttttccctg cagtccttcc atgtgggagc agagggtgtga agagaattta | 1350 |
| cgtggttgtg atgccaaaat cacagaacag aatttcatag ccagggtgc cgtgttggtt   | 1410 |
| gactcagaag gcccttctac tttagtttg aatccacaaa gaattaaaaa ctggtaacac   | 1470 |
| cacaggcttt ctgaccatcc attcgttggg ttttgcatth gaccaaccc tctgcctacc   | 1530 |
| tgaggagctt tctttggaaa ccaggatgga aacttcttcc ctgccttacc ttcctttcac  | 1590 |
| tccattcatt gtctctctg tgtgcaacct gagctgggaa aggcatttgg atgcctctct   | 1650 |
| gttggggcct ggggctgcag aacacacctg cgtttcactg gccttcatta ggtggcccta  | 1710 |
| gggagatggc tttctgcttt ggatcactgt tccctagcat gggctcttggg tctattggca | 1770 |
| tgtccatggc cttcccaatc aagtctcttc aggcctcag tgaagtttgg ctaaaggttg   | 1830 |
| gtgtaaaaat caagagaagc ctggaagaca tcatggatgc catggattag ctgtgcaact  | 1890 |
| gaccagctcc aggtttgatc aaaccaaag caacatttgt catgttgtct gaccatgtgg   | 1950 |
| agatgtttct ggacttgcta gagcctgctt agctgcatgt tttgtagtta cgatttttgg  | 2010 |
| aatcccactt tgagtgtga aagtgttaagg aagctttctt cttacacctt gggcttggat  | 2070 |
| attgccaga gaagaaattt ggcttttttt ttcttaatgg acaagagaca gttgctgttc   | 2130 |
| tcatgttcca agtctgagag caacagaccc tcatcatctg tgccctggaag agttcactgt | 2190 |
| cattgagcag cacagcctga gtgctggcct ctgtcaaccc ttattccact gccttatttg  | 2250 |
| acaaggggtt acatgtctgt caccttactg ccttgggatt aaatcagtta caggccagag  | 2310 |
| tctccttga gggcctggaa ctctgagtcc tccatgaac ctctgtagcc taaatgaaat    | 2370 |
| tcttaaaatc accgatggaa .cc  | 2392 |

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&lt;211&gt; 1416

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (55)... (840)

&lt;400&gt; 83

attgtccctg cctgcttctg gagaaagaag atattgacac catctacggg cacc atg 57

Met

1

gaa ctg ctt caa gtg acc att ctt ttt ctt ctg ccc agt att tgc agc 105

Glu Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys Ser

5

10

15

agt aac agc aca ggt gtt tta gag gca gct aat aat tca ctt gtt gtt 153

Ser Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val Val

20

25

30

act aca aca aaa cca tct ata aca aca cca aac aca gaa tca tta cag 201

Thr Thr Thr Lys Pro Ser Ile Thr Thr Pro Asn Thr Glu Ser Leu Gln

35

40

45

aaa aat gtt gtc aca cca aca act gga aca act cct aaa gga aca atc 249

Lys Asn Val Val Thr Pro Thr Thr Gly Thr Thr Pro Lys Gly Thr Ile

50

55

60

65

acc aat gaa tta ctt aaa atg tct ctg atg tca aca gct act ttt tta 297

Thr Asn Glu Leu Leu Lys Met Ser Leu Met Ser Thr Ala Thr Phe Leu

70

75

80

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|   |     |
|---|-----|
| aca agt aaa gat gaa gga ttg aaa gcc aca acc act gat gtc agg aag | 345 |
| Thr Ser Lys Asp Glu Gly Leu Lys Ala Thr Thr Thr Asp Val Arg Lys |     |
| 85 90 95  |     |
| aat gac tcc atc att tca aac gta aca gta aca agt gtt aca ctt cca | 393 |
| Asn Asp Ser Ile Ile Ser Asn Val Thr Val Thr Ser Val Thr Leu Pro |     |
| 100 105 110   |     |
| aat gct gtt tca aca tta caa agt tcc aaa ccc aag act gaa act cag | 441 |
| Asn Ala Val Ser Thr Leu Gln Ser Ser Lys Pro Lys Thr Glu Thr Gln |     |
| 115 120 125   |     |
| agt tca att aaa aca aca gaa ata cca ggt agt gtt cta caa cca gat | 489 |
| Ser Ser Ile Lys Thr Thr Glu Ile Pro Gly Ser Val Leu Gln Pro Asp |     |
| 130 135 140 145   |     |
| gca tca cct tct aaa act ggt aca tta acc tca ata cca gtt aca att | 537 |
| Ala Ser Pro Ser Lys Thr Gly Thr Leu Thr Ser Ile Pro Val Thr Ile |     |
| 150 155 160   |     |
| cca gaa aac acc tca cag tct caa gta ata ggc act gag ggt gga aaa | 585 |
| Pro Glu Asn Thr Ser Gln Ser Gln Val Ile Gly Thr Glu Gly Gly Lys |     |
| 165 170 175   |     |
| aat gca agc act tca gca acc agc cgg tct tat tcc agt att att ttg | 633 |
| Asn Ala Ser Thr Ser Ala Thr Ser Arg Ser Tyr Ser Ser Ile Ile Leu |     |
| 180 185 190   |     |
| ccg gtg gtt att gct ttg att gta ata aca ctt tca gta ttt gtt ctg | 681 |
| Pro Val Val Ile Ala Leu Ile Val Ile Thr Leu Ser Val Phe Val Leu |     |
| 195 200 205   |     |
| gtg ggt ttg tac cga atg tgc tgg aag gca gat ccg ggc aca cca gaa | 729 |

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Val Gly Leu Tyr Arg Met Cys Trp Lys Ala Asp Pro Gly Thr Pro Glu  
 210                      215                      220                      225  
 aat gga aat gat caa cct cag tct gat aaa gag agc gtg aag ctt ctt      777  
 Asn Gly Asn Asp Gln Pro Gln Ser Asp Lys Glu Ser Val Lys Leu Leu  
                          230                      235                      240  
 acc gtt aag aca att tct cat gag tct ggt gag cac tct gca caa gga      825  
 Thr Val Lys Thr Ile Ser His Glu Ser Gly Glu His Ser Ala Gln Gly  
                          245                      250                      255  
 aaa acc aag aac tga cagcttgagg aattctctcc acacctaggc aataattacg      880  
 Lys Thr Lys Asn  
                          260  
 cttaatcttc agcttctatg caccaagcgt ggaaaaggag aaagtcctgc agaatcaatc      940  
 ccgacttcca taccigctgc tggactgtac cagacgtctg tcccagtaaa gtgatgtcca      1000  
 gctgacatgc aataatttga tggaatcaaa aagaaccccg gggctctcct gttctctcac      1060  
 atttaaaaat tccattactc catttacagg agcgttccta ggaaaaggaa ttttaggagg      1120  
 agaatttgtg agcagtgaat ctgacagccc aggaggtggg ctgctgata ggcattgactt      1180  
 tccttaatgt ttaaagtttt ccgggccaag aatttttata catgaagact ttctactttt      1240  
 tctcggtgtt cttatattac ctactgttag tatttattgt ttaccactat gttaatgcag      1300  
 ggaaaagttg cacgtgtatt attaaatatt aggtagaaat cataccatgc tactttgtac      1360  
 atataagtat tttattcctg ctttcgtgtt acttttaata aataactact gtactc      1416

&lt;210&gt; 84

&lt;211&gt; 1347

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (26)... (694)

&lt;400&gt; 84

gccttggtt ttccacctg aaaga atg ttg tgg ctg ctc ttt ttt ctg gtg 52

Met Leu Trp Leu Leu Phe Phe Leu Val

1

5

act gcc att cat gct gaa ctc tgt caa cca ggt gca gaa aat gct ttt 100

Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn Ala Phe

10

15

20

25

aaa gtg aga ctt agt atc aga aca gct ctg gga gat aaa gca tat gcc 148

Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala Tyr Ala

30

35

40

tgg gat acc aat gaa gaa tac ctc ttc aaa gcg atg gta gct ttc tcc 196

Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala Phe Ser

45

50

55

atg aga aaa gtt ccc aac aga gaa gca aca gaa att tcc cat gtc cta 244

Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His Val Leu

60

65

70

ctt tgc aat gta acc cag agg gta tca ttc tgg ttt gtg gtt aca gac 292

Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val Thr Asp

75

80

85

cct tca aaa aat cac acc ctt cct gct gtt gag gtg caa tca gcc ata 340

Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser Ala Ile

90

95

100

105

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aga atg aac aag aac cgg atc aac aat gcc ttc ttt cta aat gac caa 388  
 Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp Gln  
 110 115 120  
 act ctg gaa ttt tta aaa atc cct tcc aca ctt gca cca ccc atg gac 436  
 Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro Met Asp  
 125 130 135  
 cca tct gtg ccc atc tgg att att ata ttt ggt gtg ata ttt tgc atc 484  
 Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe Cys Ile  
 140 145 150  
 atc ata gtt gca att gca cta ctg att tta tca ggg atc tgg caa cgt 532  
 Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp Gln Arg  
 155 160 165  
 aga aga aag aac aaa gaa cca tct gaa gtg gat gac gct gaa gat aag 580  
 Arg Arg Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu Asp Lys  
 170 175 180 185  
 tgt gaa aac atg atc aca att gaa aat ggc atc ccc tct gat ccc ctg 628  
 Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp Pro Leu  
 190 195 200  
 gac atg aag gga ggg cat att aat gat gcc ttc atg aca gag gat gag 676  
 Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu Asp Glu  
 205 210 215  
 agg ctc acc cct ctc tgaagggt gttgttctgc ttcctcaaga aattaaacat 730  
 Arg Leu Thr Pro Leu  
 220  
 ttgtttctgt gtgactgctg agcatcctga aataccaaga gcagatcata tattttgttt 790

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caccattctt cttttgtaat aaattttgaa tgtgcttgaa agtgaaaagc aatcaattat 850  
 acccaccaac accactgaaa tcataagcta ttcacgactc aaaatattct aaaatatttt 910  
 tctgacagta tagtgtataa atgtggtcac gtggtatttg tagttattga ttttaagcatt 970  
 ttttagaaata agatcaggca tatgtatata ttttcacact tcaaagacct aaggaaaaat 1030  
 aaattttcca gtggagaata catataatat ggtgtagaaa tcattgaaaa tggatccttt 1090  
 ttgacgatca cttatatcac tctgtatatg actaagtaaa caaaagtgag aagtaattat 1150  
 tgtaaattgga tggataaaaa tggaattact catatacagg gtggaatttt atcctgttat 1210  
 cacaccaaca gttgattata tattttctga atatcagccc ctaataggac aattctattt 1270  
 gttgaccatt tctacaattt gtaaaagtcc aatctgtgct aacttaataa agtaataatc 1330  
 atctcttttt gattgtg 1347

&lt;210&gt; 85

&lt;211&gt; 2284

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (75)... (626)

&lt;400&gt; 85

aaaatggcac agagcattga aaggaggcaa cggatgccca gtgcaagatt ctgaagaagc 60  
 aggaattcag cccg atg gga gtc cga gtt cat gtc gtg gcg gcc tca gcc 110

Met Gly Val Arg Val His Val Val Ala Ala Ser Ala

1

5

10

ctg ctg tat ttc atc ctg ctt tct ggg acc aga tgt gag gaa aac tgt 158  
 Leu Leu Tyr Phe Ile Leu Leu Ser Gly Thr Arg Cys Glu Glu Asn Cys



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|   |     |     |     |
|---|-----|-----|-----|
| 15  | 20  | 25  |     |
| ggt aat cct gaa cat tgc ctg acc aca gac tgg gta cat ctc tgg tat |     |     | 206 |
| Gly Asn Pro Glu His Cys Leu Thr Thr Asp Trp Val His Leu Trp Tyr |     |     |     |
| 30  | 35  | 40  |     |
| ata tgg ttg cta gtg gta att ggc gcg ctg ctt ctc ctg tgt ggc ctg |     |     | 254 |
| Ile Trp Leu Leu Val Val Ile Gly Ala Leu Leu Leu Leu Cys Gly Leu |     |     |     |
| 45  | 50  | 55  | 60  |
| acg tcc ctg tgc ttc cgc tgc tgc tgt ctg agc cgc cag caa aat ggg |     |     | 302 |
| Thr Ser Leu Cys Phe Arg Cys Cys Cys Leu Ser Arg Gln Gln Asn Gly |     |     |     |
| 65  | 70  | 75  |     |
| gaa gat ggg ggc cca cca ccc tgt gaa gtg acc gtc att gct ttc gat |     |     | 350 |
| Glu Asp Gly Gly Pro Pro Pro Cys Glu Val Thr Val Ile Ala Phe Asp |     |     |     |
| 80  | 85  | 90  |     |
| cac gac agc act ctc cag agc act atc aca tct ctg cag tcg gtg ttt |     |     | 398 |
| His Asp Ser Thr Leu Gln Ser Thr Ile Thr Ser Leu Gln Ser Val Phe |     |     |     |
| 95  | 100 | 105 |     |
| ggc cct gca gct cgg agg atc ctg gct gtg gct cac tcc cac agc tcc |     |     | 446 |
| Gly Pro Ala Ala Arg Arg Ile Leu Ala Val Ala His Ser His Ser Ser |     |     |     |
| 110   | 115 | 120 |     |
| ctg ggc cag ctg ccc tcc tct ttg gac acc ctc cca ggg tat gaa gaa |     |     | 494 |
| Leu Gly Gln Leu Pro Ser Ser Leu Asp Thr Leu Pro Gly Tyr Glu Glu |     |     |     |
| 125   | 130 | 135 | 140 |
| gct ctt cac atg agt cgc ttc aca gta gcc atg tgc ggg cag aaa gca |     |     | 542 |
| Ala Leu His Met Ser Arg Phe Thr Val Ala Met Cys Gly Gln Lys Ala |     |     |     |
| 145   | 150 | 155 |     |

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cct gat cta ccc cca gta cct gaa gaa aag cag ctg cct cca aca gag 590  
 Pro Asp Leu Pro Pro Val Pro Glu Glu Lys Gln Leu Pro Pro Thr Glu  
 160 165 170  
 aag gag tcg act cga ata gtt gac tct tgg aac tgatgag agctgtcatt 640  
 Lys Glu Ser Thr Arg Ile Val Asp Ser Trp Asn  
 175 180  
 ttataaatag gaggaggatg atgtccagag tctgtgggaa aatggaacac ataactttct 700  
 aaccctcaga agttttaaga tgcatctaa caccatcatt ctatgggaaa gatggttctt 760  
 actcttcgtt cacaggcctt tatatcttcc gatacagaat gctctaattg ggaactctaa 820  
 ttttgatcc aatggccaaa atctgcaagt aatctctagc cacactgatt actactaaac 880  
 caggaaagca tcaaggtatc ttgaattcct ttaactattg agtgcataata gaattcctgt 940  
 acccatga tactgcaagt tgtgtctctc tctgtcagct aatccactgc ggtaactgg 1000  
 aaaagaaaga caacagtgtc agcacagcca tcgacattaa tgcactgaat gcatgcatct 1060  
 ttctctctga gacagcaatc gattttacac cgaatgacaa tgatcatctt agacagcaca 1120  
 acataccac tcggatatct aaaagctagg gatggcattg ctgatatggg caaagagaac 1180  
 acagtatagt atttaagtgc caaatatcag tctttcttcc tctctgtgac taccctcag 1240  
 cagtatgaaa aactccatac tgtgcagtca cagttggatt aattcttcag ttctccgca 1300  
 ctgcaaacac atatattgtc gcacatgcat gtatacctgc accctgtttt aactctaaag 1360  
 gaatagtgtt gctttacttc ttctctgttt tgcctggacc acttaaagcc acaacacctc 1420  
 tatagtgaca cagctagtc tctagtgggt gccctcactg ccacctagag gagccatggt 1480  
 ggaaaacaca ctctctcctt tgagcctatc tgcacatctc tcgagttctt ggagcaaaaa 1540  
 ctaaatgctg aactaagcct gggtgagatg cttcccatgg accatgccgc agcacagtgc 1600  
 taatctatcc acaaaacata ccacctccca aagtattatt attggaaaat cgaggaagtg 1660  
 acgcacattt agggaaaaac tactcacctt agaaaagtca ctgaaatcct tttttttttt 1720  
 tttgagatgg agttttgctc ttgtagccca ggctgggatg caatggcatg gtctcagctc 1780

178/307

actgtaacct ccacctcccg gattcaagca attcttctgc ctcagcttcc cgactagctg 1840  
 ggattacagc tgcctgccac cgtgcccagc taatttttgt attttttagtg gagagggggt 1900  
 ttcacatgt tggccagtct ggtctagaac tcctgacgtc aggtgatccg cccaccttgg 1960  
 cctcccaaag tgctggaatt agaggcctga cccctgctc ctggcctgaa atctttaaag 2020  
 ccgttttttc cctaaaaaac gggaaataat aacacctcag aaggtttttg tgaagatcaa 2080  
 agaagctaaa tatatgtggc atgatttgta aagtgttatg catatgtatg ttattcttcc 2140  
 tactgtcttc taaccttccc ttgcctgcta tgacttatct gagagccatg ttcccattta 2200  
 tctttttgcc aactatgtta ctgttgcac acctgaaatg gctttgtttt tatcaataaa 2260  
 tacttggtga ttgtggtaaa cagc 2284

&lt;210&gt; 86

&lt;211&gt; 1737

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (236)... (1024)

&lt;400&gt; 86

tttcgattcc actctcttcc gtttctgtcg ctgcagtcgt ccgcgggact ccggccggtt 60  
 gccggcccca ggcggtgctt ctccccacca ccgccagct cagctcagcc cagcccagcc 120  
 cactctgccc ttagaggccc ttctcccaa agacgcactc cagaagtctc gccctcgtgc 180  
 ggctgaggag cctgggatcc cagacctgaa caagtgaac ccccgcccct gaaga atg 238

Met

1

ggg aag acg ttt tcc cag ctg ggc tct tgg cgg gag gat gag aac aag 286

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Lys | Thr | Phe | Ser | Gln | Leu | Gly | Ser | Trp | Arg | Glu | Asp | Glu | Asn | Lys |     |
|     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |     |
| tca | atc | ctg | tcc | tcc | aaa | cca | gcc | att | ggc | agc | aag | gct | gtc | aac | tac | 334 |
| Ser | Ile | Leu | Ser | Ser | Lys | Pro | Ala | Ile | Gly | Ser | Lys | Ala | Val | Asn | Tyr |     |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |     |
| tcc | agc | acc | ggt | agc | agc | aag | tct | ttt | tgt | tcc | tgt | gtg | cct | tgt | gaa | 382 |
| Ser | Ser | Thr | Gly | Ser | Ser | Lys | Ser | Phe | Cys | Ser | Cys | Val | Pro | Cys | Glu |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
| gga | act | gct | gat | gcc | agc | ttc | gtg | act | tgt | ccc | acc | tgc | cag | ggc | agt | 430 |
| Gly | Thr | Ala | Asp | Ala | Ser | Phe | Val | Thr | Cys | Pro | Thr | Cys | Gln | Gly | Ser |     |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     | 65  |     |     |     |     |
| ggc | aag | att | ccc | caa | gag | ctg | gag | aag | cag | ttg | gtg | gct | ctc | att | ccc | 478 |
| Gly | Lys | Ile | Pro | Gln | Glu | Leu | Glu | Lys | Gln | Leu | Val | Ala | Leu | Ile | Pro |     |
|     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |     |     |     |
| tat | ggg | gac | cag | agg | ctg | aag | ccc | aag | cac | acg | aag | ctc | ttt | gtg | ttc | 526 |
| Tyr | Gly | Asp | Gln | Arg | Leu | Lys | Pro | Lys | His | Thr | Lys | Leu | Phe | Val | Phe |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |     |
| ctg | gcc | gtg | ctc | atc | tgc | ctg | gtg | acc | tcc | tcc | ttc | atc | gtc | ttt | ttc | 574 |
| Leu | Ala | Val | Leu | Ile | Cys | Leu | Val | Thr | Ser | Ser | Phe | Ile | Val | Phe | Phe |     |
|     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |     |     |
| ctg | ttt | ccc | cgg | tcc | gtc | att | gtg | cag | cct | gca | ggc | ctc | aac | tcc | tcc | 622 |
| Leu | Phe | Pro | Arg | Ser | Val | Ile | Val | Gln | Pro | Ala | Gly | Leu | Asn | Ser | Ser |     |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |     |
| aca | gtg | gcc | ttt | gat | gag | gct | gat | atc | tac | ctc | aac | ata | acg | aat | atc | 670 |
| Thr | Val | Ala | Phe | Asp | Glu | Ala | Asp | Ile | Tyr | Leu | Asn | Ile | Thr | Asn | Ile |     |

180/307

|   |     |     |     |      |
|---|-----|-----|-----|------|
| 130   | 135 | 140 | 145 |      |
| tta aac atc tcc aat ggc aac tac tac ccc att atg gtg aca cag ctg |     |     |     | 718  |
| Leu Asn Ile Ser Asn Gly Asn Tyr Tyr Pro Ile Met Val Thr Gln Leu |     |     |     |      |
|   | 150 | 155 | 160 |      |
| acc ctc gag gtt ctg cac ctg tcc ctc gtg gtg ggg cag gtt tcc aac |     |     |     | 766  |
| Thr Leu Glu Val Leu His Leu Ser Leu Val Val Gly Gln Val Ser Asn |     |     |     |      |
|   | 165 | 170 | 175 |      |
| aac ctt ctc cta cac att ggc cct ttg gcc agt gaa cag atg ttt tac |     |     |     | 814  |
| Asn Leu Leu Leu His Ile Gly Pro Leu Ala Ser Glu Gln Met Phe Tyr |     |     |     |      |
|   | 180 | 185 | 190 |      |
| gca gta gct acc aag ata cgg gat gaa aac aca tac aaa atc tgt acc |     |     |     | 862  |
| Ala Val Ala Thr Lys Ile Arg Asp Glu Asn Thr Tyr Lys Ile Cys Thr |     |     |     |      |
|   | 195 | 200 | 205 |      |
| tgg ctg gaa atc aaa gtc cac cat gtg ctt ttg cac atc cag ggc acc |     |     |     | 910  |
| Trp Leu Glu Ile Lys Val His His Val Leu Leu His Ile Gln Gly Thr |     |     |     |      |
|   | 210 | 215 | 220 | 225  |
| ctg acc tgt tca tac ctg agc cat tca gag cag ctg gtc ttt cag agc |     |     |     | 958  |
| Leu Thr Cys Ser Tyr Leu Ser His Ser Glu Gln Leu Val Phe Gln Ser |     |     |     |      |
|   | 230 | 235 | 240 |      |
| tat gaa tat gtg gac tgc cga gga aac gca tct gtg ccc cac cag ctg |     |     |     | 1006 |
| Tyr Glu Tyr Val Asp Cys Arg Gly Asn Ala Ser Val Pro His Gln Leu |     |     |     |      |
|   | 245 | 250 | 255 |      |
| acc cct cac cca cca tgacctgtc tgctgtccct gtactccagg cacctgcaac  |     |     |     | 1060 |
| Thr Pro His Pro Pro   |     |     |     |      |
| 260   |     |     |     |      |

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cctggtctat atctcccaca actccctggt gactaaggaa ggactacaga ggctttgcc 1120  
 aaggagaagc cctgcctcat cacaccctta cctcccaccc cctcagcaca ggaagcttgc 1180  
 tttgaagtta acttcataca cacacactca tatcctccag ttccccccag attctttcag 1240  
 gggctgccat cagattctgc ccttggttag ttttttgttt ttttttttgg tagagacaga 1300  
 gtctcactgt tggccaggt tggttttgaa ctccctgggt caagcgatcc tcccttcttg 1360  
 gcctcccaaa gcaattggat tacagatgtg agcctgtgcc tggctggtct ttcttgagga 1420  
 aaatctgacc tggcattttc ttgaggcacc ttagattccc tggagtggca cctggccttt 1480  
 ctgtactgag cacctggtca gtctgaaggg ggcatttcac cccagctcca tcagggtgg 1540  
 cagtcctgtc tgaatgtgga gagagctgta gttttatctg gcttttaaaa catggacctg 1600  
 ccggtggggc gcagtggctt acacctgtaa tcccagtact ttgggaggcc gaagtgggtg 1660  
 gatcacttga gggcaggagt tcgtgaccag cctggtcaac atggtgaaac cttgtctcta 1720  
 ctaaaaatac aaaaatt 1737

&lt;210&gt; 87

&lt;211&gt; 1556

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (103)... (609)

&lt;400&gt; 87

agcgtcact cgctgcact cagtcgcggg aggtttcccc gcgccggccg cgtcccgcc 60  
 gctccccggc accagaagtt cctctgcgcg tccgacggcg ac atg ggc gtc ccc 114

Met Gly Val Pro

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|   |     |
|---|-----|
| acg gcc ctg gag gcc ggc agc tgg cgc tgg gga tcc ctg ctc ttc gct   | 162 |
| Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly Ser Leu Leu Phe Ala   |     |
| 5                                      10                                      15                                      20   |     |
| ctc ttc ctg gct gcg tcc cta ggc aaa gat gca cca tcc aac tgt gtg   | 210 |
| Leu Phe Leu Ala Ala Ser Leu Gly Lys Asp Ala Pro Ser Asn Cys Val   |     |
| 25                                      30                                      35  |     |
| gtg tac cca tcc tcc tcc cag gag agt gaa aac atc acg gct gca gcc   | 258 |
| Val Tyr Pro Ser Ser Ser Gln Glu Ser Glu Asn Ile Thr Ala Ala Ala   |     |
| 40                                      45                                      50  |     |
| ctg gct acg ggt gcc tgc atc gta gga atc ctc tgc ctc ccc ctc atc   | 306 |
| Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu Ile   |     |
| 55                                      60                                      65  |     |
| ctg ctc ctg gtc tac aag caa agg cag gca gcc tcc aac cgc cgt gcc   | 354 |
| Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg Arg Ala   |     |
| 70                                      75                                      80  |     |
| cag gag ctg gtg cgg atg gac agc aac att caa ggg att gaa aac ccc   | 402 |
| Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile Glu Asn Pro   |     |
| 85                                      90                                      95                                      100 |     |
| ggc ttt gaa gcc tca cca cct gcc cag ggg ata ccc gag gcc aaa gtc   | 450 |
| Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro Glu Ala Lys Val   |     |
| 105                                      110                                      115                                       |     |
| agg cac ccc ctg tcc tat gtg gcc cag cgg cag cct tct gag tct ggg   | 498 |
| Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln Pro Ser Glu Ser Gly   |     |
| 120                                      125                                      130                                       |     |
| cgg cat ctg ctt tcg gag ccc agc acc ccc ctg tct cct cca ggc ccc   | 546 |

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Arg His Leu Leu Ser Glu Pro Ser Thr Pro Leu Ser Pro Pro Gly Pro

135

140

145

gga gac gtc ttc ttc cca tcc ctg gac cct gtc cct gac tct cca aac 594

Gly Asp Val Phe Phe Pro Ser Leu Asp Pro Val Pro Asp Ser Pro Asn

150

155

160

ttt gag gtc atc tagc ccagctgggg gacagtgggc tgttgtggct gggctctgggg 650

Phe Glu Val Ile

165

caggtgcatt tgagccaggg ctggctctgt gagtggcctc cttggcctcg gccctggttc 710

cctccctcct gctctgggct cagatactgt gacatcccag aagcccagcc cctcaacccc 770

tctggatgct acatggggat gctggacggc tcagcccctg ttccaaggat tttgggggtgc 830

tgagattctc ccctagagac ctgaaattca ccagctacag atgccaaatg acttacatct 890

taagaagtct cagaacgtcc agcccttcag cagctctcgt tctgagacat gaggccttggg 950

atgtggcagc atcagtggga caagatggac actggggcac cctcccaggc accagacaca 1010

gggcacgggtg gagagacttc tccccgtgg ccgccttggc tccccgttt tgcccagggc 1070

tgctcttctg tcagacttcc tctttgtacc acagtggctc tggggccagg cctgcctgcc 1130

cactggccat cgccacctic ccagctgcc tcctaccagc agtttctctg aagatctgtc 1190

aacaggttaa gtcaatctgg ggcttccact gcctgcattc cagtcccag agcttggtgg 1250

tcccgaacg ggaagtacat attggggcat ggtggcctcc gtgagcaaat ggtgtcttgg 1310

gcaatctgag gccaggacag atgttgcccc acccactgga gatggtgctg agggaggtgg 1370

gtggggcctt ctgggaaggt gagtggagag gggcacctgc cccccccct ccccatcccc 1430

tactcccact gtcagcgcg ggccattgca agggtgccac acaatgtctt gtccaccctg 1490

ggacacttct gagtatgaag cgggatgcta ttaaaaacta catggggaaa caggtgcaaa 1550

ccctgg 1556



184/307

&lt;210&gt; 88

&lt;211&gt; 1855

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (222)... (953)

&lt;400&gt; 88

cagagatgga atttcaccgt gttgcctagg ctggtctgga gctcttgatc tcaagcgatc 60  
 ctccctgcct cggcctccca acgtgctggg attataggcg tgagccaccg ctccctggcca 120  
 gggctctgttc ctagttgcaa cagttcttgg aaaccctc gagagggcca cgctccatt 180  
 caccaggcca cgcatacaaa gaggcaacac caggagccaa c atg agc tcg ggg 233

Met Ser Ser Gly

1

act gaa ctg ctg tgg ccc gga gca gcg ctg ctg gtg ctg ttg ggg gtg 281

Thr Glu Leu Leu Trp Pro Gly Ala Ala Leu Leu Val Leu Leu Gly Val

5 10 15 20

gca gcc agt ctg tgt gtg cgc tgc tca cgc cca ggt gca aag agg tca 329

Ala Ala Ser Leu Cys Val Arg Cys Ser Arg Pro Gly Ala Lys Arg Ser

25 30 35

gag aaa atc tac cag cag aga agt ctg cgt gag gac caa cag agc ttt 377

Glu Lys Ile Tyr Gln Gln Arg Ser Leu Arg Glu Asp Gln Gln Ser Phe

40 45 50

acg ggg tcc cgg acc tac tcc ttg gtc ggg cag gca tgg cca gga ccc 425

Thr Gly Ser Arg Thr Tyr Ser Leu Val Gly Gln Ala Trp Pro Gly Pro

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|   |     |     |     |
|---|-----|-----|-----|
| 55  | 60  | 65  |     |
| ctg gcg gac atg gca ccc aca agg aag gac aag ctg ttg caa ttc tac |     |     | 473 |
| Leu Ala Asp Met Ala Pro Thr Arg Lys Asp Lys Leu Leu Gln Phe Tyr |     |     |     |
| 70  | 75  | 80  |     |
| ccc agc ctg gag gat cca gca tct tcc agg tac cag aac ttc agc aaa |     |     | 521 |
| Pro Ser Leu Glu Asp Pro Ala Ser Ser Arg Tyr Gln Asn Phe Ser Lys |     |     |     |
| 85  | 90  | 95  | 100 |
| gga agc aga cac ggg tcg gag gaa gcc tac ata gac ccc att gcc atg |     |     | 569 |
| Gly Ser Arg His Gly Ser Glu Glu Ala Tyr Ile Asp Pro Ile Ala Met |     |     |     |
| 105   | 110 | 115 |     |
| gag tat tac aac tgg ggg cgg ttc tcg aag ccc cca gaa gat gat gat |     |     | 617 |
| Glu Tyr Tyr Asn Trp Gly Arg Phe Ser Lys Pro Pro Glu Asp Asp Asp |     |     |     |
| 120   | 125 | 130 |     |
| gcc aat tcc tac gag aat gtg ctc att tgc aag cag aaa acc aca gag |     |     | 665 |
| Ala Asn Ser Tyr Glu Asn Val Leu Ile Cys Lys Gln Lys Thr Thr Glu |     |     |     |
| 135   | 140 | 145 |     |
| aca ggt gcc cag cag gag ggc ata ggt ggc ctc tgc aga ggg gac ctc |     |     | 713 |
| Thr Gly Ala Gln Gln Glu Gly Ile Gly Gly Leu Cys Arg Gly Asp Leu |     |     |     |
| 150   | 155 | 160 |     |
| agc ctg tca ctg gcc ctg aag act ggc ccc act tct ggt ctc tgt ccc |     |     | 761 |
| Ser Leu Ser Leu Ala Leu Lys Thr Gly Pro Thr Ser Gly Leu Cys Pro |     |     |     |
| 165   | 170 | 175 | 180 |
| tct gcc tcc ccg gaa gaa gat gag gaa tct gag gat tat cag aac tca |     |     | 809 |
| Ser Ala Ser Pro Glu Glu Asp Glu Glu Ser Glu Asp Tyr Gln Asn Ser |     |     |     |
| 185   | 190 | 195 |     |

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gca tcc atc cat cag tgg cgc gag tcc agg aag gtc atg ggg caa ctc 857

Ala Ser Ile His Gln Trp Arg Glu Ser Arg Lys Val Met Gly Gln Leu

200

205

210

cag aga gaa gca tcc cct ggc ccg gtg gga agc cca gac gag gag gac 905

Gln Arg Glu Ala Ser Pro Gly Pro Val Gly Ser Pro Asp Glu Glu Asp

215

220

225

ggg gaa ccg gat tac gtg aat ggg gag gtg gca gcc aca gaa gcc 950

Gly Glu Pro Asp Tyr Val Asn Gly Glu Val Ala Ala Thr Glu Ala

230

235

240

tagggcagac caagaagaaa ggagccaagg caaagaggga ccactgtgct catggaccca 1010

tcgtgcctt ccaaggacca tttcccagag ctactcaact ttttaagcccc tgccatggtt 1070

gctcctggaa ggagaaccag ccaccctgag gaccacctgg ccatgcgtgc acagcctggg 1130

aaaagacagt tactcacggg agctgcaggc ccgtcaccaa gccctctccc gaccaggt 1190

ttgtggggca ggcacctggt accaagggtta acccggtcc tggtatggac ggatgcgcag 1250

gatttaggat aagctgtcac ccagtcccca taacaaaacc actgtccaac actggtatct 1310

gtgttctttt gtctatgaa tttggattcc taattgctat tgttggttgc tggggtttta 1370

aatgattgat aagcttgtag agttaactta tagaggggga gccatattta acattctgga 1430

tttcagagta gagatttctg tgttgtctcc tagaaagcat tacatgtagt ttatttcagc 1490

atccttggtg ggtggggccc tggtctctct cccctttggt gggacctccc ctttctttgg 1550

gcttcagttc actcaggaag aaatgaggct gtcgcatct ttatgtgctt ccagtggaaa 1610

tgtcacttgc tacagacaat agtgcagtag agtctagaga agtagtgacc agaacagggc 1670

agagtaggtc cctccatgg cctgaatcc tctctgctc cagggtggc ctctgcagag 1730

ctgattaaac agtggttga ctgtctcatg ggaagagctg gggcccagag ggaccttgag 1790

tcagaaatgt tgccagaaaa agtatctcct ccaacaaaa catctcaata aaaccatttt 1850

agttg 1855

187/307

&lt;210&gt; 89

&lt;211&gt; 2530

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (28)... (1314)

&lt;400&gt; 89

agcgcggcgg ggcgatgtgt gattacc atg gcg agg agt ctc tgt ccg ggg 51

Met Ala Arg Ser Leu Cys Pro Gly

1

5

gcc tgg cta agg aaa ccc tat tac ctc cag gct cgc ttc tca tat gtg 99

Ala Trp Leu Arg Lys Pro Tyr Tyr Leu Gln Ala Arg Phe Ser Tyr Val

10

15

20

cgg atg aaa tat ctt ttc ttt tcc tgg tta gtg gtt ttt gtt gga agc 147

Arg Met Lys Tyr Leu Phe Phe Ser Trp Leu Val Val Phe Val Gly Ser

25

30

35

40

tgg att ata tat gtg cag tat tct acc tat aca gaa tta tgc aga gga 195

Trp Ile Ile Tyr Val Gln Tyr Ser Thr Tyr Thr Glu Leu Cys Arg Gly

45

50

55

aag gac tgt aag aaa ata ata tgt gac aag tac aag act gga gtt att 243

Lys Asp Cys Lys Lys Ile Ile Cys Asp Lys Tyr Lys Thr Gly Val Ile

60

65

70

gat ggg cct gca tgt aac agc ctt tgt gtt aca gaa act ctt tac ttt 291

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Asp Gly Pro Ala Cys Asn Ser Leu Cys Val Thr Glu Thr Leu Tyr Phe  
 75 80 85  
 gga aaa tgt tta tcc acc aag ccc aac aat cag atg tat tta ggg att 339  
 Gly Lys Cys Leu Ser Thr Lys Pro Asn Asn Gln Met Tyr Leu Gly Ile  
 90 95 100  
 tgg gat aat cta cca ggt gtt gtg aaa tgt caa atg gaa caa gcg ctt 387  
 Trp Asp Asn Leu Pro Gly Val Val Lys Cys Gln Met Glu Gln Ala Leu  
 105 110 115 120  
 cat ctt gat ttt gga act gaa ttg gaa cca aga aaa gaa ata gtg cta 435  
 His Leu Asp Phe Gly Thr Glu Leu Glu Pro Arg Lys Glu Ile Val Leu  
 125 130 135  
 ttt gat aag cca act aga gga act act gta caa aaa ttt aaa gaa atg 483  
 Phe Asp Lys Pro Thr Arg Gly Thr Thr Val Gln Lys Phe Lys Glu Met  
 140 145 150  
 gtc tat agt ctc ttt aag gca aaa ttg ggt gac caa gga aac ctc tct 531  
 Val Tyr Ser Leu Phe Lys Ala Lys Leu Gly Asp Gln Gly Asn Leu Ser  
 155 160 165  
 gaa ctg gtt aat ctc atc ttg acg gtg gct gat gga gac aaa gat ggc 579  
 Glu Leu Val Asn Leu Ile Leu Thr Val Ala Asp Gly Asp Lys Asp Gly  
 170 175 180  
 cag gtt tcc ttg gga gaa gca aag tcg gca tgg gca ctt ctt caa ctg 627  
 Gln Val Ser Leu Gly Glu Ala Lys Ser Ala Trp Ala Leu Leu Gln Leu  
 185 190 195 200  
 aat gaa ttt ctt ctc atg gtg ata ctt caa gat aaa gaa cat acc ccc 675  
 Asn Glu Phe Leu Leu Met Val Ile Leu Gln Asp Lys Glu His Thr Pro

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|  |     |     |      |
|--|-----|-----|------|
| 205  | 210 | 215 |      |
| aaa tta atg gga ttc tgt ggt gac ctc tat gtg atg gaa agt gtt gaa            |     |     | 723  |
| Lys Leu Met Gly Phe Cys Gly Asp Leu Tyr Val Met Glu Ser Val Glu            |     |     |      |
| 220  | 225 | 230 |      |
| tat acc tct ctt tat gga ata agc ctt cct tgg gtc att gaa ctt ttt            |     |     | 771  |
| Tyr Thr Ser Leu Tyr Gly Ile Ser Leu Pro Trp Val Ile Glu Leu Phe            |     |     |      |
| 235  | 240 | 245 |      |
| att cca tct ggg ttc aga aga agc atg gat cag ctg ttc aca cca tca            |     |     | 819  |
| Ile Pro Ser Gly Phe Arg Arg Ser Met Asp Gln Leu Phe Thr Pro Ser            |     |     |      |
| 250  | 255 | 260 |      |
| tgg cca aga aag gcc aaa ata gcc ata gga ctt cta gaa ttt gtg gaa            |     |     | 867  |
| Trp Pro Arg Lys Ala Lys Ile Ala Ile Gly Leu Leu Glu Phe Val Glu            |     |     |      |
| 265  | 270 | 275 | 280  |
| gat gtt ttc cat ggc ccc tac gga aat ttc ctc atg tgc gat act agt            |     |     | 915  |
| Asp Val Phe His Gly Pro Tyr Gly Asn Phe Leu Met Cys Asp Thr Ser            |     |     |      |
| 285  | 290 | 295 |      |
| gcc aaa aac cta gga tat aat gat aag tat gat ttg aaa atg gtg gat            |     |     | 963  |
| Ala Lys Asn Leu Gly Tyr Asn Asp Lys Tyr Asp Leu Lys Met Val Asp            |     |     |      |
| 300  | 305 | 310 |      |
| atg aga aaa att <sup>A</sup> g cca gag aca aac ctg aaa gaa ctt att aag gat |     |     | 1011 |
| Met Arg Lys Ile Val Pro Glu Thr Asn Leu Lys Glu Leu Ile Lys Asp            |     |     |      |
| 315  | 320 | 325 |      |
| cgt cac tgt gag tct gat ttg gac tgt gtc tat ggc aca gat tgt aga            |     |     | 1059 |
| Arg His Cys Glu Ser Asp Leu Asp Cys Val Tyr Gly Thr Asp Cys Arg            |     |     |      |
| 330  | 335 | 340 |      |

W

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act agc tgt gat cag agt aca atg aag tgt act tca gaa gtg ata caa 1107  
 Thr Ser Cys Asp Gln Ser Thr Met Lys Cys Thr Ser Glu Val Ile Gln  
 345 350 355 360

cca aac ttg gca aaa gct tgt cag tta ctc aaa gac tac cta ctg cgt 1155  
 Pro Asn Leu Ala Lys Ala Cys Gln Leu Leu Lys Asp Tyr Leu Leu Arg  
 365 370 375

ggc gct cca agt gaa att cgt gaa gaa tta gaa aag cag ctt tat tct 1203  
 Gly Ala Pro Ser Glu Ile Arg Glu Glu Leu Glu Lys Gln Leu Tyr Ser  
 380 385 390

tgt att gct ctc aaa gtc aca gca aat caa atg gaa atg gaa cat tct 1251  
 Cys Ile Ala Leu Lys Val Thr Ala Asn Gln Met Glu Met Glu His Ser  
 395 400 405

ttg ata cta aat aac cta aaa aca tta ttg tgg aag aaa att tcc tac 1299  
 Leu Ile Leu Asn Asn Leu Lys Thr Leu Leu Trp Lys Lys Ile Ser Tyr  
 410 415 420

act aat gac tct tagttcatt tggacataat taccatttta agaaacctgc 1350  
 Thr Asn Asp Ser  
 425

cactttttaa gaacaatttt gagcattaaa aaaaaatggc ttcaaattcc tgccagttac 1410  
 acaaaaactcc ttccccccag gcctgagaag ccatcagtat gtgattactg aagtaatggc 1470  
 aggtgtagga tcaacaggtc cccaagatgt cattcctgcc cttttagaag ccctgttaca 1530  
 tctccgaagt acattcattg tgtaactatt ttgactgact ttaaaaacca atgctgtgaa 1590  
 aagtttcatt ccataaacat caacagttag tgattttag atttacctta gccaaaatac 1650  
 caatgctgga agcatttgtt ttgcattgaa gctgctgttc aacaagaaaa ttataaatt 1710  
 tactaatgtc ttagcatggt aaagtttgca cattaacaga aattaagact gcaaagcagg 1770

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ttaaacttgc ttctttataa aacagatggt gggttaatag catggtttac tgtattaaag 1830  
 acttatacac ccatttttaa cctcattcag acatcaagtt atgtgtagct tcacaatggt 1890  
 tcaagtggct tacttcaaga aatcttatac ttgacagtac accaatttta ttgactaaaa 1950  
 atggatgaac tttcctaaag attcaaaggg cccatcttag tatcacgcag ctgactgagc 2010  
 ccttcaaaac tgacatctta aggcccaatc aagatccaca tatectgatt ttgaactatg 2070  
 tgaaagtggg actgttaagt gcaagactaa aataaattat agcagacttt ttagtaataa 2130  
 ctttccattt tcaaacagta tatcctgtgg gccaaagggc tatttcttaa agaggcatgt 2190  
 aaatgtattht atttatctaa tgthtttttc cccatgtaaa ctgatatac aaggtthtagt 2250  
 atttgctcct ctttcatatt atthttcacac gtatactcag atttggtcatg tacctthcaa 2310  
 catctccata aaattaaaca cthtttggtg aaaagatcca ctthtttctg ctcaaaggtt 2370  
 tcgcctacct aaagtggac atgttaaaaa tctatgtgac catcactgga cagctthtctc 2430  
 tcaaaactth cttcaacgc catggattag caccagthtt gthtacttta aggtacttht 2490  
 cccattcatc atctggttat aataaatgga tggaagaaat 2530

&lt;210&gt; 90

&lt;211&gt; 1911

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (232)... (1083)

&lt;400&gt; 90

aaaatatgag acggggaatc atcgtgtgat gtgtgtgctg cthttggctg agtgtgtgga 60  
 gtcctgctca ggtgttaggt acagtgtgtt tgatcgtggt ggcttgaggg gaaccgctg 120  
 ttcagagctg tgactgcggc tgcactcaga gaagctgccc ttggtgctc gtagcgccgg 180



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gccttctctc ctggtcatca tccagagcag ccagtgtccg ggaggcagaa g atg ccc 237  
Met Pro  
1

cac tcc agc ctg cat cca tcc atc ccg tgt ccc agg ggt cac ggg gcc 285  
His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His Gly Ala  
5 10 15

cag aag gca gcc ttg gtt ctg ctg agt gcc tgc ctg gtg acc ctt tgg 333  
Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr Leu Trp  
20 25 30

ggg cta gga gag cca cca gag cac act ctc cgg tac ctg gtg ctc cac 381  
Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val Leu His  
35 40 45 50

cta gcc tcc ctg cag ctg gga ctg ctg tta aac ggg gtc tgc agc ctg 429  
Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys Ser Leu  
55 60 65

gct gag gag ctg cac cac atc cac tcc agg tac cgg ggc agc tac tgg 477  
Ala Glu Glu Leu His His Ile His Ser Arg Tyr Arg Gly Ser Tyr Trp  
70 75 80

agg act gtg cgg gcc tgc ctg ggc tgc ccc ctc cgc cgt ggg gcc ctg 525  
Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly Ala Leu  
85 90 95

ttg ctg ctg tcc atc tat ttc tac tac tcc ctc cca aat gcg gtc ggc 573  
Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala Val Gly  
100 105 110

ccg ccc ttc act tgg atg ctt gcc ctc ctg ggc ctc tcg cag gca ctg 621

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Pro | Pro | Phe | Thr | Trp | Met | Leu | Ala | Leu | Leu | Gly | Leu | Ser | Gln | Ala | Leu |      |  |
| 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     | 130 |      |  |
| aac | atc | ctc | ctg | ggc | ctc | aag | ggc | ctg | gcc | cca | gct | gag | atc | tct | gca | 669  |  |
| Asn | Ile | Leu | Leu | Gly | Leu | Lys | Gly | Leu | Ala | Pro | Ala | Glu | Ile | Ser | Ala |      |  |
|     |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     | 145 |      |  |
| gtg | tgt | gaa | aaa | ggg | aat | ttc | aac | gtg | gcc | cat | ggg | ctg | gca | tgg | tca | 717  |  |
| Val | Cys | Glu | Lys | Gly | Asn | Phe | Asn | Val | Ala | His | Gly | Leu | Ala | Trp | Ser |      |  |
|     |     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |      |  |
| tat | tac | atc | gga | tat | ctg | cgg | ctg | atc | ctg | cca | gag | ctc | cag | gcc | cgg | 765  |  |
| Tyr | Tyr | Ile | Gly | Tyr | Leu | Arg | Leu | Ile | Leu | Pro | Glu | Leu | Gln | Ala | Arg |      |  |
|     |     |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |      |  |
| att | cga | act | tac | aat | cag | cat | tac | aac | aac | ctg | cta | cgg | ggt | gca | gtg | 813  |  |
| Ile | Arg | Thr | Tyr | Asn | Gln | His | Tyr | Asn | Asn | Leu | Leu | Arg | Gly | Ala | Val |      |  |
|     |     |     |     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |      |  |
| agc | cag | cgg | ctg | tat | att | ctc | ctc | cca | ttg | gac | tgt | ggg | gtg | cct | gat | 861  |  |
| Ser | Gln | Arg | Leu | Tyr | Ile | Leu | Leu | Pro | Leu | Asp | Cys | Gly | Val | Pro | Asp |      |  |
| 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     | 210 |      |  |
| aac | ctg | agt | atg | gct | gac | ccc | aac | att | cgc | ttc | ctg | gat | aaa | ctg | ccc | 909  |  |
| Asn | Leu | Ser | Met | Ala | Asp | Pro | Asn | Ile | Arg | Phe | Leu | Asp | Lys | Leu | Pro |      |  |
|     |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     | 225 |      |  |
| cag | cag | acc | gct | gac | cgt | gct | ggc | atc | aag | gat | cgg | gtt | tac | agc | aac | 957  |  |
| Gln | Gln | Thr | Ala | Asp | Arg | Ala | Gly | Ile | Lys | Asp | Arg | Val | Tyr | Ser | Asn |      |  |
|     |     |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |      |  |
| agc | atc | tat | gag | ctt | ctg | gag | aac | ggg | cag | cgg | aac | ctg | cag | atg | aca | 1005 |  |
| Ser | Ile | Tyr | Glu | Leu | Leu | Glu | Asn | Gly | Gln | Arg | Asn | Leu | Gln | Met | Thr |      |  |

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|   |     |     |      |
|---|-----|-----|------|
| 245   | 250 | 255 |      |
| gca gct tct cgc tgt ccc agg agg ttc tcc ggc acc tgc ggc agg agg   |     |     | 1053 |
| Ala Ala Ser Arg Cys Pro Arg Arg Phe Ser Gly Thr Cys Gly Arg Arg   |     |     |      |
| 260   | 265 | 270 |      |
| aaa agg aag agg tta ctg tgg gca gct tgaagacctc agcgggtgcc         |     |     | 1100 |
| Lys Arg Lys Arg Leu Leu Trp Ala Ala                               |     |     |      |
| 275   | 280 |     |      |
| agtacctcca cgatgtccca agagcctgag ctctcatca gtggaatgga aaagcccctc  |     |     | 1160 |
| cctctccgea cggatttctc ttgagaccca gggtcaccag gccagagcct ccagtgtct  |     |     | 1220 |
| ccaagcctct ggactggggg ctctcttcag tggtgaatg tccagcagag ctatttctt   |     |     | 1280 |
| ccacaggggg ccttgcaggg aagggtccag gacttgacat cttaatgac gtcttgtccc  |     |     | 1340 |
| cttgggccag tcatttcccc tctctgagcc tcggtgtctt caacctgtga aatgggatca |     |     | 1400 |
| taatcactgc cttacctccc tcacggttgt tgtgaggact gagtgtgtgg aagtttttca |     |     | 1460 |
| taaactttgg atgctagtgt acttaggggg tgtgccagg gtctttcatg gggccttcca  |     |     | 1520 |
| gacctactcc ccaccttct ccccttctt tgccgggga cgccgaactc tctaatggt     |     |     | 1580 |
| atcaacaggc tccttcgccc tctggctcct ggtcatgttc cattattggg gagccccagc |     |     | 1640 |
| agaagaatgg agaggaggag gaggtgagt ttgggtatt gaatccccg gctccaccc     |     |     | 1700 |
| tgcagcatca aggttgctat ggactctcct gccgggcaac tcttgcgtaa tcatgactat |     |     | 1760 |
| ctctaggatt ctggcaccac ttccttcctt ggccccctaa gcctagctgt gtatcggcac |     |     | 1820 |
| ccccaccca ctagagtact ccctctcact tgcggtttcc ttatactcca cccctttctc  |     |     | 1880 |
| aacggtcctt ttttaaagca catctcagat t                                |     |     | 1911 |

&lt;210&gt; 91

&lt;211&gt; 476

&lt;212&gt; PRT

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&lt;213&gt; Homo sapiens

&lt;400&gt; 91

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met

1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser

20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr

35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly

50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65 70 75 80

Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln

85 90 95

Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro

100 105 110

Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val

115 120 125

Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr

130 135 140

Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser

145 150 155 160

Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala

165 170 175

Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu

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|   |     |     |     |
|---|-----|-----|-----|
| 180   | 185 | 190 |     |
| Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys |     |     |     |
| 195   | 200 | 205 |     |
| Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg |     |     |     |
| 210   | 215 | 220 |     |
| Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser |     |     |     |
| 225   | 230 | 235 | 240 |
| Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile |     |     |     |
| 245   | 250 | 255 |     |
| Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His |     |     |     |
| 260   | 265 | 270 |     |
| Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu |     |     |     |
| 275   | 280 | 285 |     |
| Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr |     |     |     |
| 290   | 295 | 300 |     |
| Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys |     |     |     |
| 305   | 310 | 315 | 320 |
| Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro |     |     |     |
| 325   | 330 | 335 |     |
| Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly |     |     |     |
| 340   | 345 | 350 |     |
| Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys |     |     |     |
| 355   | 360 | 365 |     |
| Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn |     |     |     |
| 370   | 375 | 380 |     |

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Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu His Ser Leu

385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys

405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile

420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His

435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg

450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly

465 470 475

&lt;210&gt; 92

&lt;211&gt; 226

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 92

Met Ser Arg Ala Gln Ile Trp Ala Leu Val Ser Gly Val Gly Gly Phe

1 5 10 15

Gly Ala Leu Val Ala Ala Thr Thr Ser Asn Glu Trp Lys Val Thr Thr

20 25 30

Arg Ala Ser Ser Val Ile Thr Ala Thr Trp Val Tyr Gln Gly Leu Trp

35 40 45

Met Asn Cys Ala Gly Asn Ala Leu Gly Ser Phe His Cys Arg Pro His

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50                      55                      60  
Phe Thr Ile Phe Lys Val Ala Gly Tyr Ile Gln Ala Cys Arg Gly Leu  
65                      70                      75                      80  
Met Ile Ala Ala Val Ser Leu Gly Phe Phe Gly Ser Ile Phe Ala Leu  
85                      90                      95  
Phe Gly Met Lys Cys Thr Lys Val Gly Gly Ser Asp Lys Ala Lys Ala  
100                      105                      110  
Lys Ile Ala Cys Leu Ala Gly Ile Val Phe Ile Leu Ser Gly Leu Cys  
115                      120                      125  
Ser Met Thr Gly Cys Ser Leu Tyr Ala Asn Lys Ile Thr Thr Glu Phe  
130                      135                      140  
Phe Asp Pro Leu Phe Val Glu Gln Lys Tyr Glu Leu Gly Ala Ala Leu  
145                      150                      155                      160  
Phe Ile Gly Trp Ala Gly Ala Ser Leu Cys Ile Ile Gly Gly Val Ile  
165                      170                      175  
Phe Cys Phe Ser Ile Ser Asp Asn Asn Lys Thr Pro Arg Tyr Thr Tyr  
180                      185                      190  
Asn Gly Ala Thr Ser Val Met Ser Ser Arg Thr Lys Tyr His Gly Gly  
195                      200                      205  
Glu Asp Phe Lys Thr Thr Asn Pro Ser Lys Gln Phe Asp Lys Asn Ala  
210                      215                      220  
Tyr Val  
225

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&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 93

Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly

1 5 10 15

Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg

20 25 30

Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu

35 40 45

Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe

50 55 60

Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly

65 70 75 80

Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg

85 90 95

Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu

100 105 110

Val Ile Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly

115 120 125

Gly Lys Met Ser Gln Tyr Leu Asp Ser Leu Lys Val Gly Asp Val Val

130 135 140

Glu Phe Arg Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His

145 150 155 160

Phe Asn Ile Gln Pro Asn Lys Lys Ser Pro Pro Glu Pro Arg Val Ala



200/307

165 170 175  
Lys Lys Leu Gly Met Ile Ala Gly Gly Thr Gly Ile Thr Pro Met Leu  
180 185 190  
Gln Leu Ile Arg Ala Ile Leu Lys Val Pro Glu Asp Pro Thr Gln Cys  
195 200 205  
Phe Leu Leu Phe Ala Asn Gln Thr Glu Lys Asp Ile Ile Leu Arg Glu  
210 215 220  
Asp Leu Glu Glu Leu Gln Ala Arg Tyr Pro Asn Arg Phe Lys Leu Trp  
225 230 235 240  
Phe Thr Leu Asp His Pro Pro Lys Asp Trp Ala Tyr Ser Lys Gly Phe  
245 250 255  
Val Thr Ala Asp Met Ile Arg Glu His Leu Pro Ala Pro Gly Asp Asp  
260 265 270  
Val Leu Val Leu Leu Cys Gly Pro Pro Pro Met Val Gln Leu Ala Cys  
275 280 285  
His Pro Asn Leu Asp Lys Leu Gly Tyr Ser Gln Lys Met Arg Phe Thr  
290 295 300  
Tyr  
305

&lt;210&gt; 94

&lt;211&gt; 227

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 94

201/307

Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu

1 5 10 15

Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His

20 25 30

Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val

35 40 45

Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys

50 55 60

Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys

65 70 75 80

Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp

85 90 95

Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His

100 105 110

Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile

115 120 125

Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His

130 135 140

Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys

145 150 155 160

Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys

165 170 175

Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser

180 185 190

Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala

202/307

195 200 205  
Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile  
210 215 220  
Ala Ala Cys  
225

&lt;210&gt; 95

&lt;211&gt; 441

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 95

Met Ala Ile His Lys Ala Leu Val Met Cys Leu Gly Leu Pro Leu Phe  
1 5 10 15  
Leu Phe Pro Gly Ala Trp Ala Gln Gly His Val Pro Pro Gly Cys Ser  
20 25 30  
Gln Gly Leu Asn Pro Leu Tyr Tyr Asn Leu Cys Asp Arg Ser Gly Ala  
35 40 45  
Trp Gly Ile Val Leu Glu Ala Val Ala Gly Ala Gly Ile Val Thr Thr  
50 55 60  
Phe Val Leu Thr Ile Ile Leu Val Ala Ser Leu Pro Phe Val Gln Asp  
65 70 75 80  
Thr Lys Lys Arg Ser Leu Leu Gly Thr Gln Val Phe Phe Leu Leu Gly  
85 90 95  
Thr Leu Gly Leu Phe Cys Leu Val Phe Ala Cys Val Val Lys Pro Asp  
100 105 110

203/307

Phe Ser Thr Cys Ala Ser Arg Arg Phe Leu Phe Gly Val Leu Phe Ala

115

120

125

Ile Cys Phe Ser Cys Leu Ala Ala His Val Phe Ala Leu Asn Phe Leu

130

135

140

Ala Arg Lys Asn His Gly Pro Arg Gly Trp Val Ile Phe Thr Val Ala

145

150

155

160

Leu Leu Leu Thr Leu Val Glu Val Ile Ile Asn Thr Glu Trp Leu Ile

165

170

175

Ile Thr Leu Val Arg Gly Ser Gly Glu Gly Gly Pro Gln Gly Asn Ser

180

185

190

Ser Ala Gly Trp Ala Val Ala Ser Pro Cys Ala Ile Ala Asn Met Asp

195

200

205

Phe Val Met Ala Leu Ile Tyr Val Met Leu Leu Leu Leu Gly Ala Phe

210

215

220

Leu Gly Ala Trp Pro Ala Leu Cys Gly Arg Tyr Lys Arg Trp Arg Lys

225

230

235

240

His Gly Val Phe Val Leu Leu Thr Thr Ala Thr Ser Val Ala Ile Trp

245

250

255

Val Val Trp Ile Val Met Tyr Thr Tyr Gly Asn Lys Gln His Asn Ser

260

265

270

Pro Thr Trp Asp Asp Pro Thr Leu Ala Ile Ala Leu Ala Ala Asn Ala

275

280

285

Trp Ala Phe Val Leu Phe Tyr Val Ile Pro Glu Val Ser Gln Val Thr

290

295

300

Lys Ser Ser Pro Glu Gln Ser Tyr Gln Gly Asp Met Tyr Pro Thr Arg

204/307

305                      310                      315                      320  
 Gly Val Gly Tyr Glu Thr Ile Leu Lys Glu Gln Lys Gly Gln Ser Met  
                          325                      330                      335  
 Phe Val Glu Asn Lys Ala Phe Ser Met Asp Glu Pro Val Ala Ala Lys  
                          340                      345                      350  
 Arg Pro Val Ser Pro Tyr Ser Gly Tyr Asn Gly Gln Leu Leu Thr Ser  
                          355                      360                      365  
 Val Tyr Gln Pro Thr Glu Met Ala Leu Met His Lys Val Pro Ser Glu  
                          370                      375                      380  
 Gly Ala Tyr Asp Ile Ile Leu Pro Arg Ala Thr Ala Asn Ser Gln Val  
 385                      390                      395                      400  
 Met Gly Ser Ala Asn Ser Thr Leu Arg Ala Glu Asp Met Tyr Ser Ala  
                          405                      410                      415  
 Gln Ser His Gln Ala Ala Thr Pro Pro Lys Asp Gly Lys Asn Ser Gln  
                          420                      425                      430  
 Val Phe Arg Asn Pro Tyr Val Trp Asp  
                          435                      440

&lt;210&gt; 96

&lt;211&gt; 265

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 96

Met Ala Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys

205/307

Leu Leu Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro

20

25

30

Leu Val Leu Ala Leu Leu Leu Val Ser Ala Ala Leu Ser Ser Val Val

35

40

45

Ser Arg Thr Asp Ser Pro Ser Pro Thr Val Leu Asn Ser His Ile Ser

50

55

60

Thr Pro Asn Val Asn Ala Leu Thr His Glu Asn Gln Thr Lys Pro Ser

65

70

75

80

Ile Ser Gln Ile Ser Thr Thr Leu Pro Pro Thr Thr Ser Thr Lys Lys

85

90

95

Ser Gly Gly Ala Ser Val Val Pro His Pro Ser Pro Thr Pro Leu Ser

100

105

110

Gln Glu Glu Ala Asp Asn Asn Glu Asp Pro Ser Ile Glu Glu Glu Asp

115

120

125

Leu Leu Met Leu Asn Ser Ser Pro Ser Thr Ala Lys Asp Thr Leu Asp

130

135

140

Asn Gly Asp Tyr Gly Glu Pro Asp Tyr Asp Trp Thr Thr Gly Pro Arg

145

150

155

160

Asp Asp Asp Glu Ser Asp Asp Thr Leu Glu Glu Asn Arg Gly Tyr Met

165

170

175

Glu Ile Glu Gln Ser Val Lys Ser Phe Lys Met Pro Ser Ser Asn Ile

180

185

190

Glu Glu Glu Asp Ser His Phe Phe Phe His Leu Ile Ile Phe Ala Phe

195

200

205

Cys Ile Ala Val Val Tyr Ile Thr Tyr His Asn Lys Arg Lys Ile Phe

206/307

|   |     |     |     |
|---|-----|-----|-----|
| 210   | 215 | 220 |     |
| Leu Leu Val Gln Ser Arg Lys Trp Arg Asp Gly Leu Cys Ser Lys Thr |     |     |     |
| 225   | 230 | 235 | 240 |
| Val Glu Tyr His Arg Leu Asp Gln Asn Val Asn Glu Ala Met Pro Ser |     |     |     |
|   | 245 | 250 | 255 |
| Leu Lys Ile Thr Asn Asp Tyr Ile Phe                             |     |     |     |
|   | 260 | 265 |     |

&lt;210&gt; 97

&lt;211&gt; 208

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 97

|   |    |    |    |
|---|----|----|----|
| Met Leu Gly Leu Leu Val Ala Leu Leu Ala Leu Gly Leu Ala Val Phe |    |    |    |
| 1   | 5  | 10 | 15 |
| Ala Leu Leu Asp Val Trp Tyr Leu Val Arg Leu Pro Cys Ala Val Leu |    |    |    |
|   | 20 | 25 | 30 |
| Arg Ala Arg Leu Leu Gln Pro Arg Val Arg Asp Leu Leu Ala Glu Gln |    |    |    |
|   | 35 | 40 | 45 |
| Arg Phe Pro Gly Arg Val Leu Pro Ser Asp Leu Asp Leu Leu Leu His |    |    |    |
|   | 50 | 55 | 60 |
| Met Asn Asn Ala Arg Tyr Leu Arg Glu Ala Asp Phe Ala Arg Val Ala |    |    |    |
|   | 65 | 70 | 75 |
| His Leu Thr Arg Cys Gly Val Leu Gly Ala Leu Arg Glu Leu Arg Ala |    |    |    |
|   | 85 | 90 | 95 |

207/307

His Thr Val Leu Ala Ala Ser Cys Ala Arg His Arg Arg Ser Leu Arg

100

105

110

Leu Leu Glu Pro Phe Glu Val Arg Thr Arg Leu Leu Gly Trp Asp Asp

115

120

125

Arg Ala Phe Tyr Leu Glu Ala Arg Phe Val Ser Leu Arg Asp Gly Phe

130

135

140

Val Cys Ala Leu Leu Arg Phe Arg Gln His Leu Leu Gly Thr Ser Pro

145

150

155

160

Glu Arg Val Val Gln His Leu Cys Gln Arg Arg Val Glu Pro Pro Glu

165

170

175

Leu Pro Ala Asp Leu Gln His Trp Ile Ser Tyr Asn Glu Ala Ser Ser

180

185

190

Gln Leu Leu Arg Met Glu Ser Gly Leu Ser Asp Val Thr Lys Asp Gln

195

200

205

&lt;210&gt; 98

&lt;211&gt; 400

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 98

Met Ala Trp Arg Arg Arg Glu Ala Ser Val Gly Ala Arg Gly Val Leu

1

5

10

15

Ala Leu Ala Leu Leu Ala Leu Ala Leu Cys Val Pro Gly Ala Arg Gly

20

25

30

Arg Ala Leu Glu Trp Phe Ser Ala Val Val Asn Ile Glu Tyr Val Asp



208/307

|   |     |     |
|---|-----|-----|
| 35  | 40  | 45  |
| Pro Gln Thr Asn Leu Thr Val Trp Ser Val Ser Glu Ser Gly Arg Phe |     |     |
| 50  | 55  | 60  |
| Gly Asp Ser Ser Pro Lys Glu Gly Ala His Gly Leu Val Gly Val Pro |     |     |
| 65  | 70  | 75  |
| Trp Ala Pro Gly Gly Asp Leu Glu Gly Cys Ala Pro Asp Thr Arg Phe |     |     |
| 85  | 90  | 95  |
| Phe Val Pro Glu Pro Gly Gly Arg Gly Ala Ala Pro Trp Val Ala Leu |     |     |
| 100   | 105 | 110 |
| Val Ala Arg Gly Gly Cys Thr Phe Lys Asp Lys Val Leu Val Ala Ala |     |     |
| 115   | 120 | 125 |
| Arg Arg Asn Ala Ser Ala Val Val Leu Tyr Asn Glu Glu Arg Tyr Gly |     |     |
| 130   | 135 | 140 |
| Asn Ile Thr Leu Pro Met Ser His Ala Gly Thr Gly Asn Ile Val Val |     |     |
| 145   | 150 | 155 |
| Ile Met Ile Ser Tyr Pro Lys Gly Arg Glu Ile Leu Glu Leu Val Gln |     |     |
| 165   | 170 | 175 |
| Lys Gly Ile Pro Val Thr Met Thr Ile Gly Val Gly Thr Arg His Val |     |     |
| 180   | 185 | 190 |
| Gln Glu Phe Ile Ser Gly Gln Ser Val Val Phe Val Ala Ile Ala Phe |     |     |
| 195   | 200 | 205 |
| Ile Thr Met Met Ile Ile Ser Leu Ala Trp Leu Ile Phe Tyr Tyr Ile |     |     |
| 210   | 215 | 220 |
| Gln Arg Phe Leu Tyr Thr Gly Ser Gln Ile Gly Ser Gln Ser His Arg |     |     |
| 225   | 230 | 235 |
|   |     | 240 |

209/307

Lys Glu Thr Lys Lys Val Ile Gly Gln Leu Leu Leu His Thr Val Lys

245

250

255

His Gly Glu Lys Gly Ile Asp Val Asp Ala Glu Asn Cys Ala Val Cys

260

265

270

Ile Glu Asn Phe Lys Val Lys Asp Ile Ile Arg Ile Leu Pro Cys Lys

275

280

285

His Ile Phe His Arg Ile Cys Ile Asp Pro Trp Leu Leu Asp His Arg

290

295

300

Thr Cys Pro Met Cys Lys Leu Asp Val Ile Lys Ala Leu Gly Tyr Trp

305

310

315

320

Gly Glu Pro Gly Asp Val Gln Glu Met Pro Ala Pro Glu Ser Pro Pro

325

330

335

Gly Arg Asp Pro Ala Ala Asn Leu Ser Leu Ala Leu Pro Asp Asp Asp

340

345

350

Gly Ser Asp Glu Ser Ser Pro Pro Ser Ala Ser Pro Ala Glu Ser Glu

355

360

365

Pro Gln Cys Asp Pro Ser Phe Lys Gly Asp Ala Gly Glu Asn Thr Ala

370

375

380

Leu Leu Glu Ala Gly Arg Ser Asp Ser Arg His Gly Gly Pro Ile Ser

385

390

395

400

&lt;210&gt; 99

&lt;211&gt; 192

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

210/307

&lt;400&gt; 99

Met Phe Cys Pro Leu Lys Leu Ile Leu Leu Pro Val Leu Leu Asp Tyr

1 5 10 15

Ser Leu Gly Leu Asn Asp Leu Asn Val Ser Pro Pro Glu Leu Thr Val

20 25 30

His Val Gly Asp Ser Ala Leu Met Gly Cys Val Phe Gln Ser Thr Glu

35 40 45

Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu His

50 55 60

Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val Pro

65 70 75 80

Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Asn Leu Cys

85 90 95

Asn Asp Gly Ser Leu Leu Leu Gln Asp Val Gln Glu Ala Asp Gln Gly

100 105 110

Thr Tyr Ile Cys Glu Ile Arg Leu Lys Gly Glu Ser Gln Val Phe Lys

115 120 125

Lys Ala Val Val Leu His Val Leu Pro Glu Glu Pro Lys Glu Leu Met

130 135 140

Val His Val Gly Gly Leu Ile Gln Met Gly Cys Val Phe Gln Ser Thr

145 150 155 160

Glu Val Lys His Val Thr Lys Val Glu Trp Ile Phe Ser Gly Arg Arg

165 170 175

Ala Lys Val Thr Arg Arg Lys His His Cys Val Arg Glu Gly Ser Gly

180 185 190

211/307

&lt;210&gt; 100

&lt;211&gt; 260

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 100

Met Ala Gly Ser Pro Leu Leu Trp Gly Pro Arg Ala Gly Gly Val Gly

1 5 10 15

Leu Leu Val Leu Leu Leu Leu Gly Leu Phe Arg Pro Pro Pro Ala Leu

20 25 30

Cys Ala Arg Pro Val Lys Glu Pro Arg Gly Leu Ser Ala Ala Ser Pro

35 40 45

Pro Leu Ala Glu Thr Gly Ala Pro Arg Arg Phe Arg Arg Ser Val Pro

50 55 60

Arg Gly Glu Ala Ala Gly Ala Val Gln Glu Leu Ala Arg Ala Leu Ala

65 70 75 80

His Leu Leu Glu Ala Glu Arg Gln Glu Arg Ala Arg Ala Glu Ala Gln

85 90 95

Glu Ala Glu Asp Gln Gln Ala Arg Val Leu Ala Gln Leu Leu Arg Val

100 105 110

Trp Gly Ala Pro Arg Asn Ser Asp Pro Ala Leu Gly Leu Asp Asp Asp

115 120 125

Pro Asp Ala Pro Ala Ala Gln Leu Ala Arg Ala Leu Leu Arg Ala Arg

130 135 140

Leu Asp Pro Ala Ala Leu Ala Ala Gln Leu Val Pro Ala Pro Val Pro

212/307

145                      150                      155                      160  
 Ala Ala Ala Leu Arg Pro Arg Pro Pro Val Tyr Asp Asp Gly Pro Ala  
                                  165                      170                      175  
 Gly Pro Asp Ala Glu Glu Ala Gly Asp Glu Thr Pro Asp Val Asp Pro  
                                  180                      185                      190  
 Glu Leu Leu Arg Tyr Leu Leu Gly Arg Ile Leu Ala Gly Ser Ala Asp  
                                  195                      200                      205  
 Ser Glu Gly Val Ala Ala Pro Arg Arg Leu Arg Arg Ala Ala Asp His  
                                  210                      215                      220  
 Asp Val Gly Ser Glu Leu Pro Pro Glu Gly Val Leu Gly Ala Leu Leu  
 225                      230                      235                      240  
 Arg Val Lys Arg Leu Glu Thr Pro Ala Pro Gln Val Pro Ala Arg Arg  
                                  245                      250                      255  
 Leu Leu Pro Pro  
                                  260

&lt;210&gt; 101

&lt;211&gt; 1428

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 101

atggttggtg ccatgtggaa ggtgattgtt tcgctggtcc tgttgatgcc tggccccctgt      60  
 gatgggctgt ttcgctccct atacagaagt gtttccatgc cacctaaggg agactcagga      120  
 cagccattat ttctcacccc ttacattgaa gctgggaaga tccaaaaagg aagagaattg      180  
 agtttggtcg gccctttccc aggactgaac atgaagagtt atgccggctt cctcaccgtg      240

213/307

aataagactt acaacagcaa cctcttcttc tggttcttcc cagctcagat acagccagaa 300  
gatgccccag tagttctctg gctacagggt gggccgggag gttcatccat gtttgactc 360  
tttgtggaac atgggcctta tgttgtcaca agtaacatga ctttgcgtga cagagacttc 420  
ccctggacca caacgtcttc catgctttac attgacaatc cagtgggcac aggcttcagt 480  
tttactgatg ataccacagg atatgcagtc aatgaggacg atgtagcacg ggatttatac 540  
agtgcactaa ttcagttttt ccagatattt cctgaatata aaaataatga cttttatgtc 600  
actggggagt cttatgcagg gaaatatgtg ccagccattg cacacctcat ccattccctc 660  
aaccctgtga gagaggtgaa gatcaacctg aacggaattg ctattggaga tggatattct 720  
gatcccgaat caattatagg gggctatgca gaattcctgt accaaattgg cttgttggat 780  
gagaagcaaa aaaagtactt ccagaagcag tgccatgaat gcatagaaca catcaggaag 840  
cagaactggg ttgaggcctt tgaatactg gataaactac tagatggcga cttacaagt 900  
gatccttctt acttccagaa tgttacagga ttagtaatt actataactt tttgcgggtc 960  
acggaacctg aggatcagct ttactatgtg aaatttttgt cactcccaga ggtgagacaa 1020  
gccatccacg tggggaatca gacttttaat gatggaacta tagttgaaaa gtacttgca 1080  
gaagatacag tacagtcagt taagccatgg ttaactgaaa tcatgaataa ttataaggtt 1140  
ctgatctaca atggccaact ggacatcatc gtggcagctg ccctgacaga gcactccttg 1200  
atgggcatgg actggaaagg atcccaggaa tacaagaagg cagaaaaaaaa agtttgaag 1260  
atctttaaat ctgacagtga agtggtggt tacatccggc aagcgggtga cttccatcag 1320  
gtaattattc gaggtggagg acatatttta ccctatgacc agcctctgag agcttttgac 1380  
atgattaatc gattcattta tggaaaagga tgggacctt atgttgga 1428

&lt;210&gt; 102

&lt;211&gt; 678

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

214/307

&lt;400&gt; 102

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atgtccaggg cgcagatctg ggctctgggtg tctgggtgtcg gagggtttgg agctctcggt    60
gctgctacca cgtccaatga gtggaaagtg accacgcgag cctcctcggt gataacagcc    120
acttgggttt accaggggct gtggatgaac tgcgcaggta acgcgttggg ttctttccat    180
tgccgaccgc attttactat cttcaaagta gcaggttata tacaggcatg tagaggactt    240
atgatcgtcg ctgtcagcct gggcttcttt ggttccatat ttgcgtcttt tggaatgaag    300
tgtaccaaag tcggaggctc cgataaagcc aaagctaaaa ttgcttgttt ggctgggatt    360
gtattcatac tgtcagggct gtgctcaatg actggatgtt ccctatatgc aaacaaaatc    420
acaacggaat tctttgalcc tctctttgtt gagcaaaagt atgaattagg agccgctctg    480
tttattggat gggcaggagc ctcaactgtgc ataattgggtg gtgtcatatt ttgcttttca    540
atatctgaca acaacaaaac acccagatac acatacaacg gggccacatc tgtcatgtct    600
tctcggacaa agtatcatgg tggagaagat tttaaaacaa caaaccttc aaaacagttt    660
gataaaaatg cttatgtc                                     678

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&lt;210&gt; 103

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 103

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atggggatcc agacgagccc cgtcctgctg gcctccctgg ggggtggggct ggctactctg    60
ctcggcctgg ctgtgggtc ctacttgggtt cggagggtccc gccggcctca ggctactctc    120
ctggacccca atgaaaagta cctgctacga ctgctagaca agacgactgt gagccacaac    180
accaagaggt tccgctttgc cctgcccacc gccaccaca ctctgggggt gcctgtgggc    240
aaacatatct acctctccac ccgaattgat ggcagcctgg tcatcaggcc atacactcct    300
gtcaccagtg atgaggatca aggtatgtg gâtcttgtca tcaaggtcta cctgaagggt    360

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215/307

gtgcacccca aatttcctga gggaggggaag atgtctcagt acctggatag cctgaaggtt 420  
 ggggatgtgg tggagtttcg ggggccaagc gggttgctca cttaactgg aaaaggcat 480  
 tttacattc agcccaacaa gaaatctcca ccagaacccc gagtggcgaa gaaactggga 540  
 atgattgccg gcgggacagg aatcacccca atgctacagc tgatccgggc catcctgaaa 600  
 gtccctgaag atccaaccca gtgctttctg ctttttgcca accagacaga aaaggatatc 660  
 atcttgccgg aggacttaga ggaactgcag gcccgctatc ccaatcgctt taagctctgg 720  
 ttcactctgg atcatccccc aaaagattgg gcctacagca agggctttgt gactgccgac 780  
 atgatccggg aacacctgcc cgctccaggg gatgatgtgc tggtagtctt ttgtgggcca 840  
 cccccaatgg tgcagctggc ctgccatccc aacttggaca aactgggcta ctacacaaaag 900  
 atgcgattca cctac 915

&lt;210&gt; 104

&lt;211&gt; 681

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

atgggttga caatgaggct ggtcacagca gcactgttac tgggtctcat gatggtggtc 60  
 actggagacg aggatgagaa cagcccggtg gcccatgagg ccctcttga cgaggacacc 120  
 ctcttttgcc agggccttga agttttctac ccagagttgg ggaacattgg ctgcaaggtt 180  
 gttcctgatt gtaacaacta cagacagaag atcacctcct ggatggagcc gatagtcaag 240  
 tccccggggg ccgtggacgg cgcaacctat atcctggtga tggtagtatcc agatgccctt 300  
 agcagagcag aaccagaca gagattctgg agacattggc tggtaacaga tatcaagggc 360  
 gccgacctga agaaaggga gattcagggc caggagtat cagcctacca ggctccctcc 420  
 ccaccggcac acagtggctt ccacgctac cagttctttg tctatcttca ggaaggaaaa 480  
 gtcattcttc tccttcccaa gaaaacaaa actcgaggct cttggaaaat ggacagattt 540



216/307

ctgaaccgtt tccacctggg cgaacctgaa gcaagcacc agtccatgac ccagaactac 600  
 caggactcac caacctcca ggctcccaga gaaagggcca gcgagcccaa gcacaaaaac 660  
 caggcggaga tagctgcctg c 681

&lt;210&gt; 105

&lt;211&gt; 1323

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 105

atggccatcc acaaagcctt ggtgatgtgc ctgggactgc ctctcttctt gttcccaggg 60  
 gcctgggccc agggccatgt cccaccgggc tgcagccaag gcctcaacc cctgtactac 120  
 aacctgtgtg accgctctgg ggcggtggggc atcgctctgg aggccgtggc tggggcgggc 180  
 attgtcacca cgtttgtgct caccatcatc ctgggtggcca gcctcccctt tgtgcaggac 240  
 accaagaaac ggagcctgct ggggaccag gtattcttcc ttctggggac cctgggcctc 300  
 ttctgcctcg tgtttgctg tgtggtgaag cccgacttct ccacctgtgc ctctcggcgc 360  
 ttctcttttg gggttctgtt cgccatctgc ttctcttgtc tggcggctca cgtctttgcc 420  
 ctcaacttcc tggcccggaa gaaccacggg ccccggggct gggatgatt cactgtggct 480  
 ctgctgctga ccctggtaga ggtcatcatc aatacagagt ggctgatcat caccctggtt 540  
 cggggcagtg gcgagggcgg cctcagggc aacagcagcg caggctgggc cgtggcctcc 600  
 ccctgtgcca tcgccaacat ggactttgtc atggcactca tctacgtcat gctgctgctg 660  
 ctgggtgcct tcctgggggc ctggcccgc ctgtgtggcc gctacaagcg ctggcgtaag 720  
 catggggtct ttgtgtcct caccacagcc acctccgtt ccataagggt ggtgtggatc 780  
 gtcatgtata cttacggcaa caagcagcac aacagtccca cctgggatga cccacgctg 840  
 gccatcgcgc tcgcccgaat tgccctgggc ttctgtctct tctacgtcat ccccgaggtc 900  
 tcccaggatga ccaagtccag cccagagcaa agctaccagg gggacatgta cccacccgg 960

217/307

ggcggtgggct atgagaccat cctgaaagag cagaagggtc agagcatgtt cgtggagaac 1020  
 aaggcctttt ccatggatga gccggttgca gctaagaggc cgggtgtcacc atacagcggg 1080  
 tacaatgggc agctgctgac cagtgtgtac cagcccactg agatggccct gatgcacaaa 1140  
 gttccgtccg aaggagctta cgacatcatc ctcccacggg ccaccgcaa cagccaggtg 1200  
 atgggcagtg ccaactcgac cctgcgggct gaagacatgt actcggccca gagccaccag 1260  
 gcggccacac cgccgaaaga cggcaagaac tctcaggtct ttagaaacc ctacgtgtgg 1320  
 gac 1323

&lt;210&gt; 106

&lt;211&gt; 795

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 106

atggccgctg ccgtcccgaa gaggatgagg gggccagcac aagcgaaact gctgcccggg 60  
 tcggccatcc aagcccttgt ggggttgcg cggccgctgg tcttggcgt cctgcttgtg 120  
 tccgcccgtc tatccagtgt tgtatcacgg actgattcac cgagcccaac cgtactcaac 180  
 tcacatattt ctaccccaaa tgtgaatgct ttaacacatg aaaaccaaac caaaccttct 240  
 atttccaaa tcagcaccac cctccctccc acgacgagta ccaagaaaag tggaggagca 300  
 tctgtggtcc ctcatccctc gcctactcct ctgtctcaag aggaagctga taacaatgaa 360  
 gatcctagta tagaggagga ggatcttctc atgctgaaca gttctccatc cacagccaaa 420  
 gacactctag acaatggcga ttatggagaa ccagactatg actggaccac gggccccagg 480  
 gacgacgacg agtctgatga caccttgga gaaaacagg gttacatgga aattgaacag 540  
 tcagtgaat cttttaagat gccatcctca aatatagaag aggaagacag ccatttcttt 600  
 ttcatctta ttatttttgc tttttgcatt gctgtgttt acattacata tcacaacaaa 660  
 aggaagattt ttcttctggt tcaaagcagg aaatggcgtg atggccttg ttccaaaaca 720

218/307

gtggaatacc atcgccataga tcagaatgtt aatgaggcaa tgccttcttt gaagattacc 780  
aatgattata ttttt 795

&lt;210&gt; 107

&lt;211&gt; 624

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 107

atgctggggc tgctggtggc gttgctggcc ctggggctcg ctgtctttgc gctgctggac 60  
gtctggtacc tgggtgcgct tccgtgcgcc gtgctgcgcg cgcgcctgct gcagccgcgc 120  
gtccgtgacc tgctagctga gcagcgcttc ccgggcgcgc tgctgccctc ggacttggac 180  
ctgctgttgc acatgaacaa cgcgcgctac ctgcgcgagg ccgactttgc gcgcgtcgcg 240  
cacctgaccc gctgcggggg gctcggggcg ctgagggagt tgcgggcgca cacggtgctg 300  
gcggcctcgt gcgcgcgcca ccgccgctcg ctgcgcctgc tggagccctt cgaggtgcgc 360  
acccgcctgc tgggctggga cgaccgcgcg ttctacctgg aggcgcgctt tgtcagcctg 420  
cgggacgggt tcgtgtgcgc gctgctgcgc ttccggcagc acctgctggg cacctaccc 480  
gagcgcgtcg tgcagcacct gtgccagcgc aggggtggagc cccctgagct gcccgctgat 540  
ctgcagcact ggatctccta caacgaggcc agcagccagc tgctccgcat ggagagtggg 600  
ctcagtgatg tcaccaagga ccag 624

&lt;210&gt; 108

&lt;211&gt; 1200

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 108

219/307

atggcgtggc ggcggcgcga agccagcgtc ggggctcgcg gcgtgttggc tctggcgttg 60  
ctcgccctgg ccctgtgcgt gcccggggcc cggggccggg ctctcgagtg gttctcggcc 120  
gtggtaaaca tcgagtacgt ggaccgcag accaacctga cgggtgtggag cgtctcgag 180  
agtggccgct tcggcgacag ctcgcccaag gagggcgcgc atggcctggt gggcgctccc 240  
tgggcgcccg gcggagacct cgagggtgc gcgcccga cgcgttctt cgtgcccag 300  
cccggcggcc gaggggcccgc gccctgggtc gccctggtgg ctctggtggg ctgcaccttc 360  
aaggacaagg tgctggtggc ggcgcggagg aacgcctcgg ccgtcgtcct ctacaatgag 420  
gagcgtacg ggaacatcac cttgccatg tctcagcgg gaacaggaaa tatagtggtc 480  
attatgatta gctatccaaa aggaagagaa attttggagc tggtgcaaaa aggaattcca 540  
gtaacgatga ccataggggt tggcacccgg catgtacagg agttcatcag cggtcagtct 600  
gtggtgtttg tggccattgc cttcatcacc atgatgatta tctcgttagc ctggctaata 660  
tttactata tacagcgttt cctatatact ggctctcaga ttggaagtca gagccataga 720  
aaagaaacta agaaagttat tggccagctt ctacttcata ctgtaaagca tggagaaaag 780  
ggaattgatg ttgatgctga aaattgtgca gtgtgtattg aaaatttcaa agtaaaggat 840  
attattagaa ttctgccatg caagcatatt tttcatagaa tatgcattga cccatggctt 900  
ttggatcacc gaacatgtcc aatgtglaaa cttgatgtca tcaaagccct aggatattgg 960  
ggagagcctg gggatgtaca ggagatgcct gctccagaat ctctctctgg aagggatcca 1020  
gctgcaaatt tgagtctagc tttaccagat gatgacggaa gtgatgagag cagtccacca 1080  
tcagcctccc ctgctgaatc tgagccacag tgtgatccca gctttaaagg agatgcagga 1140  
gaaaatacgg catlgctaga agccggcagg agtgactctc ggcatggagg acccatctcc 1200

&lt;210&gt; 109

&lt;211&gt; 576

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

220/307

&lt;400&gt; 109

```

atgttttgcc cactgaaact catcctgctg ccagtggttac tggattattc cttgggcctg      60
aatgacttga atgtttcccc gcctgagcta acagtccatg tgggtgattc agctctgatg      120
ggatgtgttt tccagagcac agaagacaaa tgtatattca agatagactg gactctgtca      180
ccaggagagc acgccaagga cgaatatgtg ctatactatt actccaatct cagtgtgcct      240
attgggcgct tccagaaccg cgtacacttg atgggggaca acttatgcaa tgatggctct      300
ctcctgctcc aagatgtgca agaggctgac cagggaacct atatctgtga aatccgcctc      360
aaaggggaga gccaggtgtt caagaaggcg gtggtactgc atgtgcttcc agaggagccc      420
aaagagctca tgggtccatgt ggggtgattg attcagatgg gatgtgtttt ccagagcaca      480
gaagtgaaac acgtgaccaa ggtagaatgg atattttcag gacggcgcgc aaaggttaaca      540
aggaggaaac atcactgtgt tagagaaggc tctggc                                576

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&lt;210&gt; 110

&lt;211&gt; 780

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 110

```

atggcggggg cgcctgtgct ctggggggccg cgggccgggg gcgtcggcct tttggtgctg      60
ctgctgctcg gcctgtttcg gccgcccccc gcgctctgcg cgcggccggg aaaggagccc      120
cgcggcctaa gcgcagcgtc tccgcccttg gctgagactg gcgtcctcg ccgcttcgg      180
cggtcagtgc cccgaggtga ggccggcggg gcggtgcagg agctggcgcg ggcgttggcg      240
catctgctgg aggccgaacg tcaggagcgg gcgcggggcc aggcgcagga ggctgaggat      300
cagcaggcgc ggcctctggc gcagctgctg cgcgtctggg gcgccccccg caactctgat      360
ccggctctgg gcctggacga cgaccccgac gcgcctgcag cgcagctcgc tcgcgctctg      420
ctccgcgccc gccttgacct tgcgcacctc gcagcccgag ttgtccccgc gcccgctccc      480

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221/307

gccgcggcgc tccgaccccg gcccccggtc tacgacgacg gccccgcggg cccggatgct 540  
 gaggaggcag gcgacgagac acccgacgtg gaccccgagc tgttgaggta cttgctggga 600  
 cggatttcttg cggaagcgc ggactccgag ggggtggcag cccgcgccg cctccgccgt 660  
 gccgccgacc acgatgtggg ctctgagctg cccctgagg gcgtgctggg ggcgtgctg 720  
 cgtgtgaaac gcctagagac cccggcgcgc caggtgcctg cagccgcct cttgccaccc 780

&lt;210&gt; 111

&lt;211&gt; 1633

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (68)... (1498)

&lt;400&gt; 111

acaaccggct ggggtccttg cgcgccgcgg ctcagggagg agcaccgact gcgccgcacc 60  
 ctgagag atg gtt ggt gcc atg tgg aag gtg att gtt tcg ctg gtc ctg 109

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu

1

5

10

ttg atg cct ggc ccc tgt gat ggg ctg ttt cgc tcc cta tac aga agt 157

Leu Met Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser

15

20

25

30

gtt tcc atg cca cct aag gga gac tca gga cag cca tta ttt ctc acc 205

Val Ser Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr

35

40

45

cct tac att gaa gct ggg aag atc caa aaa gga aga gaa ttg agt ttg 253

222/307

Pro Tyr Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu  
 50 55 60  
 gtc ggc cct ttc cca gga ctg aac atg aag agt tat gcc ggc ttc ctc 301  
 Val Gly Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu  
 65 70 75  
 acc gtg aat aag act tac aac agc aac ctc ttc ttc tgg ttc ttc cca 349  
 Thr Val Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro  
 80 85 90  
 gct cag ata cag cca gaa gat gcc cca gta gtt ctc tgg cta cag ggt 397  
 Ala Gln Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly  
 95 100 105 110  
 ggg ccg gga ggt tca tcc atg ttt gga ctc ttt gtg gaa cat ggg cct 445  
 Gly Pro Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro  
 115 120 125  
 tat gtt gtc aca agt aac atg acc ttg cgt gac aga gac ttc ccc tgg 493  
 Tyr Val Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp  
 130 135 140  
 acc aca acg ctc tcc atg ctt tac att gac aat cca gtg ggc aca ggc 541  
 Thr Thr Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly  
 145 150 155  
 ttc agt ttt act gat gat acc cac gga tat gca gtc aat gag gac gat 589  
 Phe Ser Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp  
 160 165 170  
 gta gca cgg gat tta tac agt gca cta att cag ttt ttc cag ata ttt 637  
 Val Ala Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe

223/307

|   |     |     |     |      |
|---|-----|-----|-----|------|
| 175   | 180 | 185 | 190 |      |
| cct gaa tat aaa aat aat gac ttt tat gtc act ggg gag tct tat gca |     |     |     | 685  |
| Pro Glu Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala |     |     |     |      |
|   | 195 | 200 | 205 |      |
| ggg aaa tat gtg cca gcc att gca cac ctc atc cat tcc ctc aac cct |     |     |     | 733  |
| Gly Lys Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro |     |     |     |      |
|   | 210 | 215 | 220 |      |
| gtg aga gag gtg aag atc aac ctg aac gga att gct att gga gat gga |     |     |     | 781  |
| Val Arg Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly |     |     |     |      |
|   | 225 | 230 | 235 |      |
| tat tct gat ccc gaa tca att ata ggg ggc tat gca gaa ttc ctg tac |     |     |     | 829  |
| Tyr Ser Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr |     |     |     |      |
|   | 240 | 245 | 250 |      |
| caa att ggc ttg ttg gat gag aag caa aaa aag tac ttc cag aag cag |     |     |     | 877  |
| Gln Ile Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln |     |     |     |      |
|   | 255 | 260 | 265 | 270  |
| tgc cat gaa tgc ata gaa cac atc agg aag cag aac tgg ttt gag gcc |     |     |     | 925  |
| Cys His Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala |     |     |     |      |
|   | 275 | 280 | 285 |      |
| ttt gaa ata ctg gat aaa cta cta gat ggc gac tta aca agt gat cct |     |     |     | 973  |
| Phe Glu Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro |     |     |     |      |
|   | 290 | 295 | 300 |      |
| tct tac ttc cag aat gtt aca gga tgt agt aat tac tat aac ttt ttg |     |     |     | 1021 |
| Ser Tyr Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu |     |     |     |      |
|   | 305 | 310 | 315 |      |



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|   |      |
|---|------|
| cgg tgc acg gaa cct gag gat cag ctt tac tat gtg aaa ttt ttg tca | 1069 |
| Arg Cys Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser |      |
| 320 325 330   |      |
| ctc cca gag gtg aga caa gcc atc cac gtg ggg aat cag act ttt aat | 1117 |
| Leu Pro Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn |      |
| 335 340 345 350   |      |
| gat gga act ata gtt gaa aag tac ttg cga gaa gat aca gta cag tca | 1165 |
| Asp Gly Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser |      |
| 355 360 365   |      |
| gtt aag cca tgg tta act gaa atc atg aat aat tat aag gtt ctg atc | 1213 |
| Val Lys Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile |      |
| 370 375 380   |      |
| tac aat ggc caa ctg gac atc atc gtg gca gct gcc ctg aca gag cac | 1261 |
| Tyr Asn Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu His |      |
| 385 390 395   |      |
| tcc ttg atg ggc atg gac tgg aaa gga tcc cag gaa tac aag aag gca | 1309 |
| Ser Leu Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala |      |
| 400 405 410   |      |
| gaa aaa aaa gtt tgg aag atc ttt aaa tct gac agt gaa gtg gct ggt | 1357 |
| Glu Lys Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly |      |
| 415 420 425 430   |      |
| tac atc cgg caa gcg ggt gac ttc cat cag gta att att cga ggt gga | 1405 |
| Tyr Ile Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly |      |
| 435 440 445   |      |
| gga cat att tta ccc tat gac cag cct ctg aga gct ttt gac atg att | 1453 |

225/307

Gly His Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile

450

455

460

aat cga ttc att tat gga aaa gga tgg gat cct tat gtt gga taaac 1500

Asn Arg Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly

465

470

475

taccttccca aaagagaaca tcagaggttt tcattgctga aaagaaaatc gtaaaaacag 1560

aaaatgtcat aggaataaaa aaattatctt ttcatatctg caagattttt ttcataata 1620

aaaattatcc ttg 1633

&lt;210&gt; 112

&lt;211&gt; 1095

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (192)... (872)

&lt;400&gt; 112

ctttaaaatg tcattggtaa accatacttg atcctaaatt cctgtacttc ctcaggccat 60

ccgagcatga aacgctgtca cctaccacaca tccgctggct gtgacgcttg tcaaagtgtt 120

ctctatcggc tgcattgcta gaccacaaaa gcgttctgac cggacagtgt cactggagaa 180

ggcggcgcga c atg tcc agg gcg cag atc tgg gct ctg gtg tct ggt gtc 230

Met Ser Arg Ala Gln Ile Trp Ala Leu Val Ser Gly Val

1

5

10

gga ggg ttt gga gct ctc gtt gct gct acc acg tcc aat gag tgg aaa 278

Gly Gly Phe Gly Ala Leu Val Ala Ala Thr Thr Ser Asn Glu Trp Lys

226/307

|   |     |     |     |
|---|-----|-----|-----|
| 15  | 20  | 25  |     |
| gtg acc acg cga gcc tcc tcg gtg ata aca gcc act tgg gtt tac cag |     |     | 326 |
| Val Thr Thr Arg Ala Ser Ser Val Ile Thr Ala Thr Trp Val Tyr Gln |     |     |     |
| 30  | 35  | 40  | 45  |
| ggg ctg tgg atg aac tgc gca ggt aac gcg ttg ggt tct ttc cat tgc |     |     | 374 |
| Gly Leu Trp Met Asn Cys Ala Gly Asn Ala Leu Gly Ser Phe His Cys |     |     |     |
|   | 50  | 55  | 60  |
| cga ccg cat ttt act atc ttc aaa gta gca ggt tat ata cag gca tgt |     |     | 422 |
| Arg Pro His Phe Thr Ile Phe Lys Val Ala Gly Tyr Ile Gln Ala Cys |     |     |     |
|   | 65  | 70  | 75  |
| aga gga ctt atg atc gct gct gtc agc ctg ggc ttc ttt ggt tcc ata |     |     | 470 |
| Arg Gly Leu Met Ile Ala Ala Val Ser Leu Gly Phe Phe Gly Ser Ile |     |     |     |
|   | 80  | 85  | 90  |
| ttt gcg ctc ttt gga atg aag tgt acc aaa gtc gga ggc tcc gat aaa |     |     | 518 |
| Phe Ala Leu Phe Gly Met Lys Cys Thr Lys Val Gly Gly Ser Asp Lys |     |     |     |
|   | 95  | 100 | 105 |
| gcc aaa gct aaa att gct tgt ttg gct ggg att gta ttc ata ctg tca |     |     | 566 |
| Ala Lys Ala Lys Ile Ala Cys Leu Ala Gly Ile Val Phe Ile Leu Ser |     |     |     |
| 110   | 115 | 120 | 125 |
| ggg ctg tgc tca atg act gga tgt tcc cta tat gca aac aaa atc aca |     |     | 614 |
| Gly Leu Cys Ser Met Thr Gly Cys Ser Leu Tyr Ala Asn Lys Ile Thr |     |     |     |
|   | 130 | 135 | 140 |
| acg gaa ttc ttt gat cct ctc ttt gtt gag caa aag tat gaa tta gga |     |     | 662 |
| Thr Glu Phe Phe Asp Pro Leu Phe Val Glu Gln Lys Tyr Glu Leu Gly |     |     |     |
|   | 145 | 150 | 155 |

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gcc gct ctg ttt att gga tgg gca gga gcc tca ctg tgc ata att ggt 710  
 Ala Ala Leu Phe Ile Gly Trp Ala Gly Ala Ser Leu Cys Ile Ile Gly  
 160 165 170  
 ggt gtc ata ttt tgc ttt tca ata tct gac aac aac aaa aca ccc aga 758  
 Gly Val Ile Phe Cys Phe Ser Ile Ser Asp Asn Asn Lys Thr Pro Arg  
 175 180 185  
 tac aca tac aac ggg gcc aca tct gtc atg tct tct cgg aca aag tat 806  
 Tyr Thr Tyr Asn Gly Ala Thr Ser Val Met Ser Ser Arg Thr Lys Tyr  
 190 195 200 205  
 cat ggt gga gaa gat ttt aaa aca aca aac cct tca aaa cag ttt gat 854  
 His Gly Gly Glu Asp Phe Lys Thr Thr Asn Pro Ser Lys Gln Phe Asp  
 210 215 220  
 aaa aat gct tat gtc t aaaagagctc gcgggcaagc tgcctcttga 900  
 Lys Asn Ala Tyr Val  
 225  
 gtttgttata aaagcgaact gttcacaaaa tgatcccatc aaggccctcc cataattaac 960  
 actcaaaact atttttaaaa tatgcatttg aagcatctgt tgattgtatg gatgtaagtg 1020  
 ttcttacata gttagttata tactaatcat tttctgttgt ggctttctat aaaaaataaa 1080  
 cagtttattt acagg 1095

&lt;210&gt; 113

&lt;211&gt; 1602

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

228/307

&lt;221&gt; CDS

&lt;222&gt; (34)... (951)

&lt;400&gt; 113

tttgtcaggt ggtggaggaa aaggcgctcc gtc atg ggg atc cag acg agc ccc 54

Met Gly Ile Gln Thr Ser Pro

1

5

gtc ctg ctg gcc tcc ctg ggg gtg ggg ctg gtc act ctg ctc ggc ctg 102

Val Leu Leu Ala Ser Leu Gly Val Gly Leu Val Thr Leu Leu Gly Leu

10

15

20

gct gtg ggc tcc tac ttg gtt cgg agg tcc cgc cgg cct cag gtc act 150

Ala Val Gly Ser Tyr Leu Val Arg Arg Ser Arg Arg Pro Gln Val Thr

25

30

35

ctc ctg gac ccc aat gaa aag tac ctg cta cga ctg cta gac aag acg 198

Leu Leu Asp Pro Asn Glu Lys Tyr Leu Leu Arg Leu Leu Asp Lys Thr

40

45

50

55

act gtg agc cac aac acc aag agg ttc cgc ttt gcc ctg ccc acc gcc 246

Thr Val Ser His Asn Thr Lys Arg Phe Arg Phe Ala Leu Pro Thr Ala

60

65

70

cac cac act ctg ggg ctg cct gtg ggc aaa cat atc tac ctc tcc acc 294

His His Thr Leu Gly Leu Pro Val Gly Lys His Ile Tyr Leu Ser Thr

75

80

85

cga att gat ggc agc ctg gtc atc agg cca tac act cct gtc acc agt 342

Arg Ile Asp Gly Ser Leu Val Ile Arg Pro Tyr Thr Pro Val Thr Ser

90

95

100

gat gag gat caa ggc tat gtg gat ctt gtc atc aag gtc tac ctg aag 390

229/307

Asp Glu Asp Gln Gly Tyr Val Asp Leu Val Ile Lys Val Tyr Leu Lys  
 105 110 115  
 ggt gtg cac ccc aaa ttt cct gag gga ggg aag atg tct cag tac ctg 438  
 Gly Val His Pro Lys Phe Pro Glu Gly Gly Lys Met Ser Gln Tyr Leu  
 120 125 130 135  
 gat agc ctg aag gtt ggg gat gtg gtg gag ttt cgg ggg cca agc ggg 486  
 Asp Ser Leu Lys Val Gly Asp Val Val Glu Phe Arg Gly Pro Ser Gly  
 140 145 150  
 ttg ctc act tac act gga aaa ggg cat ttt aac att cag ccc aac aag 534  
 Leu Leu Thr Tyr Thr Gly Lys Gly His Phe Asn Ile Gln Pro Asn Lys  
 155 160 165  
 aaa tct cca cca gaa ccc cga gtg gcg aag aaa ctg gga atg att gcc 582  
 Lys Ser Pro Pro Glu Pro Arg Val Ala Lys Lys Leu Gly Met Ile Ala  
 170 175 180  
 ggc ggg aca gga atc acc cca atg cta cag ctg atc cgg gcc atc ctg 630  
 Gly Gly Thr Gly Ile Thr Pro Met Leu Gln Leu Ile Arg Ala Ile Leu  
 185 190 195  
 aaa gtc cct gaa gat cca acc cag tgc ttt ctg ctt ttt gcc aac cag 678  
 Lys Val Pro Glu Asp Pro Thr Gln Cys Phe Leu Leu Phe Ala Asn Gln  
 200 205 210 215  
 aca gaa aag gat atc atc ttg cgg gag gac tta gag gaa ctg cag gcc 726  
 Thr Glu Lys Asp Ile Ile Leu Arg Glu Asp Leu Glu Glu Leu Gln Ala  
 220 225 230  
 cgc tat ccc aat cgc ttt aag ctc tgg ttc act ctg gat cat ccc cca 774  
 Arg Tyr Pro Asn Arg Phe Lys Leu Trp Phe Thr Leu Asp His Pro Pro

230/307

|  |     |     |      |
|--|-----|-----|------|
| 235  | 240 | 245 |      |
| aaa gat tgg gcc tac agc aag ggc ttt gtg act gcc gac atg atc cgg    |     |     | 822  |
| Lys Asp Trp Ala Tyr Ser Lys Gly Phe Val Thr Ala Asp Met Ile Arg    |     |     |      |
| 250  | 255 | 260 |      |
| gaa cac ctg ccc gct cca ggg gat gat gtg ctg gta ctg ctt tgt ggg    |     |     | 870  |
| Glu His Leu Pro Ala Pro Gly Asp Asp Val Leu Val Leu Leu Cys Gly    |     |     |      |
| 265  | 270 | 275 |      |
| cca ccc cca atg gtg cag ctg gcc tgc cat ccc aac ttg gac aaa ctg    |     |     | 918  |
| Pro Pro Pro Met Val Gln Leu Ala Cys His Pro Asn Leu Asp Lys Leu    |     |     |      |
| 280  | 285 | 290 | 295  |
| ggc tac tca caa aag atg cga ttc acc tac tg agc atc ctc agcttc cctg |     |     | 970  |
| Gly Tyr Ser Gln Lys Met Arg Phe Thr Tyr                            |     |     |      |
| 300  | 305 |     |      |
| gtgctgttcg ctgcagttgt tccccatcag tactcaagca ctataagcct tagattcctt  |     |     | 1030 |
| tcctcagagt ttcaggtttt ttcagttaca tctagagctg aaatctggat agtacctgca  |     |     | 1090 |
| ggaacaatat tcctgtagcc atggaagagg gccaaaggctc agtcactcct tggatggcct |     |     | 1150 |
| cctaaatctc cccgtggcaa caggctccagg agaggcccat ggagcagtct ctccatgga  |     |     | 1210 |
| gtaagaagga agggagcatg tacgcttggg ccaagattgg ctagttcctt gatagcatct  |     |     | 1270 |
| tactctcacc ttctttgtgt ctgtgatgaa aggaacagtc tgtgcaatgg gttttactta  |     |     | 1330 |
| aacttcactg ttcaacctat gagcaaactc gtatgtgtga gtataagttg agcatagcat  |     |     | 1390 |
| acttcagag gtggtcttat ggagatggca agaaaggagg aaatgatttc ttcagatctc   |     |     | 1450 |
| aaaggagtct gaaatatcat atttctgtgt gtgtctctct cagccctgc ccaggctaga   |     |     | 1510 |
| gggaaacagc tactgataat cgaaaactgc tgtttgtggc aggaaccct ggctgtgcaa   |     |     | 1570 |
| ataaatgggg ctgaggcccc tgtgtgatat tg                                |     |     | 1602 |

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&lt;210&gt; 114

&lt;211&gt; 897

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (99)... (782)

&lt;400&gt; 114

agtcctccca aagtacttgt gtccgggtgg tggactggat tcgctgcgga gccctggaag 60

ctgcctttcc ttctccctgt gcttaaccag aggtgccc atg ggt tgg aca atg 113

Met Gly Trp Thr Met

1 5

agg ctg gtc aca gca gca ctg tta ctg ggt ctc atg atg gtg gtc act 161

Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu Met Met Val Val Thr

10 15 20

gga gac gag gat gag aac agc ccg tgt gcc cat gag gcc ctc ttg gac 209

Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His Glu Ala Leu Leu Asp

25 30 35

gag gac acc ctc ttt tgc cag ggc ctt gaa gtt ttc tac cca gag ttg 257

Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val Phe Tyr Pro Glu Leu

40 45 50

ggg aac att ggc tgc aag gtt gtt cct gat tgt aac aac tac aga cag 305

Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys Asn Asn Tyr Arg Gln

55 60 65

aag atc acc tcc tgg atg gag ccg ata gtc aag ttc ccg ggg gcc gtg 353



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Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys Phe Pro Gly Ala Val  
 70 75 80 85  
 gac ggc gca acc tat atc ctg gtg atg gtg gat cca gat gcc cct agc 401  
 Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp Pro Asp Ala Pro Ser  
 90 95 100  
 aga gca gaa ccc aga cag aga ttc tgg aga cat tgg ctg gta aca gat 449  
 Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His Trp Leu Val Thr Asp  
 105 110 115  
 atc aag ggc gcc gac ctg aag aaa ggg aag att cag ggc cag gag tta 497  
 Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile Gln Gly Gln Glu Leu  
 120 125 130  
 tca gcc tac cag gct ccc tcc cca ccg gca cac agt ggc ttc cat cgc 545  
 Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His Ser Gly Phe His Arg  
 135 140 145  
 tac cag ttc ttt gtc tat ctt cag gaa gga aaa gtc atc tct ctc ctt 593  
 Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys Val Ile Ser Leu Leu  
 150 155 160 165  
 ccc aag gaa aac aaa act cga ggc tct tgg aaa atg gac aga ttt ctg 641  
 Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys Met Asp Arg Phe Leu  
 170 175 180  
 aac cgt ttc cac ctg ggc gaa cct gaa gca agc acc cag ttc atg acc 689  
 Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser Thr Gln Phe Met Thr  
 185 190 195  
 cag aac tac cag gac tca cca acc ctc cag gct ccc aga gaa agg gcc 737  
 Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala Pro Arg Glu Arg Ala

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|   |     |     |     |
|---|-----|-----|-----|
| 200   | 205 | 210 |     |
| agc gag ccc aag cac aaa aac cag gcg gag ata gct gcc tgc t         |     |     | 780 |
| Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile Ala Ala Cys           |     |     |     |
| 215   | 220 | 225 |     |
| agatagccgg ctttgccatc cgggcatgtg gccacactgc ccaccaccga cgatgtgggt |     |     | 840 |
| atggaacccc ctctggatac agaaccctt cttttccaaa taaaaaaaa atcatcc      |     |     | 897 |

&lt;210&gt; 115

&lt;211&gt; 1866

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (142)... (1467)

&lt;400&gt; 115

|  |     |
|--|-----|
| gcccgcattgc gggggcgtgg cagtcaacag caacaacca cagccggca gggccagaaa | 60  |
| ctcccatctc cctcaccagc cggaagtac gagtcggctc agcctggagg gacccaacca | 120 |
| gagcctggcc tgggagccag g atg gcc atc cac aaa gcc ttg gtg atg tgc  | 171 |

Met Ala Ile His Lys Ala Leu Val Met Cys

|   |   |    |     |
|---|---|----|-----|
| 1   | 5 | 10 |     |
| ctg gga ctg cct ctc ttc ctg ttc cca ggg gcc tgg gcc cag ggc cat |   |    | 219 |
| Leu Gly Leu Pro Leu Phe Leu Phe Pro Gly Ala Trp Ala Gln Gly His |   |    |     |

|   |    |    |     |
|---|----|----|-----|
| 15  | 20 | 25 |     |
| gtc cca ccc ggc tgc agc caa ggc ctc aac ccc ctg tac tac aac ctg |    |    | 267 |
| Val Pro Pro Gly Cys Ser Gln Gly Leu Asn Pro Leu Tyr Tyr Asn Leu |    |    |     |

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|   |     |     |     |
|---|-----|-----|-----|
| 30  | 35  | 40  |     |
| tgt gac cgc tct ggg gcg tgg ggc atc gtc ctg gag gcc gtg gct ggg | 315 |     |     |
| Cys Asp Arg Ser Gly Ala Trp Gly Ile Val Leu Glu Ala Val Ala Gly |     |     |     |
| 45  | 50  | 55  |     |
| gcg ggc att gtc acc acg ttt gtg ctc acc atc atc ctg gtg gcc agc | 363 |     |     |
| Ala Gly Ile Val Thr Thr Phe Val Leu Thr Ile Ile Leu Val Ala Ser |     |     |     |
| 60  | 65  | 70  |     |
| ctc ccc ttt gtg cag gac acc aag aaa cgg agc ctg ctg ggg acc cag | 411 |     |     |
| Leu Pro Phe Val Gln Asp Thr Lys Lys Arg Ser Leu Leu Gly Thr Gln |     |     |     |
| 75  | 80  | 85  | 90  |
| gta ttc ttc ctt ctg ggg acc ctg ggc ctc ttc tgc ctc gtg ttt gcc | 459 |     |     |
| Val Phe Phe Leu Leu Gly Thr Leu Gly Leu Phe Cys Leu Val Phe Ala |     |     |     |
| 95  | 100 | 105 |     |
| tgt gtg gtg aag ccc gac ttc tcc acc tgt gcc tct cgg cgc ttc ctc | 507 |     |     |
| Cys Val Val Lys Pro Asp Phe Ser Thr Cys Ala Ser Arg Arg Phe Leu |     |     |     |
| 110   | 115 | 120 |     |
| ttt ggg gtt ctg ttc gcc atc tgc ttc tct tgt ctg gcg gct cac gtc | 555 |     |     |
| Phe Gly Val Leu Phe Ala Ile Cys Phe Ser Cys Leu Ala Ala His Val |     |     |     |
| 125   | 130 | 135 |     |
| ttt gcc ctc aac ttc ctg gcc cgg aag aac cac ggg ccc cgg ggc tgg | 603 |     |     |
| Phe Ala Leu Asn Phe Leu Ala Arg Lys Asn His Gly Pro Arg Gly Trp |     |     |     |
| 140   | 145 | 150 |     |
| gtg atc ttc act gtg gct ctg ctg ctg acc ctg gta gag gtc atc atc | 651 |     |     |
| Val Ile Phe Thr Val Ala Leu Leu Leu Thr Leu Val Glu Val Ile Ile |     |     |     |
| 155   | 160 | 165 | 170 |

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|   |      |
|---|------|
| aat aca gag tgg ctg atc atc acc ctg gtt cgg ggc agt ggc gag ggc | 699  |
| Asn Thr Glu Trp Leu Ile Ile Thr Leu Val Arg Gly Ser Gly Glu Gly |      |
| 175 180 185   |      |
| ggc cct cag ggc aac agc agc gca ggc tgg gcc gtg gcc tcc ccc tgt | 747  |
| Gly Pro Gln Gly Asn Ser Ser Ala Gly Trp Ala Val Ala Ser Pro Cys |      |
| 190 195 200   |      |
| gcc atc gcc aac atg gac ttt gtc atg gca ctc atc tac gtc atg ctg | 795  |
| Ala Ile Ala Asn Met Asp Phe Val Met Ala Leu Ile Tyr Val Met Leu |      |
| 205 210 215   |      |
| ctg ctg ctg ggt gcc ttc ctg ggg gcc tgg ccc gcc ctg tgt ggc cgc | 843  |
| Leu Leu Leu Gly Ala Phe Leu Gly Ala Trp Pro Ala Leu Cys Gly Arg |      |
| 220 225 230   |      |
| tac aag cgc tgg cgt aag cat ggg gtc ttt gtg ctc ctc acc aca gcc | 891  |
| Tyr Lys Arg Trp Arg Lys His Gly Val Phe Val Leu Leu Thr Thr Ala |      |
| 235 240 245 250   |      |
| acc tcc gtt gcc ata tgg gtg gtg tgg atc gtc atg tat act tac ggc | 939  |
| Thr Ser Val Ala Ile Trp Val Val Trp Ile Val Met Tyr Thr Tyr Gly |      |
| 255 260 265   |      |
| aac aag cag cac aac agt ccc acc tgg gat gac ccc acg ctg gcc atc | 987  |
| Asn Lys Gln His Asn Ser Pro Thr Trp Asp Asp Pro Thr Leu Ala Ile |      |
| 270 275 280   |      |
| gcc ctc gcc gcc aat gcc tgg gcc ttc gtc ctc ttc tac gtc atc ccc | 1035 |
| Ala Leu Ala Ala Asn Ala Trp Ala Phe Val Leu Phe Tyr Val Ile Pro |      |
| 285 290 295   |      |
| gag gtc tcc cag gtg acc aag tcc agc cca gag caa agc tac cag ggg | 1083 |

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Glu Val Ser Gln Val Thr Lys Ser Ser Pro Glu Gln Ser Tyr Gln Gly  
 300 305 310  
 gac atg tac ccc acc cgg ggc gtg ggc tat gag acc atc ctg aaa gag 1131  
 Asp Met Tyr Pro Thr Arg Gly Val Gly Tyr Glu Thr Ile Leu Lys Glu  
 315 320 325 330  
 cag aag ggt cag agc atg ttc gtg gag aac aag gcc ttt tcc atg gat 1179  
 Gln Lys Gly Gln Ser Met Phe Val Glu Asn Lys Ala Phe Ser Met Asp  
 335 340 345  
 gag ccg gtt gca gct aag agg ccg gtg tca cca tac agc ggg tac aat 1227  
 Glu Pro Val Ala Ala Lys Arg Pro Val Ser Pro Tyr Ser Gly Tyr Asn  
 350 355 360  
 ggg cag ctg ctg acc agt gtg tac cag ccc act gag atg gcc ctg atg 1275  
 Gly Gln Leu Leu Thr Ser Val Tyr Gln Pro Thr Glu Met Ala Leu Met  
 365 370 375  
 cac aaa gtt ccg tcc gaa gga gct tac gac atc atc ctc cca cgg gcc 1323  
 His Lys Val Pro Ser Glu Gly Ala Tyr Asp Ile Ile Leu Pro Arg Ala  
 380 385 390  
 acc gcc aac agc cag gtg atg ggc agt gcc aac tcg acc ctg cgg gct 1371  
 Thr Ala Asn Ser Gln Val Met Gly Ser Ala Asn Ser Thr Leu Arg Ala  
 395 400 405 410  
 gaa gac atg tac tcg gcc cag agc cac cag gcg gcc aca ccg ccg aaa 1419  
 Glu Asp Met Tyr Ser Ala Gln Ser His Gln Ala Ala Thr Pro Pro Lys  
 415 420 425  
 gac ggc aag aac tct cag gtc ttt aga aac ccc tac gtg tgg gac 1464  
 Asp Gly Lys Asn Ser Gln Val Phe Arg Asn Pro Tyr Val Trp Asp

237/307

| 430   | 435 | 440 |      |
|---|-----|-----|------|
| tgagtc agcgggtggcg aggagaggcg gtcggatttg gggagggccc tgaggacctg    |     |     | 1520 |
| gccccgggca agggactctc caggctcctc ctccccctgg caggcccagc aacatgtgcc |     |     | 1580 |
| ccagatgtgg aagggcctcc ctctctgcca gtgtttgggt ggggtgcatg ggtgtcccca |     |     | 1640 |
| cccactcctc agtgtttgtg gagtcgagga gccaacccca gcctcctgcc aggatcacct |     |     | 1700 |
| cggcggtcac actccagcca aatagtgttc tcggggtggt ggctgggcag cgcctatgtt |     |     | 1760 |
| tctctggaga ttcttgcaac ctcaagagac ttcccaggcg ctcaggcctg gatcttgctc |     |     | 1820 |
| ctctgtgagg aacaagggtg cctaataaat acatttctgc tttatt                |     |     | 1866 |

&lt;210&gt; 116

&lt;211&gt; 2198

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (50)... (847)

&lt;400&gt; 116

|   |    |
|---|----|
| aaaatggcgt agagcctagc aacagcgcag gctcccagcc gagtccgtt atg gcc | 55 |
|---|----|

Met Ala

1

|   |     |
|---|-----|
| gct gcc gtc ccg aag agg atg agg ggg cca gca caa gcg aaa ctg ctg | 103 |
|---|-----|

Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys Leu Leu

5

10

15

|   |     |
|---|-----|
| ccc ggg tcg gcc atc caa gcc ctt gtg ggg ttg gcg cgg ccg ctg gtc | 151 |
|---|-----|

Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro Leu Val

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|   |     |     |     |
|---|-----|-----|-----|
| 20  | 25  | 30  |     |
| ttg gcg ctc ctg ctt gtg tcc gcc gct cta tcc agt gtt gta tca cgg |     |     | 199 |
| Leu Ala Leu Leu Leu Val Ser Ala Ala Leu Ser Ser Val Val Ser Arg |     |     |     |
| 35  | 40  | 45  | 50  |
| act gat tca ccg agc cca acc gta ctc aac tca cat att tct acc cca |     |     | 247 |
| Thr Asp Ser Pro Ser Pro Thr Val Leu Asn Ser His Ile Ser Thr Pro |     |     |     |
|   | 55  | 60  | 65  |
| aat gtg aat gct tta aca cat gaa aac caa acc aaa cct tct att tcc |     |     | 295 |
| Asn Val Asn Ala Leu Thr His Glu Asn Gln Thr Lys Pro Ser Ile Ser |     |     |     |
|   | 70  | 75  | 80  |
| caa atc agc acc acc ctc cct ccc acg acg agt acc aag aaa agt gga |     |     | 343 |
| Gln Ile Ser Thr Thr Leu Pro Pro Thr Thr Ser Thr Lys Lys Ser Gly |     |     |     |
|   | 85  | 90  | 95  |
| gga gca tct gtg gtc cct cat ccc tgg cct act cct ctg tct caa gag |     |     | 391 |
| Gly Ala Ser Val Val Pro His Pro Ser Pro Thr Pro Leu Ser Gln Glu |     |     |     |
|   | 100 | 105 | 110 |
| gaa gct gat aac aat gaa gat cct agt ata gag gag gag gat ctt ctc |     |     | 439 |
| Glu Ala Asp Asn Asn Glu Asp Pro Ser Ile Glu Glu Glu Asp Leu Leu |     |     |     |
| 115   | 120 | 125 | 130 |
| atg ctg aac agt tct cca tcc aca gcc aaa gac act cta gac aat ggc |     |     | 487 |
| Met Leu Asn Ser Ser Pro Ser Thr Ala Lys Asp Thr Leu Asp Asn Gly |     |     |     |
|   | 135 | 140 | 145 |
| gat tat gga gaa cca gac tat gac tgg acc acg ggc ccc agg gac gac |     |     | 535 |
| Asp Tyr Gly Glu Pro Asp Tyr Asp Trp Thr Thr Gly Pro Arg Asp Asp |     |     |     |
|   | 150 | 155 | 160 |

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gac gag tct gat gac acc ttg gaa gaa aac agg ggt tac atg gaa att 583

Asp Glu Ser Asp Asp Thr Leu Glu Glu Asn Arg Gly Tyr Met Glu Ile

165

170

175

gaa cag tca gtg aaa tct ttt aag atg cca tcc tca aat ata gaa gag 631

Glu Gln Ser Val Lys Ser Phe Lys Met Pro Ser Ser Asn Ile Glu Glu

180

185

190

gaa gac agc cat ttc ttt ttt cat ctt att att ttt gct ttt tgc att 679

Glu Asp Ser His Phe Phe Phe His Leu Ile Ile Phe Ala Phe Cys Ile

195

200

205

210

gct gtt gtt tac att aca tat cac aac aaa agg aag att ttt ctt ctg 727

Ala Val Val Tyr Ile Thr Tyr His Asn Lys Arg Lys Ile Phe Leu Leu

215

220

225

gtt caa agc agg aaa tgg cgt gat ggc ctt tgt tcc aaa aca gtg gaa 775

Val Gln Ser Arg Lys Trp Arg Asp Gly Leu Cys Ser Lys Thr Val Glu

230

235

240

tac cat cgc cta gat cag aat gtt aat gag gca atg cct tct ttg aag 823

Tyr His Arg Leu Asp Gln Asn Val Asn Glu Ala Met Pro Ser Leu Lys

245

250

255

att acc aat gat tat att ttt taaagc actgtgattt gaatttgctt 870

Ile Thr Asn Asp Tyr Ile Phe

260

265

atgtaatttt atttgcttga ctttttatat gatattgtgc aaatgtttgc cataggcaat 930

tggtacttaa atgagaggtg agtctctctt ttgccttggt gctttggaaa ttaaagtca 990

caaacgagta tataattttt tatctgtact tttagagctg agtttaatca ggtgtccaaa 1050

atgtgagtta aacattacct tatatttaca ctgttagttt ttattgtttt agatttatta 1110



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|            |            |             |            |            |             |      |
|------------|------------|-------------|------------|------------|-------------|------|
| tgcttcttct | ggaagtatta | gtgatgctac  | ttttaaaga  | tcctaaactt | gtaactaaat  | 1170 |
| tctgacatat | ctgttactgc | tgactcacat  | tcattctccg | ccattcaaat | actatTTTTT  | 1230 |
| atccacattt | TTTTTgttc  | ccaaactgta  | atgtacaagg | atatgtgtga | taatgctttg  | 1290 |
| gatttgagta | atatTTTTT  | ttcttccaag  | aaaactgctt | tggtatTTTT | tagataattt  | 1350 |
| aaacataatt | taggataatg | atattgctca  | atctgaccac | aattttaggt | aaaacattaa  | 1410 |
| atgtgtcaag | aaatcttggc | aacagagact  | ctgcagcttg | cagtggacat | agataaaatg  | 1470 |
| ttacagagat | actatTTTT  | tggttggaa   | tactatatta | aatttagaag | cagaaactgg  | 1530 |
| taaaatgta  | aatacatgta | caattgcttt  | tagttagcaa | ttgattgtag | catgggttcc  | 1590 |
| tccaagggtt | caagcaatgg | gcagagttaa  | aaattatata | agattcggtt | acttcgttta  | 1650 |
| ttatTTTaca | gtaaatttga | ataaatctta  | gggttcatta | tcacttaa   | aatactgtac  | 1710 |
| ctaggtcttt | caaattaaaa | ttataacctga | atgaagtgtt | ttgtalacat | aaaggatatt  | 1770 |
| tgtgtacaat | tacTTTTTT  | ccccacact   | tgTTTTcttt | gTTTTgttt  | tttatggcaa  | 1830 |
| ctggaaagta | tttactatgg | gattcatTTa  | tgtctgtctt | tcattcataa | agaattgatc  | 1890 |
| aatatgtaaa | tatgtgattt | gaaccatggt  | tgacttaca  | gtgtcactac | agctTTTTtag | 1950 |
| aaaacatagc | cctaatatat | gttaagcagg  | acccgggtga | gccagtgggc | ttgcgcttta  | 2010 |
| tgtagagctg | gaagaaggcc | gtccatcctg  | tctcttgggc | ggacagtgtg | ctttccta    | 2070 |
| agggaaggga | agcacaatgg | aaatacccct  | gaaccgtttt | attgcagtaa | TTTTTTcat   | 2130 |
| atctgaaact | attatTTaat | atTTTgaata  | agatTTTaaa | aaataaatgg | caaagatata  | 2190 |
| aatctatg   |            |             |            |            |             | 2198 |

&lt;210&gt; 117

&lt;211&gt; 2180

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

241/307

&lt;221&gt; CDS

&lt;222&gt; (69)... (695)

&lt;400&gt; 117

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aaccagcgcc gcggacaccg gcaccggcgc cacggactcc gcaggacccc gcgcccgcgc      60
ccgccgct atg ctg ggg ctg ctg gtg gcg ttg ctg gcc ctg ggg ctc gct      110
      Met Leu Gly Leu Leu Val Ala Leu Leu Ala Leu Gly Leu Ala
              1              5              10
gtc ttt gcg ctg ctg gac gtc tgg tac ctg gtg cgc ctt ccg tgc gcc      158
Val Phe Ala Leu Leu Asp Val Trp Tyr Leu Val Arg Leu Pro Cys Ala
      15              20              25              30
gtg ctg cgc gcg cgc ctg ctg cag ccg cgc gtc cgt gac ctg cta gct      206
Val Leu Arg Ala Arg Leu Leu Gln Pro Arg Val Arg Asp Leu Leu Ala
              35              40              45
gag cag cgc ttc ccg ggc cgc gtg ctg ccc tcg gac ttg gac ctg ctg      254
Glu Gln Arg Phe Pro Gly Arg Val Leu Pro Ser Asp Leu Asp Leu Leu
              50              55              60
ttg cac atg aac aac gcg cgc tac ctg cgc gag gcc gac ttt gcg cgc      302
Leu His Met Asn Asn Ala Arg Tyr Leu Arg Glu Ala Asp Phe Ala Arg
              65              70              75
gtc gcg cac ctg acc cgc tgc ggg gtg ctc ggg gcg ctg agg gag ttg      350
Val Ala His Leu Thr Arg Cys Gly Val Leu Gly Ala Leu Arg Glu Leu
              80              85              90
cgg gcg cac acg gtg ctg gcg gcc tcg tgc gcg cgc cac cgc cgc tcg      398
Arg Ala His Thr Val Leu Ala Ala Ser Cys Ala Arg His Arg Arg Ser
      95              100              105              110

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ctg cgc ctg ctg gag ccc ttc gag gtg cgc acc cgc ctg ctg ggc tgg 446

Leu Arg Leu Leu Glu Pro Phe Glu Val Arg Thr Arg Leu Leu Gly Trp

115

120

125

gac gac cgc gcg ttc tac ctg gag gcg cgc ttt gtc agc ctg cgg gac 494

Asp Asp Arg Ala Phe Tyr Leu Glu Ala Arg Phe Val Ser Leu Arg Asp

130

135

140

ggc ttc gtg tgc gcg ctg ctg cgc ttc cgg cag cac ctg ctg ggc acc 542

Gly Phe Val Cys Ala Leu Leu Arg Phe Arg Gln His Leu Leu Gly Thr

145

150

155

tca ccc gag cgc gtc gtg cag cac ctg tgc cag cgc agg gtg gag ccc 590

Ser Pro Glu Arg Val Val Gln His Leu Cys Gln Arg Arg Val Glu Pro

160

165

170

cct gag ctg ccc gct gat ctg cag cac tgg atc tcc tac aac gag gcc 638

Pro Glu Leu Pro Ala Asp Leu Gln His Trp Ile Ser Tyr Asn Glu Ala

175

180

185

190

agc agc cag ctg ctc cgc atg gag agt ggg ctc agt gat gtc acc aag 686

Ser Ser Gln Leu Leu Arg Met Glu Ser Gly Leu Ser Asp Val Thr Lys

195

200

205

gac cag tgaccgcc accttcacac cgtctgccct ggccaccatc ctgggcctgg 740

Asp Gln

gggctgcccc cagatgggca gtctcagcca tactctgttc cagctggagt agcctcctga 800

ccagcctggc ccacctgct ccaccactg ggcccccca gttattgata cccctctgtg 860

ctgggctcca cgctaggcag aaggaggagt ggcattggca tctgaccca gctctgcct 920

caaggtgggg atggatgggc aaaggagagt cctgcctggc cctacgatga ggccactcat 980

gtgggcctag gtaggggagg atggtgcctg gāgcagaggg acccacaagt gcctcccgag 1040

243/307

cctagatcct ggctcggacc actgcaaggg ccgaggcagg gccagaccag agcatcctgg 1100  
gtacaggcct gggctctcca gggcctgggc ctgattcagg tgcagtgggc actcctgaag 1160  
ggtcagagcg gcatctgcca ggcagcccct ctggcttccg ctgagggtgt tgcaggcctg 1220  
gggcagagcc tgggtgggtca gaggccgggg ctagaggcag atggaaggga ggcatttgtc 1280  
gacagaggac ggggcacccg ggctcccact gcagtcggcc ttgcctctc ctcctcctc 1340  
acctccagtc aggctggacg ggagggtagc cttgtggctg agaggggtca gactaggtgg 1400  
cacaggggct cctggaaaga cagcaggctt cctgctgggc gttcccttgt tggagggaat 1460  
agagtggggg tgggactctg caggggtgtc cttgtccact cgcaccctc gccgccacc 1520  
agggccatgc tctgtgactt gggctgatcc ccacccttc tgggcctaca gcaccacagg 1580  
ccgctgtacc cccttagagc tgccctctc tggcctggcc ggcagacgtc ttcttaactc 1640  
ctctgtctc tatattcagc atgttcttg tcagctgtg gcccgccct gccttgcgt 1700  
agcagagcct ctctggcag ctctcaggt ctccctaatg gagacaccag gctactagga 1760  
cactggctgg ggccacccc tctgcctaa tgcctcacct tacagctggg gaaactgagg 1820  
cctggaatgg cccagagtca ccaaggcaaa gttggggctg gtcccagcct gaggtccag 1880  
ctgatgccct cagctcccag agagggggtg cccatctag ctgggtgcag gggtcactgc 1940  
ttgtcagctc agggccctgt gcccgcttg ctttccct acatctgtgc ctgcacatcc 2000  
agaactgcct ccttgccgct gcctccagga agcccacct gagccagagt caagggtgc 2060  
agcactgccc gatagaacac gcccgccctc actgtgttc ttgccttaca gccaccatgg 2120  
gaaagctgca acctttctgt tttattttaa gaaagcccaa cattaaaggg ttttcattgc 2180

&lt;210&gt; 118

&lt;211&gt; 1527

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

244/307

&lt;221&gt; CDS

&lt;222&gt; (103)... (1305)

&lt;400&gt; 118

agttttccag ggccggcggtg ggtgtccgct tctctctgct cttegactgc accgcactcg 60

cgcgtgaccc tgactccccc tagtcagctc agcgggtgctg cc atg gcg tgg cgg 114

Met Ala Trp Arg

1

cgg cgc gaa gcc agc gtc ggg gct cgc ggc gtg ttg gct ctg gcg ttg 162

Arg Arg Glu Ala Ser Val Gly Ala Arg Gly Val Leu Ala Leu Ala Leu

5 10 15 20

ctc gcc ctg gcc ctg tgc gtg ccc ggg gcc cgg ggc cgg gct ctc gag 210

Leu Ala Leu Ala Leu Cys Val Pro Gly Ala Arg Gly Arg Ala Leu Glu

25 30 35

tgg ttc tcg gcc gtg gta aac atc gag tac gtg gac ccg cag acc aac 258

Trp Phe Ser Ala Val Val Asn Ile Glu Tyr Val Asp Pro Gln Thr Asn

40 45 50

ctg acg gtg tgg agc gtc tcg gag agt ggc cgc ttc ggc gac agc tcg 306

Leu Thr Val Trp Ser Val Ser Glu Ser Gly Arg Phe Gly Asp Ser Ser

55 60 65

ccc aag gag ggc gcg cat ggc ctg gtg ggc gtc ccg tgg gcg ccc ggc 354

Pro Lys Glu Gly Ala His Gly Leu Val Gly Val Pro Trp Ala Pro Gly

70 75 80

gga gac ctc gag ggc tgc gcg ccc gac acg cgc ttc ttc gtg ccc gag 402

Gly Asp Leu Glu Gly Cys Ala Pro Asp Thr Arg Phe Phe Val Pro Glu

85 90 95 100

245/307

|   |     |
|---|-----|
| ccc ggc ggc cga ggg gcc gcg ccc tgg gtc gcc ctg gtg gct cgt ggg | 450 |
| Pro Gly Gly Arg Gly Ala Ala Pro Trp Val Ala Leu Val Ala Arg Gly |     |
| 105 110 115   |     |
| ggc tgc acc ttc aag gac aag gtg ctg gtg gcg gcg cgg agg aac gcc | 498 |
| Gly Cys Thr Phe Lys Asp Lys Val Leu Val Ala Ala Arg Arg Asn Ala |     |
| 120 125 130   |     |
| tgc gcc gtc gtc ctc tac aat gag gag cgc tac ggg aac atc acc ttg | 546 |
| Ser Ala Val Val Leu Tyr Asn Glu Glu Arg Tyr Gly Asn Ile Thr Leu |     |
| 135 140 145   |     |
| ccc atg tct cac gcg gga aca gga aat ata gtg gtc att atg att agc | 594 |
| Pro Met Ser His Ala Gly Thr Gly Asn Ile Val Val Ile Met Ile Ser |     |
| 150 155 160   |     |
| tat cca aaa gga aga gaa att ttg gag ctg gtg caa aaa gga att cca | 642 |
| Tyr Pro Lys Gly Arg Glu Ile Leu Glu Leu Val Gln Lys Gly Ile Pro |     |
| 165 170 175 180   |     |
| gta acg atg acc ata ggg gtt ggc acc cgg cat gta cag gag ttc atc | 690 |
| Val Thr Met Thr Ile Gly Val Gly Thr Arg His Val Gln Glu Phe Ile |     |
| 185 190 195   |     |
| agc ggt cag tct gtg gtg ttt gtg gcc att gcc ttc atc acc atg atg | 738 |
| Ser Gly Gln Ser Val Val Phe Val Ala Ile Ala Phe Ile Thr Met Met |     |
| 200 205 210   |     |
| att atc tcg tta gcc tgg cta ata ttt tac tat ata cag cgt ttc cta | 786 |
| Ile Ile Ser Leu Ala Trp Leu Ile Phe Tyr Tyr Ile Gln Arg Phe Leu |     |
| 215 220 225   |     |
| tat act ggc tct cag att gga agt cag agc cat aga aaa gaa act aag | 834 |

246/307

Tyr Thr Gly Ser Gln Ile Gly Ser Gln Ser His Arg Lys Glu Thr Lys  
 230 235 240  
 aaa gtt att ggc cag ctt cta ctt cat act gta aag cat gga gaa aag 882  
 Lys Val Ile Gly Gln Leu Leu Leu His Thr Val Lys His Gly Glu Lys  
 245 250 255 260  
 gga att gat gtt gat gct gaa aat tgt gca gtg tgt att gaa aat ttc 930  
 Gly Ile Asp Val Asp Ala Glu Asn Cys Ala Val Cys Ile Glu Asn Phe  
 265 270 275  
 aaa gta aag gat att att aga att ctg cca tgc aag cat att ttt cat 978  
 Lys Val Lys Asp Ile Ile Arg Ile Leu Pro Cys Lys His Ile Phe His  
 280 285 290  
 aga ata tgc att gac cca tgg ctt ttg gat cac cga aca tgt cca atg 1026  
 Arg Ile Cys Ile Asp Pro Trp Leu Leu Asp His Arg Thr Cys Pro Met  
 295 300 305  
 tgt aaa ctt gat gtc atc aaa gcc cta gga tat tgg gga gag cct ggg 1074  
 Cys Lys Leu Asp Val Ile Lys Ala Leu Gly Tyr Trp Gly Glu Pro Gly  
 310 315 320  
 gat gta cag gag atg cct gct cca gaa tct cct cct gga agg gat cca 1122  
 Asp Val Gln Glu Met Pro Ala Pro Glu Ser Pro Pro Gly Arg Asp Pro  
 325 330 335 340  
 gct gca aat ttg agt cta gct tta cca gat gat gac gga agt gat gag 1170  
 Ala Ala Asn Leu Ser Leu Ala Leu Pro Asp Asp Asp Gly Ser Asp Glu  
 345 350 355  
 agc agt cca cca tca gcc tcc cct gct gaa tct gag cca cag tgt gat 1218  
 Ser Ser Pro Pro Ser Ala Ser Pro Ala Glu Ser Glu Pro Gln Cys Asp

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|  |     |     |      |
|--|-----|-----|------|
| 360  | 365 | 370 |      |
| ccc agc ttt aaa gga gat gca gga gaa aat acg gca ttg cta gaa gcc    |     |     | 1266 |
| Pro Ser Phe Lys Gly Asp Ala Gly Glu Asn Thr Ala Leu Leu Glu Ala    |     |     |      |
| 375  | 380 | 385 |      |
| ggc agg agt gac tct cgg cat gga gga ccc atc tcc tagcacac           |     |     | 1310 |
| Gly Arg Ser Asp Ser Arg His Gly Gly Pro Ile Ser                    |     |     |      |
| 390  | 395 | 400 |      |
| gtgcccactg aagtggcacc aacagaagtt tggcttgaac taaaggacat tttatttttt  |     |     | 1370 |
| ttacttttagc acataatttg tatatttgaa aataatgtat attattttac ctattagatt |     |     | 1430 |
| ctgatttgat atacaaagga ctaagatatt ttcttcttga agagactttt cgattagtcc  |     |     | 1490 |
| tcatatattt atctactaaa atagagtgtt taccatg                           |     |     | 1527 |

&lt;210&gt; 119

&lt;211&gt; 1905

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (125)... (703)

&lt;400&gt; 119

|  |     |
|--|-----|
| gagcctaacc tagagtgtc gcagcagtct ttcagttgag ctgggggact gcagctgtgg | 60  |
| ggagatttca gtgcattgcc tcccctgggt gctcttcac ttggatttga aagttgagag | 120 |
| cagc atg ttt tgc cca ctg aaa ctc atc ctg ctg cca gtg tta ctg gat | 169 |

Met Phe Cys Pro Leu Lys Leu Ile Leu Leu Pro Val Leu Leu Asp



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|   |     |
|---|-----|
| tat tcc ttg ggc ctg aat gac ttg aat gtt tcc ccg cct gag cta aca | 217 |
| Tyr Ser Leu Gly Leu Asn Asp Leu Asn Val Ser Pro Pro Glu Leu Thr |     |
| 20 25 30  |     |
| gtc cat gtg ggt gat tca gct ctg atg gga tgt gtt ttc cag agc aca | 265 |
| Val His Val Gly Asp Ser Ala Leu Met Gly Cys Val Phe Gln Ser Thr |     |
| 35 40 45  |     |
| gaa gac aaa tgt ata ttc aag ata gac tgg act ctg tca cca gga gag | 313 |
| Glu Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu |     |
| 50 55 60  |     |
| cac gcc aag gac gaa tat gtg cta tac tat tac tcc aat ctc agt gtg | 361 |
| His Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val |     |
| 65 70 75  |     |
| cct att ggg cgc ttc cag aac cgc gta cac ttg atg ggg gac aac tta | 409 |
| Pro Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Asn Leu |     |
| 80 85 90 95   |     |
| tgc aat gat ggc tct ctc ctg ctc caa gat gtg caa gag gct gac cag | 457 |
| Cys Asn Asp Gly Ser Leu Leu Leu Gln Asp Val Gln Glu Ala Asp Gln |     |
| 100 105 110   |     |
| gga acc tat atc tgt gaa atc cgc ctc aaa ggg gag agc cag gtg ttc | 505 |
| Gly Thr Tyr Ile Cys Glu Ile Arg Leu Lys Gly Glu Ser Gln Val Phe |     |
| 115 120 125   |     |
| aag aag gcg gtg gta ctg cat gtg ctt cca gag gag ccc aaa gag ctc | 553 |
| Lys Lys Ala Val Val Leu His Val Leu Pro Glu Glu Pro Lys Glu Leu |     |
| 130 135 140   |     |
| atg gtc cat gtg ggt gga ttg att cag atg gga tgt gtt ttc cag agc | 601 |

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Met Val His Val Gly Gly Leu Ile Gln Met Gly Cys Val Phe Gln Ser

145

150

155

aca gaa gtg aaa cac gtg acc aag gta gaa tgg ata ttt tca gga cgg 649

Thr Glu Val Lys His Val Thr Lys Val Glu Trp Ile Phe Ser Gly Arg

160

165

170

175

cgc gca aag gta aca agg agg aaa cat cac tgt gtt aga gaa ggc tct 697

Arg Ala Lys Val Thr Arg Arg Lys His His Cys Val Arg Glu Gly Ser

180

185

190

ggc tgatggtatc aggacaaagg tagaatcagg cacatgagga ggtgttgcaa 750

Gly

gagcctgggc tttggtgctt atcagaactg gaccttctcc tagcaatttc agctttctgg 810

tgggaaagat aactccaatg aagaacaaga acaagaagat gatgatgatg cttaactttt 870

tggatgccga tatgagattg tacatgagga gattgtattt cgttactacc acaaactcag 930

gatgtctgcg gagtactccc agagctgggg ccacttccag aatcgtgtga acctggtggg 990

ggacattttc cgcaatgacg gttccatcat gttcaagga gtgagggagt cagatggagg 1050

aaactacacc tgcagtatcc acctagggaa cctggtgttc aagaaaacca ttgtgctgca 1110

tgtcageccg gaagagcctc gaacactggt gaccccgga gccctgaggc ctctggtctt 1170

gggtggtaat cagttggtga tcattgtggg aattgtctgt gccacaatcc tgctgctccc 1230

tgttctgata ttgatcgtga agaagacctg tggaaataag agttcagtga attctacagt 1290

cttggtgaag aacacgaaga agactaatcc agagataaaa gaaaaaccct gccattttga 1350

aagatgtgaa ggggagaaac acatttactc cccaataatt gtacgggagg tgatcgagga 1410

agaagaacca agtgaanaat cagaggccac ctacatgacc atgcaccag tttggccttc 1470

tctgaggtca gatcggaaca actcacttga aaaaaagtca ggtgggggaa tgccaaaaac 1530

acagcaagcc ttttgagaag aatggagagt ccttcatct cagcagcggg ggagactctc 1590

tcctgtgtgt gtcttgggcc actctaccag tgatttcaga ctcccgtct cccagctgtc 1650

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ctcctgtctc attgtttggt caatacactg aagatggaga atttggagcc tggcagagag 1710  
 actggacagc tctggaggaa caggcctgct gaggggaggg gagcatggac ttggcctctg 1770  
 gagtgggaca ctggccctgg gaaccaggct gagctgagtg gcctcaaacc ccccgttgga 1830  
 tcagaccctc ctgtgggcag ggttcttagt ggatgagtta ctgggaagaa tcagagataa 1890  
 aaaccaaccc aaatc 1905

&lt;210&gt; 120

&lt;211&gt; 998

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (50)... (832)

&lt;400&gt; 120

gcacttgcca gccagtcgc ccgccggag cccggctcgc tggggcagc atg gcg 55

Met Ala

1

ggg tcg ccg ctg ctc tgg ggg ccg cgg gcc ggg ggc gtc ggc ctt ttg 103

Gly Ser Pro Leu Leu Trp Gly Pro Arg Ala Gly Gly Val Gly Leu Leu

5

10

15

gtg ctg ctg ctg ctc ggc ctg ttt cgg ccg ccc ccc gcg ctc tgc gcg 151

Val Leu Leu Leu Leu Gly Leu Phe Arg Pro Pro Pro Ala Leu Cys Ala

20

25

30

cgg ccg gta aag gag ccc cgc ggc cta agc gca gcg tct ccg ccc ttg 199

Arg Pro Val Lys Glu Pro Arg Gly Leu Ser Ala Ala Ser Pro Pro Leu

251/307

|   |     |     |     |     |
|---|-----|-----|-----|-----|
| 35  | 40  | 45  | 50  |     |
| gct gag act ggc gct cct cgc cgc ttc cgg cgg tca gtg ccc cga ggt |     |     |     | 247 |
| Ala Glu Thr Gly Ala Pro Arg Arg Phe Arg Arg Ser Val Pro Arg Gly |     |     |     |     |
|   | 55  | 60  | 65  |     |
| gag gcg gcg ggg gcg gtg cag gag ctg gcg cgg gcg ctg gcg cat ctg |     |     |     | 295 |
| Glu Ala Ala Gly Ala Val Gln Glu Leu Ala Arg Ala Leu Ala His Leu |     |     |     |     |
|   | 70  | 75  | 80  |     |
| ctg gag gcc gaa cgt cag gag cgg gcg cgg gcc gag gcg cag gag gct |     |     |     | 343 |
| Leu Glu Ala Glu Arg Gln Glu Arg Ala Arg Ala Glu Ala Gln Glu Ala |     |     |     |     |
|   | 85  | 90  | 95  |     |
| gag gat cag cag gcg cgc gtc ctg gcg cag ctg ctg cgc gtc tgg ggc |     |     |     | 391 |
| Glu Asp Gln Gln Ala Arg Val Leu Ala Gln Leu Leu Arg Val Trp Gly |     |     |     |     |
| 100   | 105 | 110 |     |     |
| gcc ccc cgc aac tct gat ccg gct ctg ggc ctg gac gac gac ccc gac |     |     |     | 439 |
| Ala Pro Arg Asn Ser Asp Pro Ala Leu Gly Leu Asp Asp Asp Pro Asp |     |     |     |     |
| 115   | 120 | 125 | 130 |     |
| gcg cct gca gcg cag ctc gct cgc gct ctg ctc cgc gcc cgc ctt gac |     |     |     | 487 |
| Ala Pro Ala Ala Gln Leu Ala Arg Ala Leu Leu Arg Ala Arg Leu Asp |     |     |     |     |
|   | 135 | 140 | 145 |     |
| cct gcc gcc ctc gca gcc cag ctt gtc ccc gcg ccc gtc ccc gcc gcg |     |     |     | 535 |
| Pro Ala Ala Leu Ala Ala Gln Leu Val Pro Ala Pro Val Pro Ala Ala |     |     |     |     |
|   | 150 | 155 | 160 |     |
| gcg ctc cga ccc cgg ccc ccg gtc tac gac gac ggc ccc gcg ggc ccg |     |     |     | 583 |
| Ala Leu Arg Pro Arg Pro Pro Val Tyr Asp Asp Gly Pro Ala Gly Pro |     |     |     |     |
| 165   | 170 | 175 |     |     |

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gat gct gag gag gca ggc gac gag aca ccc gac gtg gac ccc gag ctg 631  
 Asp Ala Glu Glu Ala Gly Asp Glu Thr Pro Asp Val Asp Pro Glu Leu  
 180 185 190  
 ttg agg tac ttg ctg gga cgg att ctt gcg gga agc gcg gac tcc gag 679  
 Leu Arg Tyr Leu Leu Gly Arg Ile Leu Ala Gly Ser Ala Asp Ser Glu  
 195 200 205 210  
 ggg gtg gca gcc ccg cgc cgc ctc cgc cgt gcc gcc gac cac gat gtg 727  
 Gly Val Ala Ala Pro Arg Arg Leu Arg Arg Ala Ala Asp His Asp Val  
 215 220 225  
 ggc tct gag ctg ccc cct gag ggc gtg ctg ggg gcg ctg ctg cgt gtg 775  
 Gly Ser Glu Leu Pro Pro Glu Gly Val Leu Gly Ala Leu Leu Arg Val  
 230 235 240  
 aaa cgc cta gag acc ccg gcg ccc cag gtg cct gca cgc cgc ctc ttg 823  
 Lys Arg Leu Glu Thr Pro Ala Pro Gln Val Pro Ala Arg Arg Leu Leu  
 245 250 255  
 cca ccc t gagcactgcc cggatcccggt gcaccctggg acccagaagt gcccccgcca 880  
 Pro Pro  
 260  
 tccccccacc aggactgctc cccgccagca cgtccagagc aacttacccc ggccagccag 940  
 ccctctcacc cgaggatccc taccctctgg cccacaata aacatgatct gaagcagc 998

&lt;210&gt; 121

&lt;211&gt; 337

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

253/307

&lt;400&gt; 121

Met Thr Ala Gly Gly Gln Ala Glu Ala Glu Gly Ala Gly Gly Glu Pro  
 1 5 10 15  
 Gly Ala Ala Arg Leu Pro Ser Arg Val Ala Arg Leu Leu Ser Ala Leu  
 20 25 30  
 Phe Tyr Gly Thr Cys Ser Phe Leu Ile Val Leu Val Asn Lys Ala Leu  
 35 40 45  
 Leu Thr Thr Tyr Gly Phe Pro Ser Pro Ile Phe Leu Gly Ile Gly Gln  
 50 55 60  
 Met Ala Ala Thr Ile Met Ile Leu Tyr Val Ser Lys Leu Asn Lys Ile  
 65 70 75 80  
 Ile His Phe Pro Asp Phe Asp Lys Lys Ile Pro Val Lys Leu Phe Pro  
 85 90 95  
 Leu Pro Leu Leu Tyr Val Gly Asn His Ile Ser Gly Leu Ser Ser Thr  
 100 105 110  
 Ser Lys Leu Ser Leu Pro Met Phe Thr Val Leu Arg Lys Phe Thr Ile  
 115 120 125  
 Pro Leu Thr Leu Leu Leu Glu Thr Ile Ile Leu Gly Lys Gln Tyr Ser  
 130 135 140  
 Leu Asn Ile Ile Leu Ser Val Phe Ala Ile Ile Leu Gly Ala Phe Ile  
 145 150 155 160  
 Ala Ala Gly Ser Asp Leu Ala Phe Asn Leu Glu Gly Tyr Ile Phe Val  
 165 170 175  
 Phe Leu Asn Asp Ile Phe Thr Ala Ala Asn Gly Val Tyr Thr Lys Gln  
 180 185 190

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Lys Met Asp Pro Lys Glu Leu Gly Lys Tyr Gly Val Leu Phe Tyr Asn

195

200

205

Ala Cys Phe Met Ile Ile Pro Thr Leu Ile Ile Ser Val Ser Thr Gly

210

215

220

Asp Leu Gln Gln Ala Thr Glu Phe Asn Gln Trp Lys Asn Val Val Phe

225

230

235

240

Ile Leu Gln Phe Leu Leu Ser Cys Phe Leu Gly Phe Leu Leu Met Tyr

245

250

255

Ser Thr Val Leu Cys Ser Tyr Tyr Asn Ser Ala Leu Thr Thr Ala Val

260

265

270

Val Gly Ala Ile Lys Asn Val Ser Val Ala Tyr Ile Gly Ile Leu Ile

275

280

285

Gly Gly Asp Tyr Ile Phe Ser Leu Leu Asn Phe Val Gly Leu Asn Ile

290

295

300

Cys Met Ala Gly Gly Leu Arg Tyr Ser Phe Leu Thr Leu Ser Ser Gln

305

310

315

320

Leu Lys Pro Lys Pro Val Gly Glu Glu Asn Ile Cys Leu Asp Leu Lys

325

330

335

Ser

&lt;210&gt; 122

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

255/307

&lt;400&gt; 122

Met Ala Glu Ala Glu Glu Ser Pro Gly Asp Pro Gly Thr Ala Ser Pro  
1 5 10 15  
Arg Pro Leu Phe Ala Gly Leu Ser Asp Ile Ser Ile Ser Gln Asp Ile  
20 25 30  
Pro Val Glu Gly Glu Ile Thr Ile Pro Met Arg Ser Arg Ile Arg Glu  
35 40 45  
Phe Asp Ser Ser Thr Leu Asn Glu Ser Val Arg Asn Thr Ile Met Arg  
50 55 60  
Asp Leu Lys Ala Val Gly Lys Lys Phe Met His Val Leu Tyr Pro Arg  
65 70 75 80  
Lys Ser Asn Thr Leu Leu Arg Asp Trp Asp Leu Trp Gly Pro Leu Ile  
85 90 95  
Leu Cys Val Thr Leu Ala Leu Met Leu Gln Arg Asp Ser Ala Asp Ser  
100 105 110  
Glu Lys Asp Gly Gly Pro Gln Phe Ala Glu Val Phe Val Ile Val Trp  
115 120 125  
Phe Gly Ala Val Thr Ile Thr Leu Asn Ser Lys Leu Leu Gly Gly Asn  
130 135 140  
Ile Ser Phe Phe Gln Ser Leu Cys Val Leu Gly Tyr Cys Ile Leu Pro  
145 150 155 160  
Leu Thr Val Ala Met Leu Ile Cys Arg Leu Val Leu Leu Ala Asp Pro  
165 170 175  
Gly Pro Val Asn Phe Met Val Arg Leu Phe Val Val Ile Val Met Phe  
180 185 190



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Ala Trp Ser Ile Val Ala Ser Thr Ala Phe Leu Ala Asp Ser Gln Pro

195

200

205

Pro Asn Arg Arg Ala Leu Ala Val Tyr Pro Val Phe Leu Phe Tyr Phe

210

215

220

Val Ile Ser Trp Met Ile Leu Thr Phe Thr Pro Gln

225

230

235

&lt;210&gt; 123

&lt;211&gt; 560

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 123

Met Ala Ala Pro Ala Glu Ser Leu Arg Arg Arg Lys Thr Gly Tyr Ser

1

5

10

15

Asp Pro Glu Pro Glu Ser Pro Pro Ala Pro Gly Arg Gly Pro Ala Gly

20

25

30

Ser Pro Ala His Leu His Thr Gly Thr Phe Trp Leu Thr Arg Ile Val

35

40

45

Leu Leu Lys Ala Leu Ala Phe Val Tyr Phe Val Ala Phe Leu Val Ala

50

55

60

Phe His Gln Asn Lys Gln Leu Ile Gly Asp Arg Gly Leu Leu Pro Cys

65

70

75

80

Arg Val Phe Leu Lys Asn Phe Gln Gln Tyr Phe Gln Asp Arg Thr Ser

85

90

95

Trp Glu Val Phe Ser Tyr Met Pro Thr Ile Leu Trp Leu Met Asp Trp

257/307

|   |     |     |     |
|---|-----|-----|-----|
| 100   | 105 | 110 |     |
| Ser Asp Met Asn Ser Asn Leu Asp Leu Leu Ala Leu Leu Gly Leu Gly |     |     |     |
| 115   | 120 | 125 |     |
| Ile Ser Ser Phe Val Leu Ile Thr Gly Cys Ala Asn Met Leu Leu Met |     |     |     |
| 130   | 135 | 140 |     |
| Ala Ala Leu Trp Gly Leu Tyr Met Ser Leu Val Asn Val Gly His Val |     |     |     |
| 145   | 150 | 155 | 160 |
| Trp Tyr Ser Phe Gly Trp Glu Ser Gln Leu Leu Glu Thr Gly Phe Leu |     |     |     |
| 165   | 170 | 175 |     |
| Gly Ile Phe Leu Cys Pro Leu Trp Thr Leu Ser Arg Leu Pro Gln His |     |     |     |
| 180   | 185 | 190 |     |
| Thr Pro Thr Ser Arg Ile Val Leu Trp Gly Phe Arg Trp Leu Ile Phe |     |     |     |
| 195   | 200 | 205 |     |
| Arg Ile Met Leu Gly Ala Gly Leu Ile Lys Ile Arg Gly Asp Arg Cys |     |     |     |
| 210   | 215 | 220 |     |
| Trp Arg Asp Leu Thr Cys Met Asp Phe His Tyr Glu Thr Gln Pro Met |     |     |     |
| 225   | 230 | 235 | 240 |
| Pro Asn Pro Val Ala Tyr Tyr Leu His His Ser Pro Trp Trp Phe His |     |     |     |
| 245   | 250 | 255 |     |
| Arg Phe Glu Thr Leu Ser Asn His Phe Ile Glu Leu Leu Val Pro Phe |     |     |     |
| 260   | 265 | 270 |     |
| Phe Leu Phe Leu Gly Arg Arg Ala Cys Ile Ile His Gly Val Leu Gln |     |     |     |
| 275   | 280 | 285 |     |
| Ile Leu Phe Gln Ala Val Leu Ile Val Ser Gly Asn Leu Ser Phe Leu |     |     |     |
| 290   | 295 | 300 |     |

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Asn Trp Leu Thr Met Val Pro Ser Leu Ala Cys Phe Asp Asp Ala Thr  
305 310 315 320  
Leu Gly Phe Leu Phe Pro Ser Gly Pro Gly Ser Leu Lys Asp Arg Val  
325 330 335  
Leu Gln Met Gln Arg Asp Ile Arg Gly Ala Arg Pro Glu Pro Arg Phe  
340 345 350  
Gly Ser Val Val Arg Arg Ala Ala Asn Val Ser Leu Gly Val Leu Leu  
355 360 365  
Ala Trp Leu Ser Val Pro Val Val Leu Asn Leu Leu Ser Ser Arg Gln  
370 375 380  
Val Met Asn Thr His Phe Asn Ser Leu His Ile Val Asn Thr Tyr Gly  
385 390 395 400  
Ala Phe Gly Ser Ile Thr Lys Glu Arg Ala Glu Val Ile Leu Gln Gly  
405 410 415  
Thr Ala Ser Ser Asn Ala Ser Ala Pro Asp Ala Met Trp Glu Asp Tyr  
420 425 430  
Glu Phe Lys Cys Lys Pro Gly Asp Pro Ser Arg Arg Pro Cys Leu Ile  
435 440 445  
Ser Pro Tyr His Tyr Arg Leu Asp Trp Leu Met Trp Phe Ala Ala Phe  
450 455 460  
Gln Thr Tyr Glu His Asn Asp Trp Ile Ile His Leu Ala Gly Lys Leu  
465 470 475 480  
Leu Ala Ser Asp Ala Glu Ala Leu Ser Leu Leu Ala His Asn Pro Phe  
485 490 495  
Ala Gly Arg Pro Pro Pro Arg Trp Val Arg Gly Glu His Tyr Arg Tyr

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500                      505                      510  
 Lys Phe Ser Arg Pro Gly Gly Arg His Ala Ala Glu Gly Lys Trp Trp  
 515                      520                      525  
 Val Arg Lys Arg Ile Gly Ala Tyr Phe Pro Pro Leu Ser Leu Glu Glu  
 530                      535                      540  
 Leu Arg Pro Tyr Phe Arg Asp Arg Gly Trp Pro Leu Pro Gly Pro Leu  
 545                      550                      555                      560

&lt;210&gt; 124

&lt;211&gt; 406

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 124

Met Ala Glu Asn Gly Lys Asn Cys Asp Gln Arg Arg Val Ala Met Asn  
 1                      5                      10                      15  
 Lys Glu His His Asn Gly Asn Phe Thr Asp Pro Ser Ser Val Asn Glu  
 20                      25                      30  
 Lys Lys Arg Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg  
 35                      40                      45  
 Gln Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile  
 50                      55                      60  
 Leu Lys Glu Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val  
 65                      70                      75                      80  
 Ser Phe Leu Leu Leu Leu Ala Val Leu Ile Ala Thr Tyr Tyr Val Glu  
 85                      90                      95

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Gly Val His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu  
100 105 110  
Tyr Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly  
115 120 125  
Thr Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser  
130 135 140  
Val Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro  
145 150 155 160  
Pro Tyr Pro Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly  
165 170 175  
Thr Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys  
180 185 190  
Met Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met  
195 200 205  
Ala Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr  
210 215 220  
Gln Glu Phe Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Asp Phe  
225 230 235 240  
Ala Ser Arg Ala Lys Leu Ala Val Gln Lys Leu Val Gln Lys Val Gly  
245 250 255  
Phe Phe Gly Ile Leu Ala Cys Ala Ser Ile Pro Asn Pro Leu Phe Asp  
260 265 270  
Leu Ala Gly Ile Thr Cys Gly His Phe Leu Val Pro Phe Trp Thr Phe  
275 280 285  
Phe Gly Ala Thr Leu Ile Gly Lys Ala Ile Ile Lys Met His Ile Gln

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290                      295                      300  
 Lys Ile Phe Val Ile Ile Thr Phe Ser Lys His Ile Val Glu Gln Met  
 305                      310                      315                      320  
 Val Ala Phe Ile Gly Ala Val Pro Gly Ile Gly Pro Ser Leu Gln Lys  
                     325                      330                      335  
 Pro Phe Gln Glu Tyr Leu Glu Ala Gln Arg Gln Lys Leu His His Lys  
                     340                      345                      350  
 Ser Glu Met Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe  
                     355                      360                      365  
 Glu Lys Leu Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile  
                     370                      375                      380  
 Asn Ser Met Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn  
 385                      390                      395                      400  
 Ser Glu Glu Lys Thr Lys  
                     405

&lt;210&gt; 125

&lt;211&gt; 453

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 125

Met Gly Val Leu Gly Arg Val Leu Leu Trp Leu Gln Leu Cys Ala Leu  
 1                      5                      10                      15  
 Thr Gln Ala Val Ser Lys Leu Trp Val Pro Asn Thr Asp Phe Asp Val  
                     20                      25                      30

262/307

Ala Ala Asn Trp Ser Gln Asn Arg Thr Pro Cys Ala Gly Gly Ala Val

35

40

45

Glu Phe Pro Ala Asp Lys Met Val Ser Val Leu Val Gln Glu Gly His

50

55

60

Ala Val Ser Asp Met Leu Leu Pro Leu Asp Gly Glu Leu Val Leu Ala

65

70

75

80

Ser Gly Ala Gly Phe Gly Val Ser Asp Val Gly Ser His Leu Asp Cys

85

90

95

Gly Ala Gly Glu Pro Ala Val Phe Arg Asp Ser Asp Arg Phe Ser Trp

100

105

110

His Asp Pro His Leu Trp Arg Ser Gly Asp Glu Ala Pro Gly Leu Phe

115

120

125

Phe Val Asp Ala Glu Arg Val Pro Cys Arg His Asp Asp Val Phe Phe

130

135

140

Pro Pro Ser Ala Ser Phe Arg Val Gly Leu Gly Pro Gly Ala Ser Pro

145

150

155

160

Val Arg Val Arg Ser Ile Ser Ala Leu Gly Arg Thr Phe Thr Arg Asp

165

170

175

Glu Asp Leu Ala Val Phe Leu Ala Ser Arg Ala Gly Arg Leu Arg Phe

180

185

190

His Gly Pro Gly Ala Leu Ser Val Gly Pro Glu Asp Cys Ala Asp Pro

195

200

205

Ser Gly Cys Val Cys Gly Asn Ala Glu Ala Gln Pro Trp Ile Cys Ala

210

215

220

Ala Leu Leu Gln Pro Leu Gly Gly Arg Cys Pro Gln Ala Ala Cys His

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225                      230                      235                      240  
Ser Ala Leu Arg Pro Gln Gly Gln Cys Cys Asp Leu Cys Gly Ala Val  
                         245                      250                      255  
Val Leu Leu Thr His Gly Pro Ala Phe Asp Leu Glu Arg Tyr Arg Ala  
                         260                      265                      270  
Arg Ile Leu Asp Thr Phe Leu Gly Leu Pro Gln Tyr His Gly Leu Gln  
                         275                      280                      285  
Val Ala Val Ser Lys Val Pro Arg Ser Ser Arg Leu Arg Glu Ala Asp  
                         290                      295                      300  
Thr Glu Ile Gln Val Val Leu Val Glu Asn Gly Pro Glu Thr Gly Gly  
305                      310                      315                      320  
Ala Gly Arg Leu Ala Arg Ala Leu Leu Ala Asp Val Ala Glu Asn Gly  
                         325                      330                      335  
Glu Ala Leu Gly Val Leu Glu Ala Thr Met Arg Glu Ser Gly Ala His  
                         340                      345                      350  
Val Trp Gly Ser Ser Ala Ala Gly Leu Ala Gly Gly Val Ala Ala Ala  
                         355                      360                      365  
Val Leu Leu Ala Leu Leu Val Leu Leu Val Ala Pro Pro Leu Leu Arg  
                         370                      375                      380  
Arg Ala Gly Arg Leu Arg Trp Arg Arg His Glu Ala Ala Ala Pro Ala  
385                      390                      395                      400  
Gly Ala Pro Leu Gly Phe Arg Asn Pro Val Phe Asp Val Thr Ala Ser  
                         405                      410                      415  
Glu Glu Leu Pro Leu Pro Arg Arg Leu Ser Leu Val Pro Lys Ala Ala  
                         420                      425                      430



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Ala Asp Ser Thr Ser His Ser Tyr Phe Val Asn Pro Leu Phe Ala Gly

435

440

445

Ala Glu Ala Glu Ala

450

&lt;210&gt; 126

&lt;211&gt; 59

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 126

Met Thr Ser Val Ser Thr Gln Leu Ser Leu Val Leu Met Ser Leu Leu

1

5

10

15

Leu Val Leu Pro Val Val Glu Ala Val Glu Ala Gly Asp Ala Ile Ala

20

25

30

Leu Leu Leu Gly Val Val Leu Ser Ile Thr Gly Ile Cys Ala Cys Leu

35

40

45

Gly Val Tyr Ala Arg Lys Arg Asn Gly Gln Met

50

55

&lt;210&gt; 127

&lt;211&gt; 210

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 127

Met Ala Leu Pro Gln Met Cys Asp Gly Ser His Leu Ala Ser Thr Leu

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|   |     |     |     |
|---|-----|-----|-----|
| 1   | 5   | 10  | 15  |
| Arg Tyr Cys Met Thr Val Ser Gly Thr Val Val Leu Val Ala Gly Thr |     |     |     |
| 20  | 25  | 30  |     |
| Leu Cys Phe Ala Trp Trp Ser Glu Gly Asp Ala Thr Ala Gln Pro Gly |     |     |     |
| 35  | 40  | 45  |     |
| Gln Leu Ala Pro Pro Thr Glu Tyr Pro Val Pro Glu Gly Pro Ser Pro |     |     |     |
| 50  | 55  | 60  |     |
| Leu Leu Arg Ser Val Ser Phe Val Cys Cys Gly Ala Gly Gly Leu Leu |     |     |     |
| 65  | 70  | 75  | 80  |
| Leu Leu Ile Gly Leu Leu Trp Ser Val Lys Ala Ser Ile Pro Gly Pro |     |     |     |
| 85  | 90  | 95  |     |
| Pro Arg Trp Asp Pro Tyr His Leu Ser Arg Asp Leu Tyr Tyr Leu Thr |     |     |     |
| 100   | 105 | 110 |     |
| Val Glu Ser Ser Glu Lys Glu Ser Cys Arg Thr Pro Lys Val Val Asp |     |     |     |
| 115   | 120 | 125 |     |
| Ile Pro Thr Tyr Glu Glu Ala Val Ser Phe Pro Val Ala Glu Gly Pro |     |     |     |
| 130   | 135 | 140 |     |
| Pro Thr Pro Pro Ala Tyr Pro Thr Glu Glu Ala Leu Glu Pro Ser Gly |     |     |     |
| 145   | 150 | 155 | 160 |
| Ser Arg Asp Ala Leu Leu Ser Thr Gln Pro Ala Trp Pro Pro Pro Ser |     |     |     |
| 165   | 170 | 175 |     |
| Tyr Glu Ser Ile Ser Leu Ala Leu Asp Ala Val Ser Ala Glu Thr Thr |     |     |     |
| 180   | 185 | 190 |     |
| Pro Ser Ala Thr Arg Ser Cys Ser Gly Leu Val Gln Thr Ala Arg Gly |     |     |     |
| 195   | 200 | 205 |     |

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Gly Ser

210

&lt;210&gt; 128

&lt;211&gt; 165

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 128

Met Asp Ser Ser Arg Ala Arg Gln Gln Leu Arg Arg Arg Phe Leu Leu

1

5

10

15

Leu Pro Asp Ala Glu Ala Gln Leu Asp Arg Glu Gly Asp Ala Gly Pro

20

25

30

Glu Thr Ser Thr Ala Val Glu Lys Lys Glu Lys Pro Leu Pro Arg Leu

35

40

45

Asn Ile His Ser Gly Phe Trp Ile Leu Ala Ser Ile Val Val Thr Tyr

50

55

60

Tyr Val Asp Phe Phe Lys Thr Leu Lys Glu Asn Phe His Thr Ser Ser

65

70

75

80

Trp Phe Leu Cys Gly Ser Ala Leu Leu Leu Val Ser Leu Ser Ile Ala

85

90

95

Phe Tyr Cys Ile Val Tyr Leu Glu Trp Tyr Cys Gly Ile Gly Glu Tyr

100

105

110

Asp Val Lys Tyr Pro Ala Leu Ile Pro Ile Thr Thr Ala Ser Phe Ile

115

120

125

Ala Ala Gly Ile Cys Phe Asn Ile Ala Leu Trp His Val Trp Ser Phe

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130 135 140  
 Phe Thr Pro Leu Leu Leu Phe Thr Gln Phe Met Gly Val Val Met Phe  
 145 150 155 160

Ile Thr Leu Leu Gly

165

<210> 129

<211> 162

<212> PRT

<213> Homo sapiens

<400> 129

Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu  
 1 5 10 15

Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln  
 20 25 30

Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala  
 35 40 45

Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Phe  
 50 55 60

Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly  
 65 70 75 80

Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His  
 85 90 95

Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp  
 100 105 110

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Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val

115

120

125

Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro

130

135

140

His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val

145

150

155

160

Arg Arg

&lt;210&gt; 130

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 130

Met Ala Leu Ala Leu Ala Ala Leu Ala Ala Val Glu Pro Ala Cys Gly

1

5

10

15

Ser Arg Tyr Gln Gln Leu Gln Asn Glu Glu Glu Ser Gly Glu Pro Glu

20

25

30

Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile Ser Ala Glu

35

40

45

Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro

50

55

60

Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu

65

70

75

80

Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly Arg Asp Glu

85

90

95

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Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile

100

105

110

Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala Phe Leu Phe

115

120

125

Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala

130

135

140

Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp

145

150

155

160

Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr Phe Asp Gly

165

170

175

Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe Leu Leu Phe

180

185

190

Leu Arg Gly Phe Ile Asn Tyr Ala Lys Val Arg Lys Met Pro Glu Thr

195

200

205

Phe Ser Asn Leu Pro Arg Thr Arg Val Leu Phe Ile Tyr

210

215

220

&lt;210&gt; 131

&lt;211&gt; 1011

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 131

atgacggccg gcggccaggc cgaggccgag ggcgctggcg gggagcccgg cgcggcgcgg 60

ctgccctcgc ggggtggccc gctgctgtcg gcgctcttct acgggacctg ctccttcctc 120

atcgtgcttg tcaacaaggc gctgctgacc acctacggtt tcccgtcacc aattttcctt 180

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ggaattggac agatggcagc caccataatg atactatatg tgtccaagct aaacaaaatc 240  
 attcacttcc ctgattttga taagaaaatt cctgtaaage tgtttcctct gcctctcctc 300  
 tacgttggaa accacataag tggattatca agcacaagta aattaagcct accgatgttc 360  
 accgtgctca ggaaattcac cattccactt accttacttc tggaaccat catacttggg 420  
 aagcagtatt cactcaacat catcctcagt gtctttgcca ttattctcgg ggctttcata 480  
 gcagctgggt ctgaccttgc ttttaactta gaaggctata tttttgtatt cctgaatgat 540  
 atcttcacag cagcaaatgg agtttatacc aaacagaaaa tggacccaaa ggagctaggg 600  
 aaatacggag tacttttcta caatgcctgc ttcattgatta tcccaactct tattattagt 660  
 gtctccactg gagacctgca acaggctact gaattcaacc aatggaagaa tgttgtgttt 720  
 atcctacagt ttcttcttct ctgttttttg gggtttctgc tgatgtactc cacggttctg 780  
 tgcagctatt acaattcagc cctgacgaca gcagtgggtg gagccatcaa gaatgtatcc 840  
 gttgcctaca ttgggatatt aatcggtgga gactacattt tctctttgtt aaactttgta 900  
 gggttaaata tttgcatggc agggggcttg agatattcct ttttaacact gagcagccag 960  
 ttaaaaccta aacctgtggg tgaagaaaac atctgttttg atttgaagag c 1011

&lt;210&gt; 132

&lt;211&gt; 708

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 132

atggcggaag cggaggagtc tccaggagac cgggggacag catcgcccag gccctgttt 60  
 gcaggccttt cagatatatc catctcacia gacatccccg tagaaggaga aatcaccatt 120  
 cctatgagat ctgcacatcg ggagtttgac agctccacat taaatgaatc tgttcgcaat 180  
 accatcatgc gtgatctaaa agctgttggg aaaaaattca tgcattgttt gtaccaagg 240  
 aaaagtaata ctcttttgag agattgggat ttgtggggcc ctttgatcct ttgttgaca 300

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ctcgcattaa tgctgcaaag agactctgca gatagtgaag aagatggagg gcccgaattt 360  
gcagagggtg ttgtcattgt ctggtttggt gcagttacca tcacctcaa ctcaaaactt 420  
cttggaggga acatatcttt ttttcagagc ctctgtgtgc tgggttactg tatacttccc 480  
ttgacagtag caatgctgat ttgccggctg gtacttttgg ctgatccagg acctgtaaac 540  
ttcatgggtc ggctttttgt ggtgattgtg atgtttgcct ggtctatagt tgcctccaca 600  
gctttccttg ctgatagcca gcctccaaac cgcagagccc tagctgttta tcctgttttc 660  
ctgttttact ttgtcatcag ttggatgatt ctcaccttta ctctcag 708

&lt;210&gt; 133

&lt;211&gt; 1680

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 133

atggcggcgc ccgcgaggatc gctgaggagg cggaagactg ggtactcgga tccggagcct 60  
gagtcgccgc ccgcgccggg gcgtggcccc gcaggtcttc cggcccatct ccacacgggc 120  
acctcttggc tgaccgggat cgtgctctcg aaggccctag ccttcgtgta cttegtggca 180  
ttcctgggtg ctttccatca gaacaagcag ctcatcggtg acagggggct gcttcctgc 240  
agagtgttc tgaagaactt ccagcagtac ttccaggaca ggacgagctg ggaagtcttc 300  
agctacatgc ccaccatcct ctggctgatg gactggtcag acatgaactc caacctggac 360  
ttgctggctc ttctcggact gggcatctcg tctttcgtac tgatcacggg ctgcgccaac 420  
atgcttctca tggctgcct gtggggcctc tacatgtccc tggtaaagt gggccatgtc 480  
tggtactctt tcggatggga gtcccagctt ctggagacgg ggttcctggg gatcttctg 540  
tgccctctgt ggacgtgtc aaggctgccc cagcataccc ccacatccc gattgtcctg 600  
tggggcttcc ggtggctgat cttcaggatc atgcttggag caggcctgat caagatccgg 660  
ggggaccggt gctggcgaga cctcacctgc atggacttcc actatgagac ccagccgatg 720



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cccaatcctg tggcatacta cctgcaccac tcaccctggt ggttccatcg cttegagacg 780  
ctcagcaacc acttcatcga gtccttggtg cccttcttcc tcttctcgg ccggcgggcg 840  
tgcatacatcc acgggggtgct gcagatcctg ttccaggccg tctcatcgt cagcgggaac 900  
ctcagcttcc tgaactggct gactatggtg ccagcctgg cctgcttga tgacgccacc 960  
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agggacatcc gaggggcccg gcccagacc agattcggct ccgtggtgcg gcgtgcagcc 1080  
aacgtctcgc tgggcgtcct gctggcctgg ctcagcgtgc ccgtggctcct caacttgcg 1140  
agctccaggc aggtcatgaa caccacttc aactctcttc acatcgtaa cacttacggg 1200  
gccttcggaa gcatacacia ggagcggcg gagtgatcc tgcaggcac agccagctcc 1260  
aacgccagcg ccccgatgc catgtgggag gactacgagt tcaagtcaa gccaggtgac 1320  
cccagcagac ggccctgcct catctccccg taccactacc gcctggactg gctgatgtgg 1380  
ttcgcggcct tccagacctc cgagcacaac gactggatca tccacctggc tggcaagctc 1440  
ctggccagcg acgccaggc ctgtccctg ctggcacaca accccttcgc gggcaggccc 1500  
ccgccaggt gggctccagg agagcactac aggtacaagt tcagccgtcc tgggggcagg 1560  
cacgccccg agggcaagt gtgggtgcgg aagaggatcg gaggctactt ccctccgctc 1620  
agcctggagg agctgagccc ctacttcagg gaccgtgggt ggcctctgcc cgggcccctc 1680

&lt;210&gt; 134

&lt;211&gt; 1218

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 134

atggcagaga atggaacaaa ttgtgaccag agacgtgtag caatgaacaa ggaacatcat 60  
aatggaaatt tcacagaccc ctcttcagt aatgaaaaga agaggaggga gcgggaagaa 120  
aggcagaata ttgtcctgtg gagacagccg ctattacct tgcatattt ttctctggaa 180

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atccttgtaa tcttgaagga atggacctca aaattatggc atcgtcaaag cattgtggtg 240  
 tcttttttac tgtgcttgc tgtgcttata gctacgtatt atgttgaagg agtgcacaa 300  
 cagtatgtgc aacgtataga gaaacagttt cttttgtatg cctactggat aggcttagga 360  
 attttgtctt ctgttgggct tggaacaggg ctgcacacct ttctgcttta tctgggtcca 420  
 catatagcct cagttacatt agctgcttat gaatgcaatt cagttaattt tcccgaacca 480  
 ccctatcctg atcagattat ttgtccagat gaagagggca ctgaaggaaac catttctttg 540  
 tggagtatca tctcaaaagt taggattgaa gcctgcatgt ggggtatcgg tacagcaatc 600  
 ggagagctgc ctccatattt catggccaga gcagctcgcc tctcaggtgc tgaaccagat 660  
 gatgaagagt atcaggaatt tgaagagatg ctggaacatg cagagtctgc acaagacttt 720  
 gcctcccggg ccaaactggc agttcaaaaa ctagtacaga aagttggatt ttttggaaat 780  
 ttggcctgtg cttcaattcc aaatccttta ttgatctgg ctggaataac gtgtggacac 840  
 tttctgttac ctttttggac cttctttggt gcaaccctaa ttggaaaagc aataataaaa 900  
 atgcatatcc agaaaatttt tgttataata acattcagca agcacatagt ggagcaaattg 960  
 gtggctttca ttggtgctgt ccccggcata ggtccatctc tgcagaagcc atttcaggag 1020  
 tacctggagg ctcaacggca gaagcttcac cacaaaagcg aaatgggcac accacaggga 1080  
 gaaaactggt tgcctggat gtttgaagag ttggtcgttg tcatggtgtg ttacttcac 1140  
 ctatctatca ttaactccat ggcacaaagt tatgccaac gaatccagca gcggttgaac 1200  
 tcagaggaga aaactaaa 1218

&lt;210&gt; 135

&lt;211&gt; 1359

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 135

atgggcgtcc tgggccgggt cctgctgtgg ctgcagctct gcgcactgac ccaggcggtc 60

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tccaaactct ggggtcccaa cacggacttc gacgtcgag ccaactggag ccagaaccgg 120  
 accccgtgcg ccggcggcgc cgttgagttc ccggcggaca agatgggtgc agtcctgggtg 180  
 caagaaggtc acgccgtctc agacatgctc ctgccgtgg atggggaact cgtcctgggt 240  
 tcaggagccg gattcggcgt ctgagacgtg ggctcgacc tggactgtgg cgcgggcgaa 300  
 cctgccgtct tccgcgactc tgaccgcttc tcctggcatg acccgcacct gtggcgctct 360  
 ggggacgagg cacctggcct cttcttcgtg gacgccgagc gcgtgccctg ccgccacgac 420  
 gacgtcttct ttcgcctag tgcctccttc cgcgtggggc tcggccctgg cgctagcccc 480  
 gtgcgtgtcc gcagcatctc ggctctgggc cggacgttca cgcgcgacga ggacctgggt 540  
 gttttcctgg cgtcccgcgc gggccgccta cgcttcacg ggccgggcgc gctgagcgtg 600  
 ggccccgagg actgcgcgga cccgtcgggc tgcgtctgc gcaacgcgga ggcgacccg 660  
 tggatctgcg cggccctgct ccagccctg ggccggcgt gccccaggc cgcctgccac 720  
 agcgcctcc ggccccaggg gcagtgtgt gacctctgtg gagccgttgt gttgctgacc 780  
 cacggccccg catttgacct ggagcggtag cgggcgcgga tactggacac cttcctgggt 840  
 ctgccicagt accacgggt gcaggtggcc gtgtccaagg tgccacgtc gtcccggctc 900  
 cgtgaggccg atacggagat ccaggtgggt ctggtggaga atgggcccga gacaggcgga 960  
 gcggggcggc tggccgggc cctcctggcg gacgtcgccg agaacggcga ggccctcggc 1020  
 gtcctggagg cgaccatgcg ggagtcgggc gcacacgtct ggggcagctc cgcggctggg 1080  
 ctggcgggcg gcgtggcggc tgccgtgctg ctggcgctgc tggctcctgt ggtggcgccg 1140  
 ccgctgctgc gccgcgcggg gaggctcagg tggaggaggc acgaggcggc ggccccggct 1200  
 ggagcgcccc tcggcttcg caaccgggtg ttcgacgtga cggcctccga ggagctgccc 1260  
 ctgccgcggc ggctcagcct ggttcggaag gggccgcag acagcaccag ccacagttac 1320  
 ttcgtcaacc ctctgttcgc cggggccgag gccgaggcc 1359

&lt;210&gt; 136

&lt;211&gt; 177

275/307

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 136

```
atgacctcag tttcaacaca gttgtcctta gtcctcatgt cactgctttt ggtgctgcct    60
gttgtggaag cagtagaagc cggatgatgca atcgcccttt tgtaggtgt ggttctcagc    120
attacaggca tttgtgcctg cttgggggta tatgcacgaa aaagaaatgg acagatg      177
atgacctcag tttcaacaca gttgtcctta gtcctcatgt cactgctttt ggtgctgcct    60
gttgtggaag cagtagaagc cggatgatgca atcgcccttt tgtaggtgt ggttctcagc    120
attacaggca tttgtgcctg cttgggggta tatgcacgaa aaagaaatgg acagatg      177
```

&lt;210&gt; 137

&lt;211&gt; 630

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 137

```
atggccctgc cccagatgtg tgacgggagc cacttggcct ccacctccg ctattgcatg    60
acagtcagcg gcacagtggg tctgggtggc gggacgctct gcttcgcttg gtggagcgaa    120
ggggatgcaa ccgccagcc tggccagctg gccccacca cggagtatcc ggtgcctgag    180
ggccccagcc cctgctcag gtccgtcagc ttcgtctgct gcggtgcagg tggcctgctg    240
ctgctcattg gctgctgtg gtccgtcaag gccagcatcc cagggccacc tcgatgggac    300
ccctatcacc tctccagaga cctgtactac ctactgtgg agtcctcaga gaaggagagc    360
tgcaggaccc ccaaagtggg tgacatcccc acttacgagg aagccgtgag cttcccagtg    420
gccgaggggc cccaacacc acctgcatac cctacggagg aagccctgga gccaaagtga    480
tcgagggatg ccctgctcag caccagccc gcctggcctc caccagcta tgagagcatc    540
agccttgctc ttgatgccgt ttctgcagag acgacaccga gtgccacacg ctctgctca    600
```

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ggcctggttc agactgcacg gggaggaagt

630

&lt;210&gt; 138

&lt;211&gt; 495

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 138

atggactcct cgcgggcccg acagcagctc cggcggcgat tcctcctcct gccggacgcc 60

gaggcccagc tggaccgcga gggtgacgcc gggccggaaa cctccacagc tgttgagaaa 120

aaggagaaac ctcttccaag acttaataac cattctggat tctggatttt ggcatccatt 180

gttgtgacct attatgttga cttctttaa acccttaaag aaaacttcca cactagcagc 240

tggtttctct gtggcagtgc cttgttgctt gtcagtttat caattgcatt ttactgcata 300

gtctacctgg aatggtattg lggaattgga gaatatgatg tcaagtatcc agccttgata 360

cccattacca ctgcctcctt tattgcagca ggaatttgct tcaacattgc tttatggcat 420

gtgtggtcgt ttttcaactc attgttggtt ttaccacagt ttatgggggt tgtcatgttt 480

atcacactcc ttgga 495

&lt;210&gt; 139

&lt;211&gt; 486

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 139

atgctccaga ccagtaacta cagcctgggtg ctctctctgc agttcctgct gctgtcctat 60

gacctctttg tcaattcctt ctccagaactg ctccaaaaga ctctgtcat ccagcttggt 120

ctcttcatca tccaggatat tgcagtcctc ttcaacatca tcatcatttt cctcatgttc 180

277/307

|   |     |
|---|-----|
| ttcaacacct tcgtcttcca ggttggcctg gtcaacctcc tattccataa gttcaaaggg | 240 |
| accatcatcc tgacagctgt gtactttgcc ctcagcatct cccttcatgt ctgggtcatg | 300 |
| aacttacgct ggaaaaactc caacagcttc atatggacag atggacttca aatgctgttt | 360 |
| gtattccaga gactagcagc agtggtgtac tgctacttct ataaacggac agccgtaaga | 420 |
| ctaggcgatc ctcacttcta ccaggactct ttgtggctgc gcaaggagtt catgcaagtt | 480 |
| cgaagg  | 486 |

&lt;210&gt; 140

&lt;211&gt; 663

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 140

|   |     |
|---|-----|
| atggcgttgg cgttggcggc gctggcgcg gtcgagccgg cctgcggcag ccggtaccag  | 60  |
| cagttgcaga atgaagaaga gtctggagaa cctgaacagg ctgcaggtga tgctcctcca | 120 |
| ccttacagca gcatttctgc agagagcgca gcataatttg actacaagga tgagtctggg | 180 |
| tttccaaagc ccccatctta caatgtagct acaacactgc ccagttatga tgaagcggag | 240 |
| aggaccaagg ctgaagctac tatccctttg gttcctggga gagatgagga ttttgtgggt | 300 |
| cgggatgatt ttgatgatgc tgaccagctg aggataggaa atgatgggat tttcatgtta | 360 |
| acttttttca tggcattcct cttaactgg attgggtttt tctgtcttt ttgcctgacc   | 420 |
| acttcagctg caggaaggta tggggccatt tcaggatttg gtctctctct aattaaatgg | 480 |
| atcctgattg tcaggttttc cacctatttc cctggatatt ttgatggcca gtactggctc | 540 |
| tggtgggtgt tccttgtttt aggtttctc ctgtttctca gaggatttat caattatgca  | 600 |
| aaagttcgga agatgccaga aactttctca aatctcccca ggaccagagt tctctttatt | 660 |
| tat   | 663 |

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&lt;210&gt; 141

&lt;211&gt; 1622

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (78)... (1091)

&lt;400&gt; 141

ctcttccccc gcccgccgg gcgggaccag tgcgcagccg gggctggcgg gcggcggggt 60

ccgcggggcc gcaggag atg acg gcc ggc ggc cag gcc gag gcc gag ggc 110

Met Thr Ala Gly Gly Gln Ala Glu Ala Glu Gly

1

5

10

gct ggc ggg gag ccc ggc gcg gcg cgg ctg ccc tcg cgg gtg gcc cgg 158

Ala Gly Gly Glu Pro Gly Ala Ala Arg Leu Pro Ser Arg Val Ala Arg

15

20

25

ctg ctg tcg gcg ctc ttc tac ggg acc tgc tcc ttc ctc atc gtg ctt 206

Leu Leu Ser Ala Leu Phe Tyr Gly Thr Cys Ser Phe Leu Ile Val Leu

30

35

40

gtc aac aag gcg ctg ctg acc acc tac ggt ttc ccg tca cca att ttc 254

Val Asn Lys Ala Leu Leu Thr Thr Tyr Gly Phe Pro Ser Pro Ile Phe

45

50

55

ctt gga att gga cag atg gca gcc acc ata atg ata cta tat gtg tcc 302

Leu Gly Ile Gly Gln Met Ala Ala Thr Ile Met Ile Leu Tyr Val Ser

60

65

70

75

aag cta aac aaa atc att cac ttc cct gat ttt gat aag aaa att cct 350

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|   |     |
|---|-----|
| Lys Leu Asn Lys Ile Ile His Phe Pro Asp Phe Asp Lys Lys Ile Pro |     |
| 80 85 90  |     |
| gta aag ctg ttt cct ctg cct ctc ctc tac gtt gga aac cac ata agt | 398 |
| Val Lys Leu Phe Pro Leu Pro Leu Leu Tyr Val Gly Asn His Ile Ser |     |
| 95 100 105  |     |
| gga tta tca agc aca agt aaa tta agc cta ccg atg ttc acc gtg ctc | 446 |
| Gly Leu Ser Ser Thr Ser Lys Leu Ser Leu Pro Met Phe Thr Val Leu |     |
| 110 115 120   |     |
| agg aaa ttc acc att cca ctt acc tta ctt ctg gaa acc atc ata ctt | 494 |
| Arg Lys Phe Thr Ile Pro Leu Thr Leu Leu Leu Glu Thr Ile Ile Leu |     |
| 125 130 135   |     |
| ggg aag cag tat tca ctc aac atc atc ctc agt gtc ttt gcc att att | 542 |
| Gly Lys Gln Tyr Ser Leu Asn Ile Ile Leu Ser Val Phe Ala Ile Ile |     |
| 140 145 150 155   |     |
| ctc ggg gct ttc ata gca gct ggg tct gac ctt gct ttt aac tta gaa | 590 |
| Leu Gly Ala Phe Ile Ala Ala Gly Ser Asp Leu Ala Phe Asn Leu Glu |     |
| 160 165 170   |     |
| ggc tat att ttt gta ttc ctg aat gat atc ttc aca gca gca aat gga | 638 |
| Gly Tyr Ile Phe Val Phe Leu Asn Asp Ile Phe Thr Ala Ala Asn Gly |     |
| 175 180 185   |     |
| gtt tat acc aaa cag aaa atg gac cca aag gag cta ggg aaa tac gga | 686 |
| Val Tyr Thr Lys Gln Lys Met Asp Pro Lys Glu Leu Gly Lys Tyr Gly |     |
| 190 195 200   |     |
| gta ctt ttc tac aat gcc tgc ttc atg att atc cca act ctt att att | 734 |
| Val Leu Phe Tyr Asn Ala Cys Phe Met Ile Ile Pro Thr Leu Ile Ile |     |



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|   |     |     |      |
|---|-----|-----|------|
| 205   | 210 | 215 |      |
| agt gtc tcc act gga gac ctg caa cag gct act gaa ttc aac caa tgg |     |     | 782  |
| Ser Val Ser Thr Gly Asp Leu Gln Gln Ala Thr Glu Phe Asn Gln Trp |     |     |      |
| 220   | 225 | 230 | 235  |
| aag aat gtt gtg ttt atc cta cag ttt ctt ctt tcc tgt ttt ttg ggg |     |     | 830  |
| Lys Asn Val Val Phe Ile Leu Gln Phe Leu Leu Ser Cys Phe Leu Gly |     |     |      |
|   | 240 | 245 | 250  |
| ttt ctg ctg atg tac tcc acg gtt ctg tgc agc tat tac aat tca gcc |     |     | 878  |
| Phe Leu Leu Met Tyr Ser Thr Val Leu Cys Ser Tyr Tyr Asn Ser Ala |     |     |      |
|   | 255 | 260 | 265  |
| ctg acg aca gca gtg gtt gga gcc atc aag aat gta tcc gtt gcc tac |     |     | 926  |
| Leu Thr Thr Ala Val Val Gly Ala Ile Lys Asn Val Ser Val Ala Tyr |     |     |      |
| 270   | 275 | 280 |      |
| att ggg ata tta atc ggt gga gac tac att ttc tct ttg tta aac ttt |     |     | 974  |
| Ile Gly Ile Leu Ile Gly Gly Asp Tyr Ile Phe Ser Leu Leu Asn Phe |     |     |      |
| 285   | 290 | 295 |      |
| gta ggg tta aat att tgc atg gca ggg ggc ttg aga tat tcc ttt tta |     |     | 1022 |
| Val Gly Leu Asn Ile Cys Met Ala Gly Gly Leu Arg Tyr Ser Phe Leu |     |     |      |
| 300   | 305 | 310 | 315  |
| aca ctg agc agc cag tta aaa cct aaa cct gtg ggt gaa gaa aac atc |     |     | 1070 |
| Thr Leu Ser Ser Gln Leu Lys Pro Lys Pro Val Gly Glu Glu Asn Ile |     |     |      |
|   | 320 | 325 | 330  |
| tgt ttg gat ttg aag agc ta aagagtcctgc agcaggattg gagactgact    |     |     | 1120 |
| Cys Leu Asp Leu Lys Ser   |     |     |      |

335

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tgtgactgcg ggctgggggg gcattcccag taggaatgtg aagccagagg tttcggattc 1180
gtgacatcca cccctgggc aagtgagagc atctgcaaaa tgcaaagaga actacctcat 1240
atgcaggatg agccaatggc agtctcaaga aatgtactcg ggcgacacct tacctgtgga 1300
aagcaaatct tttcaaaata agccactggg actcggtagg tggagcccca gctgctcttc 1360
tagggaccta tggggccttc gtggcatctc tgtgctgtgt gctggggagg aggttgatgt 1420
aatggtgact cttttctgat cagcaccttg gccgtgattc ccaaggtccc agccaaagca 1480
aagggccagt tgtttcagtt taaacagaca tgtctttagt ctaataaaat tagttaactg 1540
ccagtaaagt tatttgtag ctttgatgaa agctatgttg gtatctttcc ctaatcatca 1600
aagtaaataa aaaatcattt ct 1622

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&lt;210&gt; 142

&lt;211&gt; 2475

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (36)... (746)

&lt;400&gt; 142

```

acctgtggga gcgacccggg agaaggaggg ccaag atg gcg gaa gcg gag gag 53

```

Met Ala Glu Ala Glu Glu

1

5

```

tct cca gga gac ccg ggg aca gca tcg ccc agg ccc ctg ttt gca ggc 101

```

Ser Pro Gly Asp Pro Gly Thr Ala Ser Pro Arg Pro Leu Phe Ala Gly

10

15

20

```

ctt tca gat ata tcc atc tca caa gac atc ccc gta gaa gga gaa atc 149

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Leu Ser Asp Ile Ser Ile Ser Gln Asp Ile Pro Val Glu Gly Glu Ile  
 25 30 35  
 acc att cct atg aga tct cgc atc cgg gag ttt gac agc tcc aca tta 197  
 Thr Ile Pro Met Arg Ser Arg Ile Arg Glu Phe Asp Ser Ser Thr Leu  
 40 45 50  
 aat gaa tct gtt cgc aat acc atc atg cgt gat cta aaa gct gtt ggg 245  
 Asn Glu Ser Val Arg Asn Thr Ile Met Arg Asp Leu Lys Ala Val Gly  
 55 60 65 70  
 aaa aaa ttc atg cat gtt ttg tac cca agg aaa agt aat act ctt ttg 293  
 Lys Lys Phe Met His Val Leu Tyr Pro Arg Lys Ser Asn Thr Leu Leu  
 75 80 85  
 aga gat tgg gat ttg tgg ggc cct ttg atc ctt tgt gtg aca ctc gca 341  
 Arg Asp Trp Asp Leu Trp Gly Pro Leu Ile Leu Cys Val Thr Leu Ala  
 90 95 100  
 tta atg ctg caa aga gac tct gca gat agt gaa aaa gat gga ggg ccc 389  
 Leu Met Leu Gln Arg Asp Ser Ala Asp Ser Glu Lys Asp Gly Gly Pro  
 105 110 115  
 caa ttt gca gag gtg ttt gtc att gtc tgg ttt ggt gca gtt acc atc 437  
 Gln Phe Ala Glu Val Phe Val Ile Val Trp Phe Gly Ala Val Thr Ile  
 120 125 130  
 acc ctc aac tca aaa ctt ctt gga ggg aac ata tct ttt ttt cag agc 485  
 Thr Leu Asn Ser Lys Leu Leu Gly Gly Asn Ile Ser Phe Phe Gln Ser  
 135 140 145 150  
 ctc tgt gtg ctg ggt tac tgt ata ctt ccc ttg aca gta gca atg ctg 533  
 Leu Cys Val Leu Gly Tyr Cys Ile Leu Pro Leu Thr Val Ala Met Leu

283/307

|   |     |     |      |
|---|-----|-----|------|
| 155   | 160 | 165 |      |
| att tgc cgg ctg gta ctt ttg gct gat cca gga cct gta aac ttc atg   |     |     | 581  |
| Ile Cys Arg Leu Val Leu Leu Ala Asp Pro Gly Pro Val Asn Phe Met   |     |     |      |
| 170   | 175 | 180 |      |
| gtt cgg ctt ttt gtg gtg att gtg atg ttt gcc tgg tct ata gtt gcc   |     |     | 629  |
| Val Arg Leu Phe Val Val Ile Val Met Phe Ala Trp Ser Ile Val Ala   |     |     |      |
| 185   | 190 | 195 |      |
| tcc aca gct ttc ctt gct gat agc cag cct cca aac cgc aga gcc cta   |     |     | 677  |
| Ser Thr Ala Phe Leu Ala Asp Ser Gln Pro Pro Asn Arg Arg Ala Leu   |     |     |      |
| 200   | 205 | 210 |      |
| gct gtt tat cct gtt ttc ctg ttt tac ttt gtc atc agt tgg atg att   |     |     | 725  |
| Ala Val Tyr Pro Val Phe Leu Phe Tyr Phe Val Ile Ser Trp Met Ile   |     |     |      |
| 215   | 220 | 225 | 230  |
| ctc acc ttt act cct cag taaatca ggaatgggaa attaaaaacc agtgaattga  |     |     | 780  |
| Leu Thr Phe Thr Pro Gln   |     |     |      |
| 235   |     |     |      |
| aagcacatct gaaagatgca attcaccatg gagctttgtc tctggccctt atttgtctaa |     |     | 840  |
| ttttggaggt atttgataac tgagtaggtg aggagattaa aaggagacca tatagcactg |     |     | 900  |
| tcacccctta tttgaggaac tgatgtttga aaggctgttc ttttctctct taatgtcatt |     |     | 960  |
| tctttaaaaa tacatgtgca tactacacac agtatataat gcctccttaa ggcatgatgg |     |     | 1020 |
| agtcaccgtg gtccatttgg gtgacaacca gtgacttggg aagcacatag atacatctta |     |     | 1080 |
| caagttgaat agagttgata actattttca gttttgagaa taccagttca ggtgcagctc |     |     | 1140 |
| ttaaacacat tgccttatga ctattagaat atgcctctct tttcataaat aaaaatacat |     |     | 1200 |
| ggctctatct cattttcttt tatttctctc tcttaagctt aaaaaggcaa tgagagaggt |     |     | 1260 |
| taggagtggg ttcatacacg gagaatgaga aaacatgcat taaccaatat tcagattttg |     |     | 1320 |

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atcaggggaa attctacact tgttgcaaaa aaaaaaaaaa aaaaagcaaa gggcctctaa 1380
agaatcagcc tctttgggcc ctttgtgctg tcaccttttt gccatgttta acagcatctt 1440
ggttgccact ctagtcttaa tcttgctcct taactttgaa tatgcagtct aaaatgtcag 1500
tagtcaacat gtaattttcc tttgaaattc tgaatatcc agtgctggaa cttatccaaa 1560
aagaagacct cagaaactta gattggtaga tctctagtgc atattatcat gtgggcacct 1620
tctcttaggg tggaatgagg cagtctggat gcagcatagt taaaaggagc tgtttaatat 1680
tctctgtagt ctggcctctt aactagaaag taaagctaaa tcagaagcct gtatttaacc 1740
atgtgaacag ggagggattt agtgttctga tggctgatta atagaacagc tagatactta 1800
gagcatgacg tgggatggga tgagtttaca gctgctgcct tttcatggtg agcttagcag 1860
ttttctcatt agatgtgttt ttttgggttg gggaatagca atttatttta ttgattttag 1920
actttatcaa gctaattagc tcccccttag ataagtacat gttgcacatg tgcacctact 1980
tgtaatctca gatatttatg cacacaagtg tgaaggtttt tcaggagca gagcatctgg 2040
gacaggctga ttctgagcta aacagggtc ctttaaggca atatgaactg ttgccttcta 2100
taaattgcac attgaggaac tctaatagac aaagattagg tgtcaggcag aaaacactca 2160
ttgtaaatat actattagtt gataaacata ggactttctt attccccagt ttttctttat 2220
catataattt aaatatttat tcattttgta tttaaagact acctacacat agatatatga 2280
ttccaaagtc atactttctc catccccaca ttagccaagt gaatacaggg ccaaatgggt 2340
tcttggaatg ataataacaa agcattacaa agtgggtccc cttggttcca gccttgcca 2400
gagtttttgg ttatatatit ctatttatta caatttacct tttaaattgt aaaataaacc 2460
tttgtgtgga cagag 2475

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&lt;210&gt; 143

&lt;211&gt; 1739

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

285/307

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (21)... (1703)

&lt;400&gt; 143

tgcgccctga cagcccaaca atg gcg gcg ccc gcg gag tcg ctg agg agg 50

Met Ala Ala Pro Ala Glu Ser Leu Arg Arg

1 5 10

cgg aag act ggg tac tcg gat ccg gag cct gag tcg ccg ccc gcg ccg 98

Arg Lys Thr Gly Tyr Ser Asp Pro Glu Pro Glu Ser Pro Pro Ala Pro

15 20 25

ggg cgt ggc ccc gca ggc tct ccg gcc cat ctc cac acg ggc acc ttc 146

Gly Arg Gly Pro Ala Gly Ser Pro Ala His Leu His Thr Gly Thr Phe

30 35 40

tgg ctg acc cgg atc gtg ctc ctg aag gcc cta gcc ttc gtg tac ttc 194

Trp Leu Thr Arg Ile Val Leu Leu Lys Ala Leu Ala Phe Val Tyr Phe

45 50 55

gtg gca ttc ctg gtg gct ttc cat cag aac aag cag ctc atc ggt gac 242

Val Ala Phe Leu Val Ala Phe His Gln Asn Lys Gln Leu Ile Gly Asp

60 65 70

agg ggg ctg ctt ccc tgc aga gtg ttc ctg aag aac ttc cag cag tac 290

Arg Gly Leu Leu Pro Cys Arg Val Phe Leu Lys Asn Phe Gln Gln Tyr

75 80 85 90

ttc cag gac agg acg agc tgg gaa gtc ttc agc tac atg ccc acc atc 338

Phe Gln Asp Arg Thr Ser Trp Glu Val Phe Ser Tyr Met Pro Thr Ile

95 100 105

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|   |     |
|---|-----|
| ctc tgg ctg atg gac tgg tca gac atg aac tcc aac ctg gac ttg ctg | 386 |
| Leu Trp Leu Met Asp Trp Ser Asp Met Asn Ser Asn Leu Asp Leu Leu |     |
| 110 115 120   |     |
| gct ctt ctc gga ctg ggc atc tcg tct ttc gta ctg atc acg ggc tgc | 434 |
| Ala Leu Leu Gly Leu Gly Ile Ser Ser Phe Val Leu Ile Thr Gly Cys |     |
| 125 130 135   |     |
| gcc aac atg ctt ctc atg gct gcc ctg tgg ggc ctc tac atg tcc ctg | 482 |
| Ala Asn Met Leu Leu Met Ala Ala Leu Trp Gly Leu Tyr Met Ser Leu |     |
| 140 145 150   |     |
| gtt aat gtg ggc cat gtc tgg tac tct ttc gga tgg gag tcc cag ctt | 530 |
| Val Asn Val Gly His Val Trp Tyr Ser Phe Gly Trp Glu Ser Gln Leu |     |
| 155 160 165 170   |     |
| ctg gag acg ggg ttc ctg ggg atc ttc ctg tgc cct ctg tgg acg ctg | 578 |
| Leu Glu Thr Gly Phe Leu Gly Ile Phe Leu Cys Pro Leu Trp Thr Leu |     |
| 175 180 185   |     |
| tca agg ctg ccc cag cat acc ccc aca tcc cgg att gtc ctg tgg ggc | 626 |
| Ser Arg Leu Pro Gln His Thr Pro Thr Ser Arg Ile Val Leu Trp Gly |     |
| 190 195 200   |     |
| ttc cgg tgg ctg atc ttc agg atc atg ctt gga gca ggc ctg atc aag | 674 |
| Phe Arg Trp Leu Ile Phe Arg Ile Met Leu Gly Ala Gly Leu Ile Lys |     |
| 205 210 215   |     |
| atc cgg ggg gac cgg tgc tgg cga gac ctc acc tgc atg gac ttc cac | 722 |
| Ile Arg Gly Asp Arg Cys Trp Arg Asp Leu Thr Cys Met Asp Phe His |     |
| 220 225 230   |     |
| tat gag acc cag ccg atg ccc aat cct gtg gca tac tac ctg cac cac | 770 |

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Tyr Glu Thr Gln Pro Met Pro Asn Pro Val Ala Tyr Tyr Leu His His  
 235                      240                      245                      250  
 tca ccc tgg tgg ttc cat cgc ttc gag acg ctc agc aac cac ttc atc      818  
 Ser Pro Trp Trp Phe His Arg Phe Glu Thr Leu Ser Asn His Phe Ile  
                                  255                      260                      265  
 gag ctc ctg gtg ccc ttc ttc ctc ttc ctc ggc cgg cgg gcg tgc atc      866  
 Glu Leu Leu Val Pro Phe Phe Leu Phe Leu Gly Arg Arg Ala Cys Ile  
                                  270                      275                      280  
 atc cac ggg gtg ctg cag atc ctg ttc cag gcc gtc ctc atc gtc agc      914  
 Ile His Gly Val Leu Gln Ile Leu Phe Gln Ala Val Leu Ile Val Ser  
                                  285                      290                      295  
 ggg aac ctc agc ttc ctg aac tgg ctg act atg gtg ccc agc ctg gcc      962  
 Gly Asn Leu Ser Phe Leu Asn Trp Leu Thr Met Val Pro Ser Leu Ala  
                                  300                      305                      310  
 tgc ttt gat gac gcc acc ctg gga ttc ttg ttc ccc tct ggg cca ggc      1010  
 Cys Phe Asp Asp Ala Thr Leu Gly Phe Leu Phe Pro Ser Gly Pro Gly  
 315                      320                      325                      330  
 agc ctg aag gac cga gtt ctg cag atg cag agg gac atc cga ggg gcc      1058  
 Ser Leu Lys Asp Arg Val Leu Gln Met Gln Arg Asp Ile Arg Gly Ala  
                                  335                      340                      345  
 cgg ccc gag ccc aga ttc ggc tcc gtg gtg cgg cgt gca gcc aac gtc      1106  
 Arg Pro Glu Pro Arg Phe Gly Ser Val Val Arg Arg Ala Ala Asn Val  
                                  350                      355                      360  
 tcg ctg ggc gtc ctg ctg gcc tgg ctc agc gtg ccc gtg gtc ctc aac      1154  
 Ser Leu Gly Val Leu Leu Ala Trp Leu Ser Val Pro Val Val Leu Asn



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|   |     |     |      |
|---|-----|-----|------|
| 365   | 370 | 375 |      |
| ttg ctg agc tcc agg cag gtc atg aac acc cac ttc aac tct ctt cac |     |     | 1202 |
| Leu Leu Ser Ser Arg Gln Val Met Asn Thr His Phe Asn Ser Leu His |     |     |      |
| 380   | 385 | 390 |      |
| atc gtc aac act tac ggg gcc ttc gga agc atc acc aag gag cgg gcg |     |     | 1250 |
| Ile Val Asn Thr Tyr Gly Ala Phe Gly Ser Ile Thr Lys Glu Arg Ala |     |     |      |
| 395   | 400 | 405 | 410  |
| gag gtg atc ctg cag ggc aca gcc agc tcc aac gcc agc gcc ccc gat |     |     | 1298 |
| Glu Val Ile Leu Gln Gly Thr Ala Ser Ser Asn Ala Ser Ala Pro Asp |     |     |      |
| 415   | 420 | 425 |      |
| gcc atg tgg gag gac tac gag ttc aag tgc aag cca ggt gac ccc agc |     |     | 1346 |
| Ala Met Trp Glu Asp Tyr Glu Phe Lys Cys Lys Pro Gly Asp Pro Ser |     |     |      |
| 430   | 435 | 440 |      |
| aga cgg ccc tgc ctc atc tcc ccg tac cac tac cgc ctg gac tgg ctg |     |     | 1394 |
| Arg Arg Pro Cys Leu Ile Ser Pro Tyr His Tyr Arg Leu Asp Trp Leu |     |     |      |
| 445   | 450 | 455 |      |
| atg tgg ttc gcg gcc ttc cag acc tac gag cac aac gac tgg atc atc |     |     | 1442 |
| Met Trp Phe Ala Ala Phe Gln Thr Tyr Glu His Asn Asp Trp Ile Ile |     |     |      |
| 460   | 465 | 470 |      |
| cac ctg gct ggc aag ctc ctg gcc agc gac gcc gag gcc ttg tcc ctg |     |     | 1490 |
| His Leu Ala Gly Lys Leu Leu Ala Ser Asp Ala Glu Ala Leu Ser Leu |     |     |      |
| 475   | 480 | 485 | 490  |
| ctg gca cac aac ccc ttc gcg ggc agg ccc ccg ccc agg tgg gtc cga |     |     | 1538 |
| Leu Ala His Asn Pro Phe Ala Gly Arg Pro Pro Pro Arg Trp Val Arg |     |     |      |
| 495   | 500 | 505 |      |

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gga gag cac tac agg tac aag ttc agc cgt cct ggg ggc agg cac gcc 1586  
 Gly Glu His Tyr Arg Tyr Lys Phe Ser Arg Pro Gly Gly Arg His Ala  
           510                    515                    520  
 gcc gag ggc aag tgg tgg gtg cgg aag agg atc gga gcc tac ttc cct 1634  
 Ala Glu Gly Lys Trp Trp Val Arg Lys Arg Ile Gly Ala Tyr Phe Pro  
           525                    530                    535  
 ccg ctc agc ctg gag gag ctg agg ccc tac ttc agg gac cgt ggg tgg 1682  
 Pro Leu Ser Leu Glu Glu Leu Arg Pro Tyr Phe Arg Asp Arg Gly Trp  
           540                    545                    550  
 cct ctg ccc ggg ccc ctc tagacgtgca ccagaaataa aggccaagac 1730  
 Pro Leu Pro Gly Pro Leu  
 555                    560  
 ccagccccc 1739

&lt;210&gt; 144

&lt;211&gt; 2005

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (107)... (1327)

&lt;400&gt; 144

ggagcccagc ggcgggtgtg agagtccgta aggagcagct tccaggatcc tgagatccgg 60

agcagccggg gtcggagcgg ctccctcaaga gttactgatc tatgaa atg gca gag 115

Met Ala Glu

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1

aat gga aaa aat tgt gac cag aga cgt gta gca atg aac aag gaa cat 163

Asn Gly Lys Asn Cys Asp Gln Arg Arg Val Ala Met Asn Lys Glu His

5

10

15

cat aat gga aat ttc aca gac ccc tct tca gtg aat gaa aag aag agg 211

His Asn Gly Asn Phe Thr Asp Pro Ser Ser Val Asn Glu Lys Lys Arg

20

25

30

35

agg gag cgg gaa gaa agg cag aat att gtc ctg tgg aga cag ccg ctc 259

Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln Pro Leu

40

45

50

att acc ttg cag tat ttt tct ctg gaa atc ctt gta atc ttg aag gaa 307

Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu Lys Glu

55

60

65

tgg acc tca aaa tta tgg cat cgt caa agc att gtg gtg tct ttt tta 355

Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val Ser Phe Leu

70

75

80

ctg ctg ctt gct gtg ctt ata gct acg tat tat gtt gaa gga gtg cat 403

Leu Leu Leu Ala Val Leu Ile Ala Thr Tyr Tyr Val Glu Gly Val His

85

90

95

caa cag tat gtg caa cgt ata gag aaa cag ttt ctt ttg tat gcc tac 451

Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu Tyr Ala Tyr

100

105

110

115

tgg ata ggc tta gga att ttg tct tct gtt ggg ctt gga aca ggg ctg 499

Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly Thr Gly Leu

120

125

130

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|   |     |
|---|-----|
| cac acc ttt ctg ctt tat ctg ggt cca cat ata gcc tca gtt aca tta | 547 |
| His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser Val Thr Leu |     |
| 135 140 145   |     |
| gct gct tat gaa tgc aat tca gtt aat ttt ccc gaa cca ccc tat cct | 595 |
| Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro Pro Tyr Pro |     |
| 150 155 160   |     |
| gat cag att att tgt cca gat gaa gag ggc act gaa gga acc att tct | 643 |
| Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly Thr Ile Ser |     |
| 165 170 175   |     |
| ttg tgg agt atc atc tca aaa gtt agg att gaa gcc tgc atg tgg ggt | 691 |
| Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys Met Trp Gly |     |
| 180 185 190 195   |     |
| atc ggt aca gca atc gga gag ctg cct cca tat ttc atg gcc aga gca | 739 |
| Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met Ala Arg Ala |     |
| 200 205 210   |     |
| gct cgc ctc tca ggt gct gaa cca gat gat gaa gag tat cag gaa ttt | 787 |
| Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr Gln Glu Phe |     |
| 215 220 225   |     |
| gaa gag atg ctg gaa cat gca gag tct gca caa gac ttt gcc tcc cgg | 835 |
| Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Asp Phe Ala Ser Arg |     |
| 230 235 240   |     |
| gcc aaa ctg gca gtt caa aaa cta gta cag aaa gtt gga ttt ttt gga | 883 |
| Ala Lys Leu Ala Val Gln Lys Leu Val Gln Lys Val Gly Phe Phe Gly |     |
| 245 250 255   |     |
| att ttg gcc tgt gct tca att cca aat cct tta ttt gat ctg gct gga | 931 |

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Ile Leu Ala Cys Ala Ser Ile Pro Asn Pro Leu Phe Asp Leu Ala Gly  
 260                      265                      270                      275  
 ata acg tgt gga cac ttt ctg gta cct ttt tgg acc ttc ttt ggt gca      979  
 Ile Thr Cys Gly His Phe Leu Val Pro Phe Trp Thr Phe Phe Gly Ala  
                          280                      285                      290  
 acc cta att gga aaa gca ata ata aaa atg cat atc cag aaa att ttt      1027  
 Thr Leu Ile Gly Lys Ala Ile Ile Lys Met His Ile Gln Lys Ile Phe  
                          295                      300                      305  
 gtt ata ata aca ttc agc aag cac ata gtg gag caa atg gtg gct ttc      1075  
 Val Ile Ile Thr Phe Ser Lys His Ile Val Glu Gln Met Val Ala Phe  
                          310                      315                      320  
 att ggt gct gtc ccc ggc ata ggt cca tct ctg cag aag cca ttt cag      1123  
 Ile Gly Ala Val Pro Gly Ile Gly Pro Ser Leu Gln Lys Pro Phe Gln  
                          325                      330                      335  
 gag tac ctg gag gct caa cgg cag aag ctt cac cac aaa agc gaa atg      1171  
 Glu Tyr Leu Glu Ala Gln Arg Gln Lys Leu His His Lys Ser Glu Met  
 340                      345                      350                      355  
 ggc aca cca cag gga gaa aac tgg ttg tcc tgg atg ttt gaa aag ttg      1219  
 Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe Glu Lys Leu  
                          360                      365                      370  
 gtc gtt gtc atg gtg tgt tac ttc atc cta tct atc att aac tcc atg      1267  
 Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile Asn Ser Met  
                          375                      380                      385  
 gca caa agt tat gcc aaa cga atc cag cag cgg ttg aac tca gag gag      1315  
 Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn Ser Glu Glu

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| 390  | 395 | 400 |      |
|--|-----|-----|------|
| aaa act aaa taagta gagaaagttt taaactgcag aaattggagt ggatgggttc     |     |     | 1370 |
| Lys Thr Lys  |     |     |      |
| 405  |     |     |      |
| tgccttaaatt tgggaggact ccaagccggg aaggaaaatt cccttttcca acctgtatca |     |     | 1430 |
| atttttacaa cttttttcct gaaagcagtt tagtccatac tttgactga catacttttt   |     |     | 1490 |
| cccttctgtgc taaggtaagg tatccaccct cgatgcaatc caccttgtgt tttcttaggg |     |     | 1550 |
| tggaatgtga tgttcagcag caaacttgca acagactggc cttctgtttg ttactttcaa  |     |     | 1610 |
| aaggcccaca tgatacaatt agagaattcc caccgcacaa aaaaagttcc taagtatgtt  |     |     | 1670 |
| aaatatgtca agcttttttag gcttgtcaca aatgattgct ttgttttcct aagtcacaa  |     |     | 1730 |
| aatgtatata aattatctag attggataac agtcttgcac gtttatcatg ttacaattta  |     |     | 1790 |
| atattccatc ctgcccacc cttcctctcc catcctcaaa aaagggccat tttatgatgc   |     |     | 1850 |
| attgcacacc ctctggggaa attgatcttt aaattttgag acagtataag gaaaatctgg  |     |     | 1910 |
| ttgggtgtctt acaagtgagc tgacaccatt ttttattctg tgtatttaga atgaagtctt |     |     | 1970 |
| gaaaaaaact ttataaagac atctttaatc attcc                             |     |     | 2005 |

&lt;210&gt; 145

&lt;211&gt; 1558

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (31)... (1392)

&lt;400&gt; 145

|  |    |
|--|----|
| tcccggtcgg gtgcaaggag ccgaggcgag atg ggc gtc ctg ggc cgg gtc ctg | 54 |
|--|----|

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Met Gly Val Leu Gly Arg Val Leu

1

5

ctg tgg ctg cag ctc tgc gca ctg acc cag gcg gtc tcc aaa ctc tgg 102

Leu Trp Leu Gln Leu Cys Ala Leu Thr Gln Ala Val Ser Lys Leu Trp

10

15

20

gtc ccc aac acg gac ttc gac gtc gca gcc aac tgg agc cag aac cgg 150

Val Pro Asn Thr Asp Phe Asp Val Ala Ala Asn Trp Ser Gln Asn Arg

25

30

35

40

acc ccg tgc gcc ggc ggc gcc gtt gag ttc ccg gcg gac aag atg gtg 198

Thr Pro Cys Ala Gly Gly Ala Val Glu Phe Pro Ala Asp Lys Met Val

45

50

55

tca gtc ctg gtg caa gaa ggt cac gcc gtc tca gac atg ctc ctg ccg 246

Ser Val Leu Val Gln Glu Gly His Ala Val Ser Asp Met Leu Leu Pro

60

65

70

ctg gat ggg gaa ctc gtc ctg gct tca gga gcc gga ttc ggc gtc tca 294

Leu Asp Gly Glu Leu Val Leu Ala Ser Gly Ala Gly Phe Gly Val Ser

75

80

85

gac gtg ggc tcg cac ctg gac tgt ggc gcg ggc gaa cct gcc gtc ttc 342

Asp Val Gly Ser His Leu Asp Cys Gly Ala Gly Glu Pro Ala Val Phe

90

95

100

cgc gac tct gac cgc ttc tcc tgg cat gac ccg cac ctg tgg cgc tct 390

Arg Asp Ser Asp Arg Phe Ser Trp His Asp Pro His Leu Trp Arg Ser

105

110

115

120

ggg gac gag gca cct ggc ctc ttc ttc gtg gac gcc gag cgc gtg ccc 438

Gly Asp Glu Ala Pro Gly Leu Phe Phe Val Asp Ala Glu Arg Val Pro

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|   |     |     |     |
|---|-----|-----|-----|
| 125   | 130 | 135 |     |
| tgc cgc cac gac gac gtc ttc ttt ccg cct agt gcc tcc ttc cgc gtg |     |     | 486 |
| Cys Arg His Asp Asp Val Phe Phe Pro Pro Ser Ala Ser Phe Arg Val |     |     |     |
| 140   | 145 | 150 |     |
| ggg ctc ggc cct ggc gct agc ccc gtg cgt gtc cgc agc atc tcg gct |     |     | 534 |
| Gly Leu Gly Pro Gly Ala Ser Pro Val Arg Val Arg Ser Ile Ser Ala |     |     |     |
| 155   | 160 | 165 |     |
| ctg ggc cgg acg ttc acg cgc gac gag gac ctg gct gtt ttc ctg gcg |     |     | 582 |
| Leu Gly Arg Thr Phe Thr Arg Asp Glu Asp Leu Ala Val Phe Leu Ala |     |     |     |
| 170   | 175 | 180 |     |
| tcc cgc gcg ggc cgc cta cgc ttc cac ggg ccg ggc gcg ctg agc gtg |     |     | 630 |
| Ser Arg Ala Gly Arg Leu Arg Phe His Gly Pro Gly Ala Leu Ser Val |     |     |     |
| 185   | 190 | 195 | 200 |
| ggc ccc gag gac tgc gcg gac ccg tcg ggc tgc gtc tgc ggc aac gcg |     |     | 678 |
| Gly Pro Glu Asp Cys Ala Asp Pro Ser Gly Cys Val Cys Gly Asn Ala |     |     |     |
| 205   | 210 | 215 |     |
| gag gcg cag ccg tgg atc tgc gcg gcc ctg ctc cag ccc ctg ggc ggc |     |     | 726 |
| Glu Ala Gln Pro Trp Ile Cys Ala Ala Leu Leu Gln Pro Leu Gly Gly |     |     |     |
| 220   | 225 | 230 |     |
| cgc tgc ccc cag gcc gcc tgc cac agc gcc ctc cgg ccc cag ggg cag |     |     | 774 |
| Arg Cys Pro Gln Ala Ala Cys His Ser Ala Leu Arg Pro Gln Gly Gln |     |     |     |
| 235   | 240 | 245 |     |
| tgc tgt gac ctc tgt gga gcc gtt gtg ttg ctg acc cac ggc ccc gca |     |     | 822 |
| Cys Cys Asp Leu Cys Gly Ala Val Val Leu Leu Thr His Gly Pro Ala |     |     |     |
| 250   | 255 | 260 |     |



|   |      |
|---|------|
| ttt gac ctg gag cgg tac cgg gcg cgg ata ctg gac acc ttc ctg ggt | 870  |
| Phe Asp Leu Glu Arg Tyr Arg Ala Arg Ile Leu Asp Thr Phe Leu Gly |      |
| 265 270 275 280   |      |
| ctg cct cag tac cac ggg ctg cag gtg gcc gtg tcc aag gtg cca cgc | 918  |
| Leu Pro Gln Tyr His Gly Leu Gln Val Ala Val Ser Lys Val Pro Arg |      |
| 285 290 295   |      |
| tcg tcc cgg ctc cgt gag gcc gat acg gag atc cag gtg gtg ctg gtg | 966  |
| Ser Ser Arg Leu Arg Glu Ala Asp Thr Glu Ile Gln Val Val Leu Val |      |
| 300 305 310   |      |
| gag aat ggg ccc gag aca ggc gga gcg ggg cgg ctg gcc cgg gcc ctc | 1014 |
| Glu Asn Gly Pro Glu Thr Gly Gly Ala Gly Arg Leu Ala Arg Ala Leu |      |
| 315 320 325   |      |
| ctg gcg gac gtc gcc gag aac ggc gag gcc ctc ggc gtc ctg gag gcg | 1062 |
| Leu Ala Asp Val Ala Glu Asn Gly Glu Ala Leu Gly Val Leu Glu Ala |      |
| 330 335 340   |      |
| acc atg cgg gag tcg ggc gca cac gtc tgg ggc agc tcc gcg gct ggg | 1110 |
| Thr Met Arg Glu Ser Gly Ala His Val Trp Gly Ser Ser Ala Ala Gly |      |
| 345 350 355 360   |      |
| ctg gcg ggc ggc gtg gcg gct gcc gtg ctg ctg gcg ctg ctg gtc ctg | 1158 |
| Leu Ala Gly Gly Val Ala Ala Ala Val Leu Leu Ala Leu Leu Val Leu |      |
| 365 370 375   |      |
| ctg gtg gcg ccg ccg ctg ctg cgc cgc gcg ggg agg ctc agg tgg agg | 1206 |
| Leu Val Ala Pro Pro Leu Leu Arg Arg Ala Gly Arg Leu Arg Trp Arg |      |
| 380 385 390   |      |
| agg cac gag gcg gcg gcc ccg gct gga gcg ccc ctc ggc ttc cgc aac | 1254 |

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Arg His Glu Ala Ala Ala Pro Ala Gly Ala Pro Leu Gly Phe Arg Asn  
 395 400 405  
 ccg gtg ttc gac gtg acg gcc tcc gag gag ctg ccc ctg ccg cgg cgg 1302  
 Pro Val Phe Asp Val Thr Ala Ser Glu Glu Leu Pro Leu Pro Arg Arg  
 410 415 420  
 ctc agc ctg gtt ccg aag gcg gcc gca gac agc acc agc cac agt tac 1350  
 Leu Ser Leu Val Pro Lys Ala Ala Ala Asp Ser Thr Ser His Ser Tyr  
 425 430 435 440  
 ttc gtc aac cct ctg ttc gcc ggg gcc gag gcc gag gcc t gacgggccgc 1400  
 Phe Val Asn Pro Leu Phe Ala Gly Ala Glu Ala Glu Ala  
 445 450  
 ctgaccgtcg accttggggc tctccacccc ctctggcccc agtcgaactg ggggctagcc 1460  
 acctcctcgt ccagccccca aacctcccct tcttttcccc ctctccggg ggccaaggac 1520  
 aggggtggcct tactcagtaa aggtgtttcc tgcacctg 1558

&lt;210&gt; 146

&lt;211&gt; 1005

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (151)... (330)

&lt;400&gt; 146

attcctgtaa tggctgcttc ctagaaggtc gtgtcacgtg gaacctctta atctcagcat 60  
 ccggagctcc aggaaggga aatttcaagt cagatagaat tctatatata ccatttcttt 120

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ggaaccttca gccctcaaga ttccaacatc atg acc tca gtt tca aca cag ttg 174  
 Met Thr Ser Val Ser Thr Gln Leu  
 1 5  
 tcc tta gtc ctc atg tca ctg ctt ttg gtg ctg cct gtt gtg gaa gca 222  
 Ser Leu Val Leu Met Ser Leu Leu Leu Val Leu Pro Val Val Glu Ala  
 10 15 20  
 gta gaa gcc ggt gat gca atc gcc ctt ttg tta ggt gtg gtt ctc agc 270  
 Val Glu Ala Gly Asp Ala Ile Ala Leu Leu Leu Gly Val Val Leu Ser  
 25 30 35 40  
 att aca ggc att tgt gcc tgc ttg ggg gta tat gca cga aaa aga aat 318  
 Ile Thr Gly Ile Cys Ala Cys Leu Gly Val Tyr Ala Arg Lys Arg Asn  
 45 50 55  
 gga cag atg tga ctttgaaagg cctactgagt caaacctcac cctgaaaacc 370  
 Gly Gln Met  
 tttgcgcttt agaggctaaa cctgagatgtt ggtgltgaa aggttccaag aatcagtaaa 430  
 taaggaggtt tcacatTTTT catgttttcc atgaaatggc acaaacata catttataaa 490  
 ttgaaaaaaa aatgttttct ttacaacaaa taatgcacag aaaaatgcag cctataattt 550  
 gctagttagg tagtcaaaga agtaagatgg ctgaaattta cataagtaat atttcataat 610  
 cttagaattc tctcaaagca tgtgaaatag gaagaaggaa gttcttgccc agaattcttag 670  
 gaaatcacca ctgttcggtt ataatactg cctcctgaat cgttgaggag tcttttaaat 730  
 tagatTTTTg ttttgtgtc tcccaagtta atattatatt tagatatcag agagtcaggc 790  
 aaaaaggaaa acttttatct ctagggaaaa aacatttaga aaaatgtatt cagtgtatct 850  
 aatactgaaa tgcggaaaaa aatttaatgt taaaaaaaaa actatagaca ttgacatgga 910  
 aaagagatTT aatgttttga aaaaaaactt tatattaact gagtaacatc ctcctgatga 970  
 gaagtactat attaaatata aaccattat gttat 1005

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&lt;210&gt; 147

&lt;211&gt; 969

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (151)... (783)

&lt;400&gt; 147

gctggacacc tggagctgcc cgaggacgcg gaggagagac ccgagggtcg ccgctggtag 60

ggtcgctcag ccctgcgcgc cttcaccacc acaccttcac ctgcgccag ctccctgcgc 120

gcctggacag cgctgctgc ccgcctcccg atg gcc ctg ccc cag atg tgt gac 174

Met Ala Leu Pro Gln Met Cys Asp

1

5

ggg agc cac ttg gcc tcc acc ctc cgc tat tgc atg aca gtc agc ggc 222

Gly Ser His Leu Ala Ser Thr Leu Arg Tyr Cys Met Thr Val Ser Gly

10

15

20

aca gtg gtt ctg gtg gcc ggg acg ctc tgc ttc gct tgg tgg agc gaa 270

Thr Val Val Leu Val Ala Gly Thr Leu Cys Phe Ala Trp Trp Ser Glu

25

30

35

40

ggg gat gca acc gcc cag cct ggc cag ctg gcc cca ccc acg gag tat 318

Gly Asp Ala Thr Ala Gln Pro Gly Gln Leu Ala Pro Pro Thr Glu Tyr

45

50

55

ccg gtg cct gag ggc ccc agc ccc ctg ctc agg tcc gtc agc ttc gtc 366

Pro Val Pro Glu Gly Pro Ser Pro Leu Leu Arg Ser Val Ser Phe Val

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|   |     |     |     |
|---|-----|-----|-----|
| 60  | 65  | 70  |     |
| tgc tgc ggt gca ggt ggc ctg ctg ctg ctc att ggc ctg ctg tgg tcc |     |     | 414 |
| Cys Cys Gly Ala Gly Gly Leu Leu Leu Leu Ile Gly Leu Leu Trp Ser |     |     |     |
| 75  | 80  | 85  |     |
| gtc aag gcc agc atc cca ggg cca cct cga tgg gac ccc tat cac ctc |     |     | 462 |
| Val Lys Ala Ser Ile Pro Gly Pro Pro Arg Trp Asp Pro Tyr His Leu |     |     |     |
| 90  | 95  | 100 |     |
| tcc aga gac ctg tac tac ctc act gtg gag tcc tca gag aag gag agc |     |     | 510 |
| Ser Arg Asp Leu Tyr Tyr Leu Thr Val Glu Ser Ser Glu Lys Glu Ser |     |     |     |
| 105   | 110 | 115 | 120 |
| tgc agg acc ccc aaa gtg gtt gac atc ccc act tac gag gaa gcc gtg |     |     | 558 |
| Cys Arg Thr Pro Lys Val Val Asp Ile Pro Thr Tyr Glu Glu Ala Val |     |     |     |
| 125   | 130 | 135 |     |
| agc ttc cca gtg gcc gag ggg ccc cca aca cca cct gca tac cct acg |     |     | 606 |
| Ser Phe Pro Val Ala Glu Gly Pro Pro Thr Pro Pro Ala Tyr Pro Thr |     |     |     |
| 140   | 145 | 150 |     |
| gag gaa gcc ctg gag cca agt gga tcg agg gat gcc ctg ctc agc acc |     |     | 654 |
| Glu Glu Ala Leu Glu Pro Ser Gly Ser Arg Asp Ala Leu Leu Ser Thr |     |     |     |
| 155   | 160 | 165 |     |
| cag ccc gcc tgg cct cca ccc agc tat gag agc atc agc ctt gct ctt |     |     | 702 |
| Gln Pro Ala Trp Pro Pro Pro Ser Tyr Glu Ser Ile Ser Leu Ala Leu |     |     |     |
| 170   | 175 | 180 |     |
| gat gcc gtt tct gca gag acg aca ccg agt gcc aca cgc tcc tgc tca |     |     | 750 |
| Asp Ala Val Ser Ala Glu Thr Thr Pro Ser Ala Thr Arg Ser Cys Ser |     |     |     |
| 185   | 190 | 195 | 200 |

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ggc ctg gtt cag act gca cgg gga gga agt taaaggctcc tagcaggctcc 800

Gly Leu Val Gln Thr Ala Arg Gly Gly Ser

205

210

tgaatccaga gacaaaaatg ctgtgccttc tccagagtct tatgcagtgc ctgggacaca 860

gtaggcactc agcaaacgtt cgttgttgaa ggctgttcta tttatctatt gctgtataac 920

aaaccacccc agaatttagt ggcttaaaat aaatccatt ttattatgt 969

<210> 148

<211> 1241

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (20)... (517)

<400> 148

atttcggggc ggtaccaag atg gac tcc tcg cgg gcc cga cag cag ctc cgg 52

Met Asp Ser Ser Arg Ala Arg Gln Gln Leu Arg

1

5

10

cgg cga ttc ctc ctc ctg ccg gac gcc gag gcc cag ctg gac cgc gag 100

Arg Arg Phe Leu Leu Leu Pro Asp Ala Glu Ala Gln Leu Asp Arg Glu

15

20

25

ggt gac gcc ggg ccg gaa acc tcc aca gct gtt gag aaa aag gag aaa 148

Gly Asp Ala Gly Pro Glu Thr Ser Thr Ala Val Glu Lys Lys Glu Lys

30

35

40

cct ctt cca aga ctt aat atc cat tct gga ttc tgg att ttg gca tcc 196

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Pro Leu Pro Arg Leu Asn Ile His Ser Gly Phe Trp Ile Leu Ala Ser  
 45 50 55  
 att gtt gtg acc tat tat gtt gac ttc ttt aaa acc ctt aaa gaa aac 244  
 Ile Val Val Thr Tyr Tyr Val Asp Phe Phe Lys Thr Leu Lys Glu Asn  
 60 65 70 75  
 ttc cac act agc agc tgg ttt ctc tgt ggc agt gcc ttg ttg ctt gtc 292  
 Phe His Thr Ser Ser Trp Phe Leu Cys Gly Ser Ala Leu Leu Leu Val  
 80 85 90  
 agt tta tca att gca ttt tac tgc ata gtc tac ctg gaa tgg tat tgt 340  
 Ser Leu Ser Ile Ala Phe Tyr Cys Ile Val Tyr Leu Glu Trp Tyr Cys  
 95 100 105  
 gga att gga gaa tat gat gtc aag tat cca gcc ttg ata ccc att acc 388  
 Gly Ile Gly Glu Tyr Asp Val Lys Tyr Pro Ala Leu Ile Pro Ile Thr  
 110 115 120  
 act gcc tcc ttt att gca gca gga att tgc ttc aac att gct tta tgg 436  
 Thr Ala Ser Phe Ile Ala Ala Gly Ile Cys Phe Asn Ile Ala Leu Trp  
 125 130 135  
 cat gtg tgg tcg ttt ttc act cca ttg ttg ttg ttt acc cag ttt atg 484  
 His Val Trp Ser Phe Phe Thr Pro Leu Leu Leu Phe Thr Gln Phe Met  
 140 145 150 155  
 ggg gtt gtc atg ttt atc aca ctc ctt gga tgattt ccgaagagac 530  
 Gly Val Val Met Phe Ile Thr Leu Leu Gly  
 160 165  
 aggggtcttct atgttgccca ggctgtcttt gaactcctgg gatcaagtga tcctcctgcc 590  
 tcagccttcg aagtagttgg gactacaggc ccagccacc gtgcctggct ggacatgtaa 650

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atttgaagtg aatgggttaa catccagcta gctgaaagca tggcagaccc taacagaaaa 710  
 gctacagtgt gtttttgcag ctatgaagtg aatggtttcc tggggaaaat tgtgactttg 770  
 tataactgtt gttgaaacca gaataaatta tatttcactt gcataatgcat aaattattaa 830  
 aattttcaga agtcagtgat acagaagtac tattttgcaa tgtaaatctg tttgagtctt 890  
 tggagaaagt ggtttcattg taggtacata gtgcactgtt aatattttta acaagtagtt 950  
 cactcttcca ttttaaggat agcagttcct tgtataaaat gactggatgt gtataaagga 1010  
 attatgttgt catgtgcctt taaccagctt tagtaattac tataatctca tatttatgat 1070  
 agttttgtta ggtgacagga ccaaataaaa atattttatg ttttctcatc acttttagatt 1130  
 ttatcattat gtacattact gggtttttag catttcttaa tgtgaagttt taatcacttt 1190  
 taagtataca tttttttctg tatcatttaa ataaaatatt tttataactt t 1241

&lt;210&gt; 149

&lt;211&gt; 1174

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (187)... (675)

&lt;400&gt; 149

ggaagccggg acgatgtccg catgacaacc gacgttggag tttggaggtg cttgccttag 60  
 agcaaggga acagctctca ttcaaaggaa ctagaagcct ctccctcagt ggtagggaga 120  
 cagccaggag cggttttctg ggaactgtgg gatgtgccct tgggggcccg agaaaacaga 180  
 aggaag atg ctc cag acc agt aac tac agc ctg gtg ctc tct ctg cag 228

Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln



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|   |     |
|---|-----|
| ttc ctg ctg ctg tcc tat gac ctc ttt gtc aat tcc ttc tca gaa ctg | 276 |
| Phe Leu Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu |     |
| 15 20 25 30   |     |
| ctc caa aag act cct gtc atc cag ctt gtg ctc ttc atc atc cag gat | 324 |
| Leu Gln Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp |     |
| 35 40 45  |     |
| att gca gtc ctc ttc aac atc atc atc att ttc ctc atg ttc ttc aac | 372 |
| Ile Ala Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn |     |
| 50 55 60  |     |
| acc ttc gtc ttc cag gct ggc ctg gtc aac ctc cta ttc cat aag ttc | 420 |
| Thr Phe Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe |     |
| 65 70 75  |     |
| aaa ggg acc atc atc ctg aca gct gtg tac ttt gcc ctc agc atc tcc | 468 |
| Lys Gly Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser |     |
| 80 85 90  |     |
| ctt cat gtc tgg gtc atg aac tta cgc tgg aaa aac tcc aac agc ttc | 516 |
| Leu His Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe |     |
| 95 100 105 110  |     |
| ata tgg aca gat gga ctt caa atg ctg ttt gta ttc cag aga cta gca | 564 |
| Ile Trp Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala |     |
| 115 120 125   |     |
| gca gtg ttg tac tgc tac ttc tat aaa cgg aca gcc gta aga cta ggc | 612 |
| Ala Val Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly |     |
| 130 135 140   |     |
| gat cct cac ttc tac cag gac tct ttg tgg ctg cgc aag gag ttc atg | 660 |

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Asp Pro His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met

145

150

155

caa gtt cga agg tgacctct tgtcacactg atggatactt ttccttcctg 710

Gln Val Arg Arg

160

atagaagcca catttgctgc ttgacagga gagttggccc tatgcatggg caaacagctg 770

gactttccaa ggaagggtca gactagctgt gttcagcatt caagaaggaa gatcctccct 830

cttgacaaat tagagtgtcc ccacgggtct ccagtgcggc atcccttctt tgcctttctac 890

ctctgttcca ccccttttcc ttccttttct ctctgtacca ttcatcttcc ctgaccggcc 950

tttcttgccg agggttctgt ggctcttacc cttgtgaagc ttttccttta gcctgggaca 1010

gaaggacctc ccagccccca aaggatctcc cagtgcacaa aggatgcgaa gagtgatagt 1070

tacgtgtctc tgactgatca caccgcagac atttagattt ttatacccaa ggcactttaa 1130

aaaaatgttt tataaataga gaataaattg aattcttggt ccat 1174

&lt;210&gt; 150

&lt;211&gt; 1012

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (208)... (873)

&lt;400&gt; 150

gcctcttccc cagggggccgc gtcggagcct ccgcggcggc ggcggtgctt acagcctgag 60

aagagcgtct cgcccgggag cggcggcggc catcgagacc cacccaaggc gcgtccccct 120

cggcctccca gcgtcccaa gccgcagcgg ccgcgccct tcagctagct cgctcgtctg 180

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|   |     |
|---|-----|
| ctctgcttcc ctgctgccgg ctgcgcc atg gcg ttg gcg ttg gcg gcg ctg   | 231 |
| Met Ala Leu Ala Leu Ala Ala Leu                                 |     |
| 1 5   |     |
| gcg gcg gtc gag ccg gcc tgc ggc agc cgg tac cag cag ttg cag aat | 279 |
| Ala Ala Val Glu Pro Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln Asn |     |
| 10 15 20  |     |
| gaa gaa gag tct gga gaa cct gaa cag gct gca ggt gat gct cct cca | 327 |
| Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro Pro |     |
| 25 30 35 40   |     |
| cct tac agc agc att tct gca gag agc gca gca tat ttt gac tac aag | 375 |
| Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr Lys |     |
| 45 50 55  |     |
| gat gag tct ggg ttt cca aag ccc cca tct tac aat gta gct aca aca | 423 |
| Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr Thr |     |
| 60 65 70  |     |
| ctg ccc agt tat gat gaa gcg gag agg acc aag gct gaa gct act atc | 471 |
| Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr Ile |     |
| 75 80 85  |     |
| cct ttg gtt cct ggg aga gat gag gat ttt gtg ggt cgg gat gat ttt | 519 |
| Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp Phe |     |
| 90 95 100   |     |
| gat gat gct gac cag ctg agg ata gga aat gat ggg att ttc atg tta | 567 |
| Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met Leu |     |
| 105 110 115 120   |     |
| act ttt ttc atg gca ttc ctc ttt aac tgg att ggg ttt ttc ctg tct | 615 |

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Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu Ser  
 125 130 135  
 ttt tgc ctg acc act tca gct gca gga agg tat ggg gcc att tca gga 663  
 Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser Gly  
 140 145 150  
 ttt ggt ctc tct cta att aaa tgg atc ctg att gtc agg ttt tcc acc 711  
 Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Thr  
 155 160 165  
 tat ttc cct gga tat ttt gat ggt cag tac tgg ctc tgg tgg gtg ttc 759  
 Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val Phe  
 170 175 180  
 ctt gtt tta ggc ttt ctc ctg ttt ctc aga gga ttt atc aat tat gca 807  
 Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr Ala  
 185 190 195 200  
 aaa gtt cgg aag atg cca gaa act ttc tca aat ctc ccc agg acc aga 855  
 Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr Arg  
 205 210 215  
 gtt ctc ttt att tat taaagatgtt ttctggcaaa ggccttcctg catttatgaa 910  
 Val Leu Phe Ile Tyr  
 220  
 ttctctctca agaagcaaga gaacacctgc aggaagtga tcaagatgca gaacacagag 970  
 gaataatcac ctgctttaaa aaaataaagt actgttgaaa ag 1012